Resource Summary Report

Generated by NIF on May 19, 2025

FRAGFOLD

RRID:SCR_014561
Type: Tool

Proper Citation

FRAGFOLD (RRID:SCR_014561)

Resource Information

URL: http://bioinf.cs.ucl.ac.uk/introduction/

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Description: A structural folding computational tool. The method is based on the assembly of supersecondary structural fragments taken from highly resolved protein structures using a simulated annealing algorithm.

Synonyms: GPUFRAGFOLD, GPGPUFRAGFOLD

Resource Type: software application, software resource, data analysis software, data processing software

Keywords: protein folding, structural folding, computational tool, cuda

Funding:

Availability: Available for download, Free for academic use, Commercial users should consult EBISU for advice on licensing prior to downloading

Resource Name: FRAGFOLD

Resource ID: SCR_014561

Alternate URLs: http://bioinfadmin.cs.ucl.ac.uk/downloads/gpufragfold/

Record Creation Time: 20220129T080321+0000

Record Last Update: 20250517T060137+0000

Ratings and Alerts

No rating or validation information has been found for FRAGFOLD.

No alerts have been found for FRAGFOLD.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 11 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Sitinjak MC, et al. (2024) Antiviral effect of the viroporin inhibitors against Taiwan isolates of infectious bronchitis virus (IBV). Virus research, 349, 199458.

Savinov A, et al. (2023) High-throughput computational discovery of inhibitory protein fragments with AlphaFold. bioRxiv : the preprint server for biology.

Liu Z, et al. (2021) A viroporin-like 2B protein of duck hepatitis A virus 1 that induces incomplete autophagy in DEF cells. Poultry science, 100(10), 101331.

Cheong DE, et al. (2021) A designed fusion tag for soluble expression and selective separation of extracellular domains of fibroblast growth factor receptors. Scientific reports, 11(1), 21453.

Roche R, et al. (2021) Hybridized distance- and contact-based hierarchical structure modeling for folding soluble and membrane proteins. PLoS computational biology, 17(2), e1008753.

Shi F, et al. (2020) Identification of 22 Novel Motifs of the Cell Entry Fusion Glycoprotein B of Oncolytic Herpes Simplex Viruses: Sequence Analysis and Literature Review. Frontiers in oncology, 10, 1386.

Strtak AC, et al. (2019) Recovirus NS1-2 Has Viroporin Activity That Induces Aberrant Cellular Calcium Signaling To Facilitate Virus Replication. mSphere, 4(5).

Wi?ch A, et al. (2019) The intrinsically disordered C-terminal F domain of the ecdysteroid receptor from Aedes aegypti exhibits metal ion-binding ability. The Journal of steroid biochemistry and molecular biology, 186, 42.

Tu Y, et al. (2019) Mutant hFGF23(A12D) stimulates osteoblast differentiation through FGFR3. Journal of cellular and molecular medicine, 23(4), 2933.

Cui X, et al. (2018) Heterologous expression of an agarase gene in Bacillus subtilis, and characterization of the agarase. International journal of biological macromolecules, 120(Pt A), 657.

Tan CW, et al. (2008) Using neural networks and evolutionary information in decoy discrimination for protein tertiary structure prediction. BMC bioinformatics, 9, 94.