Resource Summary Report

Generated by <u>dkNET</u> on May 20, 2025

Evolutionary Couplings Server

RRID:SCR_018745 Type: Tool

Proper Citation

Evolutionary Couplings Server (RRID:SCR_018745)

Resource Information

URL: https://evcouplings.org/

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Description: Web server provides functional and structural information about proteins from their evolutionary record using methods from statistical physics. Computes evolutionary couplings from sequence alignments and predicts 3D structure for your protein of interest. Allows to run former EVcouplings, EVmutation, EVfold and EVcomplex jobs.

Synonyms: EVcouplings

Resource Type: data access protocol, service resource, production service resource, analysis service resource, web service, software resource

Defining Citation: PMID:30304492

Keywords: Coevolutionary sequence analysis, evolutionary coupling, protein sequence, RNA sequence alignment, predict protein structure, evolutionary sequence covariantion, 3D protein structure prediction, , bio.tools

Funding: NSF GRFP DGE1144152; DOE CSGF fellowship ; NIGMS R01 GM106303

Availability: Free, Freely available

Resource Name: Evolutionary Couplings Server

Resource ID: SCR_018745

Alternate IDs: biotools:EVcouplings

Alternate URLs: https://github.com/debbiemarkslab/evcouplings, https://bio.tools/EVcouplings

License: MIT License

License URLs: https://github.com/debbiemarkslab/EVcouplings/blob/develop/LICENSE

Record Creation Time: 20220129T080341+0000

Record Last Update: 20250519T204043+0000

Ratings and Alerts

No rating or validation information has been found for Evolutionary Couplings Server.

No alerts have been found for Evolutionary Couplings Server.

Data and Source Information

Source: <u>SciCrunch Registry</u>

Usage and Citation Metrics

We found 21 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>dkNET</u>.

Landwehr GM, et al. (2025) Accelerated enzyme engineering by machine-learning guided cell-free expression. Nature communications, 16(1), 865.

Swapna GVT, et al. (2024) Modeling Alternative Conformational States of Pseudo-Symmetric Solute Carrier Transporters using Methods from Machine Learning. bioRxiv : the preprint server for biology.

Fram B, et al. (2024) Simultaneous enhancement of multiple functional properties using evolution-informed protein design. Nature communications, 15(1), 5141.

Ding K, et al. (2024) Machine learning-guided co-optimization of fitness and diversity facilitates combinatorial library design in enzyme engineering. Nature communications, 15(1), 6392.

Tang X, et al. (2024) Pathogenicity of de novo CACNA1D Ca2+ channel variants predicted from sequence co-variation. European journal of human genetics : EJHG, 32(9), 1065.

van Hooren M, et al. (2024) Ectopic Expression of Distinct PLC Genes Identifies 'Compactness' as a Possible Architectural Shoot Strategy to Cope with Drought Stress. Plant & cell physiology, 65(6), 885.

Johnston KE, et al. (2024) A combinatorially complete epistatic fitness landscape in an enzyme active site. Proceedings of the National Academy of Sciences of the United States of America, 121(32), e2400439121.

Dibley K, et al. (2024) The wheat stripe rust resistance gene YrNAM is Yr10. Nature communications, 15(1), 3291.

Frank HM, et al. (2024) Structural basis of ligand specificity and channel activation in an insect gustatory receptor. Cell reports, 43(4), 114035.

Kohga H, et al. (2022) Crystal structure of the lipid flippase MurJ in a "squeezed" form distinct from its inward- and outward-facing forms. Structure (London, England : 1993), 30(8), 1088.

Li P, et al. (2022) PcoB is a defense outer membrane protein that facilitates cellular uptake of copper. Protein science : a publication of the Protein Society, 31(7), e4364.

Gomes G, et al. (2021) New Findings on LMO7 Transcripts, Proteins and Regulatory Regions in Human and Vertebrate Model Organisms and the Intracellular Distribution in Skeletal Muscle Cells. International journal of molecular sciences, 22(23).

McCallum M, et al. (2021) CryoEM map of Pseudomonas aeruginosa PilQ enables structural characterization of TsaP. Structure (London, England : 1993), 29(5), 457.

Roche R, et al. (2021) Hybridized distance- and contact-based hierarchical structure modeling for folding soluble and membrane proteins. PLoS computational biology, 17(2), e1008753.

Chaudhuri D, et al. (2021) In Silico Study of Mutational Stability of SARS-CoV-2 Proteins. The protein journal, 40(3), 328.

Stiffler MA, et al. (2020) Protein Structure from Experimental Evolution. Cell systems, 10(1), 15.

Chiasson MA, et al. (2020) Multiplexed measurement of variant abundance and activity reveals VKOR topology, active site and human variant impact. eLife, 9.

Mejhert N, et al. (2020) Partitioning of MLX-Family Transcription Factors to Lipid Droplets Regulates Metabolic Gene Expression. Molecular cell, 77(6), 1251.

Olarte MJ, et al. (2020) Determinants of Endoplasmic Reticulum-to-Lipid Droplet Protein Targeting. Developmental cell, 54(4), 471.

Thompson MJ, et al. (2020) The functional role of the ?M4 transmembrane helix in the muscle nicotinic acetylcholine receptor probed through mutagenesis and coevolutionary

analyses. The Journal of biological chemistry, 295(32), 11056.