

Resource Summary Report

Generated by [NIF](#) on Aug 16, 2026

[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: 20260815T183212+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 [NIF](#) .

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.