

Resource Summary Report

Generated by T1D on Sep 5, 2026

ConSurf-DB

RRID:SCR_007609

Type: Tool

Proper Citation

ConSurf-DB (RRID:SCR_007609)

Resource Information

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

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Description: Collection of pre-calculated evolutionary conservation profiles for proteins of known structure in the Protein DataBase (PDB).

Synonyms: consurf-db, ConSurf-DataBase, ConSurf-DB, ConSurf- Data Base

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

Keywords: evolution, conservation, protein, structure, pre-calculated, profile

Availability: Free, Acknowledgement requested

Resource Name: ConSurf-DB

Resource ID: SCR_007609

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

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

Record Creation Time: 20220129T080242+0000

Record Last Update: 20260903T234925+0000

Ratings and Alerts

No rating or validation information has been found for ConSurf-DB.

No alerts have been found for ConSurf-DB.

Data and Source Information

Usage and Citation Metrics

We found 17 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

Olajide OM, et al. (2023) Evolutionarily conserved amino acids in MHC-II mediate bat influenza A virus entry into human cells. PLoS biology, 21(7), e3002182.

Luo L, et al. (2022) The Inhibitors of CDK4/6 from a Library of Marine Compound Database: A Pharmacophore, ADMET, Molecular Docking and Molecular Dynamics Study. Marine drugs, 20(5).

Choudhury A, et al. (2021) Structural genomics approach to investigate deleterious impact of nsSNPs in conserved telomere maintenance component 1. Scientific reports, 11(1), 10202.

Sharir-Ivry A, et al. (2021) Quantifying evolutionary importance of protein sites: A Tale of two measures. PLoS genetics, 17(4), e1009476.

Gouridis G, et al. (2021) Structural dynamics in the evolution of a bilobed protein scaffold. Proceedings of the National Academy of Sciences of the United States of America, 118(49).

Shi S, et al. (2021) Theaflavin binds to a druggable pocket of TMEM16A channel and inhibits lung adenocarcinoma cell viability. The Journal of biological chemistry, 297(3), 101016.

Villafana RT, et al. (2020) Signatures of TRI5, TRI8 and TRI11 Protein Sequences of Fusarium incarnatum-equiseti Species Complex (FIESC) Indicate Differential Trichothecene Analogue Production. Toxins, 12(6).

Wako H, et al. (2019) Dynamic properties of oligomers that characterize low-frequency normal modes. Biophysics and physicobiology, 16, 220.

R S, et al. (2018) Purification, characterization, molecular modeling and docking study of fish waste protease. International journal of biological macromolecules, 118(Pt A), 569.

Kim J, et al. (2017) A dynamic hydrophobic core orchestrates allostery in protein kinases. Science advances, 3(4), e1600663.

Panigrahi P, et al. (2015) Engineering Proteins for Thermostability with iRDP Web Server. PloS one, 10(10), e0139486.

Melnikov A, et al. (2014) Comprehensive mutational scanning of a kinase in vivo reveals substrate-dependent fitness landscapes. Nucleic acids research, 42(14), e112.

Chen YC, et al. (2014) Identifying RNA-binding residues based on evolutionary conserved structural and energetic features. Nucleic acids research, 42(3), e15.

Doncheva NT, et al. (2014) Integrative visual analysis of protein sequence mutations. BMC proceedings, 8(Suppl 2 Proceedings of the 3rd Annual Symposium on Biologica), S2.

Gao J, et al. (2012) Comparison of different ranking methods in protein-ligand binding site prediction. International journal of molecular sciences, 13(7), 8752.

Han L, et al. (2012) Identification of catalytic residues using a novel feature that integrates the microenvironment and geometrical location properties of residues. PloS one, 7(7), e41370.

Wainreb G, et al. (2011) Protein stability: a single recorded mutation aids in predicting the effects of other mutations in the same amino acid site. Bioinformatics (Oxford, England), 27(23), 3286.