

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, software resource, source code

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: 20260813T055323+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 149 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.

de Lange EMF, et al. (2026) Competition between binding partners of yeast Pex3 affects peroxisome biology. *The FEBS journal*, 293(1), 175.

Esposito-Verza A, et al. (2026) Molecular requirements for PLK1 activation by T-loop phosphorylation. *The EMBO journal*, 45(5), 1496.

Wang D, et al. (2026) PRMT5 is Frequently Upregulated and a Potential Therapeutic Target in MTAP-deficient Malignant Peripheral Nerve Sheath Tumors. *bioRxiv : the preprint server for biology*.

Schnapka V, et al. (2026) Atomic resolution ensembles of intrinsically disordered proteins with AlphaFold. *Nature communications*, 17(1).

Gu C, et al. (2026) CTMP-REV7 axis modulates MHC-I antigen presentation via CDK1-AKT crosstalk in MSI-L/MSS colorectal cancer. *Cellular oncology (Dordrecht, Netherlands)*, 49(3).

Hourigan D, et al. (2026) The Hungate1000 prokaryotic culture collection encodes a wide variety of bacteriocins. *mSystems*, 11(6), e0019526.

Feddersen H, et al. (2026) Membrane binding controls the ATPase cycle and localization of MinD in *Bacillus subtilis*. *eLife*, 13.

Abbas DK, et al. (2026) Evolutionarily conserved spliceosome-exosome pathway in nuclear mRNA surveillance. *Genes & development*, 40(13-14), 1119.

Zhao W, et al. (2026) A fungi-derived cyclic peptide enhances Th9-mediated antitumor immunity by targeting ZAP70 and SREBP1. *The Journal of clinical investigation*, 136(3).

Feng Q, et al. (2026) Hexosamine biosynthesis drives hemocyanin O-GlcNAcylation to potentiate antibacterial immunity in shrimp. *The Journal of biological chemistry*, 302(7), 113213.

Lin H, et al. (2026) A Comparative Review of Artificial Intelligence Applications in Small Molecule Versus Peptide Drug Discovery. *International journal of molecular sciences*, 27(7).

Lim SK, et al. (2026) Targeted computational design of an interleukin-7 superkine with enhanced folding efficiency and immunotherapeutic efficacy. *eLife*, 14.

Zhu Y, et al. (2026) BolAG-BolRPI2-BolBAM4 Module Regulates the Bolting of Curd by Modulating Starch Metabolism in Broccoli (*Brassica oleracea* var. *italica*). *Plant biotechnology journal*, 24(3), 1465.

Huang Y, et al. (2026) SR-B1-Mediated Transplacental Transfer of Hydrophobic Toxicants Disrupts Fetal Development During Barrierogenesis. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(23), e15742.

Tao Y, et al. (2026) TENT5A Maintains MYC mRNA Stability to Enhance Osteosarcoma Stemness. *Cancer research*, 86(9), 2161.

Scholl D, et al. (2026) The filamentous ultrastructure of the PopZ condensate is required for its cellular function. *Nature structural & molecular biology*, 33(3), 420.

Narayanasamy A, et al. (2026) Ion Mobility Mass Spectrometry Guided Modeling with AlphaFold and Rosetta Improves Protein Complex Structure Prediction. *bioRxiv : the preprint server for biology*.

Lu J, et al. (2026) Benchmarking TCR-pMHC structure prediction: a unified evaluation and CDR3-based functional insights. *Briefings in bioinformatics*, 27(3).

Jmii S, et al. (2026) Structure-guided optimization of SLY1 expression and purification in *Escherichia coli*. *Protein science : a publication of the Protein Society*, 35(5), e70592.