

Resource Summary Report

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

Foldseek

RRID:SCR_027018

Type: Tool

Proper Citation

Foldseek (RRID:SCR_027018)

Resource Information

URL: <https://github.com/steineggerlab/foldseek>

Proper Citation: Foldseek (RRID:SCR_027018)

Description: Software tool for fast and sensitive comparisons of large structure sets. Used for comparisons of large protein structure sets, supporting monomer and multimer searches, as well as clustering. It runs on CPU, supports GPU acceleration for faster searches, and optionally allows ultra-fast and sensitive comparisons directly from protein sequence inputs using a language model, bypassing the need for structures.

Resource Type: source code, software application, software resource

Keywords: comparisons of large structure sets, protein structure sets, monomer and multimer searches, clustering

Availability: Free, Available for download, Freely available

Resource Name: Foldseek

Resource ID: SCR_027018

License: GNU GPL v3

Record Creation Time: 20250604T055933+0000

Record Last Update: 20260815T183254+0000

Ratings and Alerts

No rating or validation information has been found for Foldseek.

No alerts have been found for Foldseek.

Data and Source Information

Usage and Citation Metrics

We found 15 mentions in open access literature.

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

Qiu K, et al. (2026) pLM-Repeat: Exploiting the sequence representations of protein language models for sensitive repeat detection. Protein science : a publication of the Protein Society, 35(5), e70541.

Dall'Armellina F, et al. (2026) AlphaFold-driven discovery of oxysterol-binding protein-related protein-phosphoinositide 3-, 4-, and 5-phosphatase interactions using new generation confidence scores. Protein science : a publication of the Protein Society, 35(5), e70572.

Qi X, et al. (2026) Atlas of predicted protein complex structures across kingdoms. Nature communications, 17(1).

Stephens TG, et al. (2026) Cosmopolitan Gene Families With Known Functions Are Hotspots for the Evolution of Novel Genes in Stony Corals. Genome biology and evolution, 18(4).

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

Black JJ, et al. (2026) The Legionella pneumophila effector SidL is an adenylyltransferase that modifies the glycolytic intermediate 3-phosphoglycerate. Molecular cell.

Schraivesande WEW, et al. (2025) Lettuce Big-Vein Associated Virus ORF3 Encodes a Functional 30K Movement Protein. Molecular plant pathology, 26(9), e70153.

Hu H, et al. (2025) Discovery of novel non-retroviral endogenous viral elements reveals their long-term integration history in spiders. Nature communications, 16(1), 6006.

Garg SG, et al. (2025) A General Substitution Matrix for Structural Phylogenetics. Molecular biology and evolution, 42(6).

Wu B, et al. (2025) Harnessing protein language model for structure-based discovery of highly efficient and robust PET hydrolases. Nature communications, 16(1), 6211.

Rose K, et al. (2025) In situ cryo-ET visualization of mitochondrial depolarization and mitophagic engulfment. Proceedings of the National Academy of Sciences of the United States of America, 122(31), e2511890122.

Xu H, et al. (2025) Pdgf mediates a transient regeneration-activated cell state in planarian tissue regeneration. Proceedings of the National Academy of Sciences of the United States of America, 122(36), e2501874122.

Chen L, et al. (2025) A prevalent huge phage clade in human and animal gut microbiomes. *bioRxiv : the preprint server for biology*.

Guo X, et al. (2025) Pangenome-scale annotation of mycobacteriophages for dissecting phage-host interactions based on a sequence clustering and structural homology analysis strategy. *mSystems*, 10(8), e0050825.

Jiang J, et al. (2025) Functional consequences of reductive protein evolution in a minimal eukaryotic genome. *Cell reports*, 44(10), 116333.