

Resource Summary Report

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ColabFold

RRID:SCR_025453

Type: Tool

Proper Citation

ColabFold (RRID:SCR_025453)

Resource Information

URL: <https://github.com/sokrypton/ColabFold>

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Description: Software application offers accelerated prediction of protein structures and complexes by combining homology search of MMseqs2 with AlphaFold2 or RoseTTAFold. Used for protein folding.

Resource Type: source code, software resource

Defining Citation: [PMID:35637307](#)

Keywords: prediction of protein structures and complexes, protein folding, protein structure prediction,

Funding: Max Planck Society ;
University of Göttingen ;
National Research Foundation of Korea ;
Seoul National University ;
NIH Office of the Director DP5OD026389;
NIAID R21AI156595;
NSF

Availability: Free, Available for download, Freely available

Resource Name: ColabFold

Resource ID: SCR_025453

Alternate URLs: <https://github.com/sokrypton/ColabFold/blob/main/AlphaFold2.ipynb>

License: MIT license

Record Creation Time: 20240709T053252+0000

Ratings and Alerts

No rating or validation information has been found for ColabFold.

No alerts have been found for ColabFold.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 391 mentions in open access literature.

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

Mitic I, et al. (2026) Assessing the validity of leucine zipper constructs predicted by AlphaFold. Protein science : a publication of the Protein Society, 35(1), e70438.

Maurstad MF, et al. (2026) The green lacewing venom system and the complex mechanisms underlying its evolution. Molecular biology and evolution, 43(1).

Chen W, et al. (2025) Trastuzumab Deruxtecan (T-DXd) Resistance via Loss of HER2 Expression and Binding. Cancer discovery.

Dong R, et al. (2025) Exploring the repository of de novo-designed bifunctional antimicrobial peptides through deep learning. eLife, 13.

Li C, et al. (2025) Mining the UniProtKB/Swiss-Prot database for antimicrobial peptides. Protein science : a publication of the Protein Society, 34(4), e70083.

Mychack A, et al. (2025) Staphylococcus aureus uses a GGDEF protein to recruit diacylglycerol kinase to the membrane for lipid recycling. Proceedings of the National Academy of Sciences of the United States of America, 122(12), e2414696122.

De Koch MD, et al. (2025) Novel lineage of anelloviruses with large genomes identified in dolphins. Journal of virology, 99(1), e0137024.

Kimbrough H, et al. (2025) A tunable affinity fusion tag for protein self-assembly. bioRxiv : the preprint server for biology.

Ramirez AG, et al. (2025) Biochemical and physiological characterization of Aedes aegypti midgut chymotrypsin. Scientific reports, 15(1), 9685.

O'Donoghue AJ, et al. (2025) Comprehensive proteolytic profiling of Aedes aegypti mosquito midgut extracts: Unraveling the blood meal protein digestion system. PLoS neglected tropical diseases, 19(2), e0012555.

Rahmati S, et al. (2025) Computational structure-based design of antiviral peptides as potential protein-protein interaction inhibitors of rabies virus phosphoprotein and human LC8. *Heliyon*, 11(1), e41520.

Bruguera ES, et al. (2025) The co-receptor Tetraspanin12 directly captures Norrin to promote ligand-specific β -catenin signaling. *eLife*, 13.

Warschkau D, et al. (2025) Proteomic identification of a *Toxoplasma gondii* sporozoite-specific antigen using HDAC3 inhibitor-treated tachyzoites as surrogate. *FEMS microbes*, 6, xtae034.

Cesaro S, et al. (2025) A crucial active site network of titratable residues guides catalysis and NAD⁺ binding in human succinic semialdehyde dehydrogenase. *Protein science : a publication of the Protein Society*, 34(1), e70024.

Sahakyan H, et al. (2025) In silico evolution of globular protein folds from random sequences. *Proceedings of the National Academy of Sciences of the United States of America*, 122(27), e2509015122.

Ngo K, et al. (2025) Harnessing AlphaFold to reveal hERG channel conformational state secrets. *eLife*, 13.

Zahnow F, et al. (2025) The evolutionary path of the epithelial sodium channel β -subunit in *Cetartiodactyla* points to a role in sodium sensing. *Communications biology*, 8(1), 1004.

Ali S, et al. (2025) Comparative proteomics of biofilm development in *Pseudoalteromonas tunicata* discovers a distinct family of Ca²⁺-dependent adhesins. *mBio*, 16(6), e0106925.

Lipp NF, et al. (2025) An origin for a eukaryotic lipid transfer protein fold in Asgard archaea. *bioRxiv : the preprint server for biology*.

Riedersberger M, et al. (2025) Effects of open-channel blocking peptides in NaV1.5 β KPQ. *Biophysical journal*, 124(14), 2263.