Resource Summary Report

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Foldit

RRID:SCR_003788
Type: Tool

Proper Citation

Foldit (RRID:SCR_003788)

Resource Information

URL: http://fold.it/

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Description: Foldit is a revolutionary new multiplayer online computer game that engages non-scientists in solving hard prediction problems, enabling you to contribute to important scientific research. Foldit players interact with protein structures using direct manipulation tools and user-friendly versions of algorithms from the Rosetta structure prediction methodology, while they compete and collaborate to optimize the computed energy. Here are the basic principles to keep in mind when folding proteins. Your score on each protein is based on how well you do with these three things: # Pack the protein: The smaller the protein, the better. More precisely, you want to avoid empty spaces (voids) in the structure of the protein where water molecules can get inside. So you want the atoms in the protein to be as close together as possible. Certain structures, such as sheets, will even connect together with hydrogen bonds if you line them up right and get them close together. This is also good. Key word: Compact. # Hide the hydrophobics: Hydrophobics are the sidechains that don't want to be touching water, just like oil or wax. Since most proteins float around in water, you want to keep the hydrophobics (orange sidechains) surrounded by as many atoms as possible so the water won't get to them. The other side of this rule is that hydrophilics (blue sidechains) do want to be touching water, so they should be exposed as much as possible. Key word: Buried. # Clear the clashes: Two atoms can't occupy the same space at the same time. If you've folded a protein so two sidechains are too close together, your score will go down a lot. This is represented by a red spiky ball (clash) where the two sidechains are intersecting. If there are clashes, you know something is wrong with your protein. So make sure everything is far enough apart. Key word: Apart. The current series of Science Puzzles, the Grand Challenges, are meant to generate the evidence needed to prove that human protein folders can be more effective than computers at certain aspects of protein structure prediction. That's what all the puzzles in Foldit are about right now: predicting the structure of a protein based on its amino acid sequence. The three rules mentioned above describe the characteristics of correct protein structures.

Abbreviations: Foldit

Synonyms: Fold It, Foldit: Solve Puzzles for Science

Resource Type: portal, software resource, community building portal, data or information resource

Defining Citation: PMID:20686574

Keywords: crowd-source

Funding: Howard Hughes Medical Institute ;
Microsoft ;
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Resource Name: Foldit

Resource ID: SCR_003788

Alternate IDs: nlx_143530

Record Creation Time: 20220129T080220+0000

Record Last Update: 20250418T055029+0000

Ratings and Alerts

No rating or validation information has been found for Foldit.

No alerts have been found for Foldit.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 26 mentions in open access literature.

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

Sahtoe DD, et al. (2024) Design of amyloidogenic peptide traps. Nature chemical biology,

20(8), 981.

Kojima M, et al. (2024) High-throughput structure determination of an intrinsically disordered protein using cell-free protein crystallization. Proceedings of the National Academy of Sciences of the United States of America, 121(25), e2322452121.

Strasser BJ, et al. (2023) Quantifying online citizen science: Dynamics and demographics of public participation in science. PloS one, 18(11), e0293289.

Miller JA, et al. (2023) Practical recommendations from a multi-perspective needs and challenges assessment of citizen science games. PloS one, 18(5), e0285367.

Nawarathnage S, et al. (2022) Crystals of TELSAM-target protein fusions that exhibit minimal crystal contacts and lack direct inter-TELSAM contacts. Open biology, 12(3), 210271.

Muth LT, et al. (2021) A toolbox for digitally enhanced teaching in synthetic biology. FEMS microbiology letters, 368(17).

Klatt O, et al. (2021) Endogenous ?-neurexins on axons and within synapses show regulated dynamic behavior. Cell reports, 35(11), 109266.

Alsulami AF, et al. (2021) SARS-CoV-2 3D database: understanding the coronavirus proteome and evaluating possible drug targets. Briefings in bioinformatics, 22(2), 769.

Stollar EJ, et al. (2020) Uncovering protein structure. Essays in biochemistry, 64(4), 649.

Hameduh T, et al. (2020) Homology modeling in the time of collective and artificial intelligence. Computational and structural biotechnology journal, 18, 3494.

Zhang J, et al. (2020) Identifying mutation hotspots reveals pathogenetic mechanisms of KCNQ2 epileptic encephalopathy. Scientific reports, 10(1), 4756.

Koepnick B, et al. (2019) De novo protein design by citizen scientists. Nature, 570(7761), 390.

Griner SL, et al. (2019) Structure-based inhibitors of amyloid beta core suggest a common interface with tau. eLife, 8.

Khatib F, et al. (2019) Building de novo cryo-electron microscopy structures collaboratively with citizen scientists. PLoS biology, 17(11), e3000472.

Zhou N, et al. (2018) Crowdsourcing image analysis for plant phenomics to generate ground truth data for machine learning. PLoS computational biology, 14(7), e1006337.

Ellwood ER, et al. (2018) Worldwide Engagement for Digitizing Biocollections (WeDigBio): The Biocollections Community's Citizen-Science Space on the Calendar. Bioscience, 68(2), 112.

Krotee P, et al. (2017) Atomic structures of fibrillar segments of hIAPP suggest tightly mated

?-sheets are important for cytotoxicity. eLife, 6.

Roskams J, et al. (2016) Power to the People: Addressing Big Data Challenges in Neuroscience by Creating a New Cadre of Citizen Neuroscientists. Neuron, 92(3), 658.

Hirschman L, et al. (2016) Crowdsourcing and curation: perspectives from biology and natural language processing. Database : the journal of biological databases and curation, 2016.

Curtis V, et al. (2014) Online citizen science games: Opportunities for the biological sciences. Applied & translational genomics, 3(4), 90.