Resource Summary Report

Generated by PRECISE-TBI on Sep 7, 2026

FreeContact

RRID:SCR_016113
Type: Tool

Proper Citation

FreeContact (RRID:SCR_016113)

Resource Information

URL: https://rostlab.org/node/960

Proper Citation: FreeContact (RRID:SCR_016113)

Description: Alignment software for large-scale protein contact or protein-protein interaction prediction optimized for speed through shorter runtimes. FreeContact provides the opportunity to compute contact predictions in any environment (desktop or cloud).

Resource Type: alignment software, data processing software, image analysis software, software application, software resource

Defining Citation: PMID:24669753, DOI:10.1186/1471-2105-15-85

Keywords: protein, structure, prediction, sequence, analysis, fast, contact, alignment, multiple

Funding: Alexander von Humboldt Foundation ;
German Ministry for Research and Education (BMBF: Bundesministerium fuer Bildung und Forschung) ;
Research Council of Norway 208481

Availability: Open source, Free, Available for download

Resource Name: FreeContact

Resource ID: SCR_016113

Alternate IDs: OMICS_03520

Alternate URLs: https://rostlab.org/owiki/index.php/FreeContact, https://sources.debian.org/src/libfreecontact-perl/

License: GPLv3

Record Creation Time: 20220129T080328+0000

Record Last Update: 20260905T133007+0000

Ratings and Alerts

No rating or validation information has been found for FreeContact.

No alerts have been found for FreeContact.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 22 mentions in open access literature.

Listed below are recent publications. The full list is available at PRECISE-TBI .

Dong B, et al. (2026) MAKA-Map: Real-Valued Distance Prediction for Protein Folding Mechanisms via a Hybrid Neural Framework Integrating the Mamba and Kolmogorov-Arnold Networks. Biomolecules, 16(2).

Sun J, et al. (2023) TMKit: a Python interface for computational analysis of transmembrane proteins. Briefings in bioinformatics, 24(5).

Rahman J, et al. (2022) Enhancing protein inter-residue real distance prediction by scrutinising deep learning models. Scientific reports, 12(1), 787.

Sun J, et al. (2021) Improved sequence-based prediction of interaction sites in ?-helical transmembrane proteins by deep learning. Computational and structural biotechnology journal, 19, 1512.

Zheng W, et al. (2021) Folding non-homologous proteins by coupling deep-learning contact maps with I-TASSER assembly simulations. Cell reports methods, 1(3).

Mortuza SM, et al. (2021) Improving fragment-based ab initio protein structure assembly using low-accuracy contact-map predictions. Nature communications, 12(1), 5011.

Bhattacharya S, et al. (2020) Evaluating the significance of contact maps in low-homology protein modeling using contact-assisted threading. Scientific reports, 10(1), 2908.

Wu T, et al. (2020) Analysis of several key factors influencing deep learning-based inter-residue contact prediction. Bioinformatics (Oxford, England), 36(4), 1091.

Xiao Y, et al. (2020) Experimental determination and data-driven prediction of homotypic transmembrane domain interfaces. Computational and structural biotechnology journal, 18, 3230.

Téletchéa S, et al. (2019) Repository of Enriched Structures of Proteins Involved in the Red Blood Cell Environment (RESPIRE). PloS one, 14(2), e0211043.

Hou J, et al. (2019) Protein tertiary structure modeling driven by deep learning and contact distance prediction in CASP13. Proteins, 87(12), 1165.

Kandathil SM, et al. (2019) Prediction of interresidue contacts with DeepMetaPSICOV in CASP13. Proteins, 87(12), 1092.

Wang Y, et al. (2019) Fueling ab initio folding with marine metagenomics enables structure and function predictions of new protein families. Genome biology, 20(1), 229.

Adhikari B, et al. (2018) DNCON2: improved protein contact prediction using two-level deep convolutional neural networks. Bioinformatics (Oxford, England), 34(9), 1466.

Thomas JMH, et al. (2017) Approaches to ab initio molecular replacement of ?-helical transmembrane proteins. Acta crystallographica. Section D, Structural biology, 73(Pt 12), 985.

de Oliveira SH, et al. (2017) Comparing co-evolution methods and their application to template-free protein structure prediction. Bioinformatics (Oxford, England), 33(3), 373.

Buchan DWA, et al. (2017) EigenTHREADER: analogous protein fold recognition by efficient contact map threading. Bioinformatics (Oxford, England), 33(17), 2684.

Alcock F, et al. (2016) Assembling the Tat protein translocase. eLife, 5.

Fox G, et al. (2016) Using de novo protein structure predictions to measure the quality of very large multiple sequence alignments. Bioinformatics (Oxford, England), 32(6), 814.

Rawi R, et al. (2016) COUSCOus: improved protein contact prediction using an empirical Bayes covariance estimator. BMC bioinformatics, 17(1), 533.