



AlphaFold

AI-powered protein structure prediction system that accurately predicts 3D protein structures from amino acid sequences

<https://alphafold.ebi.ac.uk/>

Overview

AlphaFold is a revolutionary artificial intelligence system developed by Google DeepMind in partnership with EMBL-EBI that predicts a protein's 3D structure from its amino acid sequence with accuracy competitive with experimental methods. The AlphaFold Database provides free access to over 200 million structure predictions covering a significant portion of known proteins across 48+ species. This breakthrough technology has transformed structural biology by making protein structure prediction accessible to researchers worldwide, accelerating drug discovery, disease research, and fundamental biological understanding. The system uses deep learning trained on existing protein structures to generate highly accurate predictions, complete with confidence metrics for each residue.

Key Features

- Predicts 3D protein structures from amino acid sequences with experimental-level accuracy
- Access to 200+ million pre-computed structure predictions via AlphaFold Database
- AlphaMissense integration for proteome-wide missense variant effect prediction
- Multimer prediction capabilities through open-source code
- Downloadable multiple sequence alignments (MSAs) for each prediction
- Confidence metrics (pLDDT scores) for prediction quality assessment
- RESTful API for programmatic access to structure predictions
- Regular database updates synchronized with UniProt releases

Pricing

Model: Free

Completely free for both academic and commercial use. All data available under CC-BY-4.0 license. Open-source code available on GitHub under Apache 2.0 license.

Target Company Size: Academic Institutions, Research Labs, Pharmaceutical Companies, Biotechnology Startups, Enterprise Biotech, Government Research Agencies

Integrations

UniProt, Protein Data Bank (PDB), EMBL-EBI Services, GitHub, Python scientific stack (JAX, NumPy), Docker/Singularity containers, NVIDIA GPU infrastructure

Compliance & Certifications

Open Source Initiative Approved License (Apache 2.0), Creative Commons BY 4.0 for data

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