

Resource Summary Report

Generated by [RRID](#) on Aug 15, 2026

[AlphaFold3](#)

RRID:SCR_028034

Type: Tool

Proper Citation

AlphaFold3 (RRID:SCR_028034)

Resource Information

URL: <https://github.com/google-deepmind/alphafold3>

Proper Citation: AlphaFold3 (RRID:SCR_028034)

Description: Software package provides implementation of the inference pipeline of AlphaFold 3.

Resource Type: software toolkit, source code, software resource

Keywords: inference pipeline, AlphaFold 3,

Availability: Free, Available for download, Freely available

Resource Name: AlphaFold3

Resource ID: SCR_028034

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Record Creation Time: 20260228T070219+0000

Record Last Update: 20260815T183307+0000

Ratings and Alerts

No rating or validation information has been found for AlphaFold3.

No alerts have been found for AlphaFold3.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 30 mentions in open access literature.

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

Rinaldi AJ, et al. (2026) Molecular and Structural Characterization of Foam Proteins from *Mahanarva spectabilis* (Distant, 1909) (Hemiptera: Cercopidae) Nymphs Reveals Adaptive Features and Potential Targets for Pest Control. Archives of insect biochemistry and physiology, 121(2), e70130.

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).

Howard JB, et al. (2026) Improving Protein Structure Prediction Using Integrative Cryo-EM and Ion Mobility Mass Spectrometry Modeling. bioRxiv : the preprint server for biology.

Ghoreyshi ZS, et al. (2026) A biophysical framework for accurately identifying antigen single-amino acid escape variants and corresponding variant-specific compensatory TCR sequences. bioRxiv : the preprint server for biology.

Bifsa F, et al. (2026) Predictive modelling of the COMATOSE transporter reveals a conserved ligand binding pocket for acyl-CoAs. Scientific reports, 16(1).

Yang LY, et al. (2026) The LiPP Benchmark Set for Modeling Lipid-Protein Complexes: Comparison of Co-Folding and Docking Methods. Journal of chemical information and modeling, 66(12), 7231.

Kahlous NA, et al. (2026) Molecular mechanisms of native ligand selectivity in catecholamine G protein-coupled receptors. Nature communications, 17(1).

Sang Z, et al. (2026) Repertoire-scale antibody structural prediction informs therapeutic design. Science advances, 12(17), eaef7163.

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

Gladysheva AV, et al. (2026) Solution Structure of Nucleoprotein Domain 1 from the Emerging Yezo Virus. International journal of molecular sciences, 27(12).

Berman P, et al. (2026) Complete biosynthesis of psychedelic tryptamines from three kingdoms in plants. Science advances, 12(14), eaeb3034.

Kuhlmann K, et al. (2026) Crucial Gram-positive type IV secretion system protein TraF is a structural homolog of type VII secretion system protein EssB/YuC. microLife, 7, uqag009.

Shi WO, et al. (2026) A lipid-binding protein in black-legged tick saliva selectively recognizes *Borrelia burgdorferi* lipids. bioRxiv : the preprint server for biology.

Ramongolalaina C, et al. (2026) Optimized optogenetic anti-CRISPR for endogenous gene regulation in *Drosophila*. Nucleic acids research, 54(9).

Dospinescu VM, et al. (2026) CO₂-dependent opening of connexin 43 hemichannels. *eLife*, 14.

Hall S, et al. (2026) Purified zymogens reveal mechanisms of snake venom metalloproteinase auto-activation. *eLife*, 15.

Francette AM, et al. (2026) Evolutionary analysis of transcription elongation factors reveals conserved and lineage-specific regulatory domains. *PLoS biology*, 24(6), e3003855.

Mirgaux M, et al. (2026) AI-guided competitive docking for virtual screening and compound efficacy prediction. *npj drug discovery*, 3(1).

Sone K, et al. (2026) Crystal structure of plant γ -glutamyl peptidase 1: implications for sulfur metabolism and secondary metabolite biosynthesis. *The FEBS journal*, 293(5), 1400.

Walstein K, et al. (2026) M18BP1 valency and a distributed interaction footprint determine epigenetic centromere specification in humans. *The EMBO journal*, 45(5), 1537.