

Resource Summary Report

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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, software resource, web service, analysis service resource

Defining Citation: [PMID:30304492](#)

Keywords: Coevolutionary sequence analysis, evolutionary coupling, protein sequence, RNA sequence alignment, predict protein structure, evolutionary sequence covariation, 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: 20260801T190618+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: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 24 mentions in open access literature.

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

Swapna GVT, et al. (2025) Memorization bias impacts modeling of alternative conformational states of solute carrier membrane proteins with methods from deep learning. PLoS computational biology, 21(10), e1013590.

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

Simonsen S, et al. (2025) Extreme multivalency and a composite short linear motif facilitate PCNA-binding, localisation and abundance of p21 (CDKN1A). The FEBS journal, 292(16), 4314.

Meng Y, et al. (2025) Protein structure prediction via deep learning: an in-depth review. Frontiers in pharmacology, 16, 1498662.

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

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.

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.

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.

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.

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).

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.

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

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.