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: source code, software toolkit, 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: 20250423T061359+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 42 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Patel DT, et al. (2025) Global atlas of predicted functional domains in Legionella pneumophila Dot/Icm translocated effectors. Molecular systems biology, 21(1), 59.

Bruguera ES, et al. (2025) The co-receptor Tetraspanin12 directly captures Norrin to promote ligand-specific ?-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.

Bogdanow B, et al. (2025) Redesigning error control in cross-linking mass spectrometry enables more robust and sensitive protein-protein interaction studies. Molecular systems biology, 21(1), 90.

Bal?kç? E, et al. (2025) Structure of the Nipah virus polymerase complex. The EMBO journal, 44(2), 563.

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

Chothe SK, et al. (2025) Marked neurotropism and potential adaptation of H5N1 clade 2.3.4.4.b virus in naturally infected domestic cats. Emerging microbes & infections, 14(1), 2440498.

Ding Y, et al. (2025) The ortholog of human DNAJC9 promotes histone H3-H4 degradation and is counteracted by Asf1 in fission yeast. Nucleic acids research, 53(3).

Zhegalova IV, et al. (2025) Convergent pairs of highly transcribed genes restrict chromatin looping in Dictyostelium discoideum. Nucleic acids research, 53(2).

Jang SJ, et al. (2024) Genome-Wide Transcriptional Roles of KSHV Viral Interferon Regulatory Factors in Oral Epithelial Cells. Viruses, 16(6).

Duller S, et al. (2024) Targeted isolation of Methanobrevibacter strains from fecal samples expands the cultivated human archaeome. Nature communications, 15(1), 7593.

Dreckmann TM, et al. (2024) Biosynthesis of the corallorazines, a widespread class of antibiotic cyclic lipodipeptides. RSC chemical biology, 5(10), 970.

Pérez-Chávez I, et al. (2024) Tracking fructose 1,6-bisphosphate dynamics in liver cancer cells using a fluorescent biosensor. iScience, 27(12), 111336.

Camacho J, et al. (2024) Sugar assimilation underlying dietary evolution of Neotropical bats. Nature ecology & evolution, 8(9), 1735.

Denieva ZG, et al. (2024) Human Immunodeficiency Virus Type 1 Gag Polyprotein Modulates Membrane Physical Properties like a Surfactant: Potential Implications for Virus Assembly. ACS infectious diseases, 10(8), 2870.

Datler J, et al. (2024) Multi-modal cryo-EM reveals trimers of protein A10 to form the palisade layer in poxvirus cores. Nature structural & molecular biology, 31(7), 1114.

Maire J, et al. (2024) Chlamydiae as symbionts of photosynthetic dinoflagellates. The ISME journal, 18(1).

Wu D, et al. (2024) Structural characterization and AlphaFold modeling of human T cell receptor recognition of NRAS cancer neoantigens. bioRxiv : the preprint server for biology.

Garrido-Rodríguez P, et al. (2024) Analysis of AlphaFold and molecular dynamics structure predictions of mutations in serpins. PloS one, 19(7), e0304451.

Seong K, et al. (2024) Engineering the plant intracellular immune receptor Sr50 to restore recognition of the AvrSr50 escape mutant. bioRxiv : the preprint server for biology.