

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: software resource, source code

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 [RRID](#) .

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.

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

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.

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.

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

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

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

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

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

Jumadila O, et al. (2025) Development of a self-assembling multimeric Bann-RBD fusion protein in *Pichia pastoris* as a potential COVID-19 vaccine candidate. *Scientific reports*, 15(1), 18467.

Ford JJ, et al. (2025) Identification of the lydiamycin biosynthetic gene cluster in a plant pathogen guides structural revision and identification of molecular target. *Proceedings of the National Academy of Sciences of the United States of America*, 122(21), e2424388122.

Matusiak R, et al. (2025) Revisiting phage tail spike architecture: evidence for undetected receptor-binding proteins in Caudoviricetes with non-contractile tails. *Frontiers in microbiology*, 16, 1625765.

Páez-Pérez ED, et al. (2025) Simplified method for purifying full-length major type IV pilins: PilA from *Acidithiobacillus thiooxidans*. *MethodsX*, 15, 103520.

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.

Kloeber JA, et al. (2025) KCTD10 is a sensor for co-directional transcription-replication conflicts. *Nature*, 648(8092), 210.

Lang F, et al. (2025) Highly efficient degradation of polybutylene succinate (PBS) and polycaprolactone (PCL) by a recombinant marine fungal cutinase. *Applied and environmental microbiology*, 91(9), e0083325.