

Resource Summary Report

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AlphaFold

RRID:SCR_025454

Type: Tool

Proper Citation

AlphaFold (RRID:SCR_025454)

Resource Information

URL: <https://github.com/google-deepmind/alphafold>

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Description: Software package provides implementation of inference pipeline of AlphaFold v2. Incorporates physical and biological knowledge about protein structure, leveraging multi-sequence alignments, into design of deep learning algorithm. Used for protein structure prediction.

Synonyms: , AlphaFold v2, AlphaFold2

Resource Type: software toolkit, source code, software resource

Defining Citation: [PMID:34265844](#)

Keywords: inference pipeline, protein structure prediction, protein structure,

Funding: National Research Foundation of Korea ;
Seoul National University

Availability: Free, Available for download, Freely available

Resource Name: AlphaFold

Resource ID: SCR_025454

License: Apache-2.0

Record Creation Time: 20240709T053252+0000

Record Last Update: 20260729T044621+0000

Ratings and Alerts

No rating or validation information has been found for AlphaFold.

No alerts have been found for AlphaFold.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 107 mentions in open access literature.

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

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.

Lupton CJ, et al. (2026) Structure of the lysosomal KICSTOR-GATOR1-SAMTOR nutrient-sensing supercomplex. Cell.

White K, et al. (2025) Lactococcal phage-host profiling through binding studies between cell wall polysaccharide types and Skunavirus receptor-binding proteins. Microbial genomics, 11(4).

Kropp A, et al. (2025) Quinone extraction drives atmospheric carbon monoxide oxidation in bacteria. Nature chemical biology, 21(7), 1058.

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

Kocot AM, et al. (2025) Deep eutectic solvent enhances antibacterial activity of a modular lytic enzyme against *Acinetobacter baumannii*. Scientific reports, 15(1), 2047.

Abugable AA, et al. (2025) ADP-ribosylation of NuMA promotes DNA single-strand break repair and transcription. Cell reports, 44(6), 115737.

Walker MWG, et al. (2025) Relaxed DNA substrate specificity of transposases involved in programmed genome rearrangement. bioRxiv : the preprint server for biology.

Wang S, et al. (2025) Bond-centric modular design of protein assemblies. Nature materials, 24(10), 1644.

Patnaik R, et al. (2025) Curcumin Inhibits Protease Activated Receptor 2-Induced ERK Phosphorylation Calcium Mobilization and Anti-Apoptotic Signaling in Inflammation-Driven Colorectal Cancer Cells. Cells, 14(18).

Chirasani VR, et al. (2025) Structural interactions of ankyrin B with NrCAM and β 2 spectrin. The Journal of biological chemistry, 301(12), 110872.

Migliorini A, et al. (2025) Multiscale Computational Dissection of CCRL2-Mediated Chemerin Presentation. *Journal of chemical information and modeling*, 65(24), 13400.

Köller Z, et al. (2025) To be, or not to be cleaved: Directed evolution of a canonical serine protease inhibitor against active and inactive protease pair identifies binding loop residue critical for prevention of proteolytic cleavage. *Protein science : a publication of the Protein Society*, 34(5), e70146.

Bayam E, et al. (2025) Bi-allelic variants in WDR47 cause a complex neurodevelopmental syndrome. *EMBO molecular medicine*, 17(1), 129.

Zheng Q, et al. (2025) The photoinduced β -carotene synthesis in *Blakeslea trispora* is dependent on WC-2A. *Frontiers in microbiology*, 16, 1554367.

Kim M, et al. (2025) DeepFold-PLM: accelerating protein structure prediction via efficient homology search using protein language models. *Bioinformatics (Oxford, England)*, 41(11).

Hanna MG, et al. (2025) BLTP3A is associated with membranes of the late endocytic pathway and is an effector of CASM. *The EMBO journal*, 44(21), 6168.

Ng JK, et al. (2025) Proteome-wide assessment of differential missense variant clustering in neurodevelopmental disorders and cancer. *Cell genomics*, 5(4), 100807.

Munder F, et al. (2025) High-affinity PQQ import is widespread in Gram-negative bacteria. *Science advances*, 11(22), eadr2753.

Shaw DR, et al. (2025) Independently evolved extracellular electron transfer pathways in ecologically diverse Desulfobacterota. *The ISME journal*, 19(1).