Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Mar 31, 2025

QUARK

RRID:SCR_018777
Type: Tool

Proper Citation

QUARK (RRID:SCR_018777)

Resource Information

URL: https://zhanglab.ccmb.med.umich.edu/QUARK/

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Description: Computer algorithm for ab initio protein structure prediction and protein peptide folding, which aims to construct correct protein 3D model from amino acid sequence only. Server is suitable for proteins that do not have homologous templates in PDB library.

Resource Type: data access protocol, web service, service resource, software resource

Keywords: Ab initio protein structure, protein structure, protein structure prediction, protein peptide folding, construct protein 3D model, amino acid sequence, Monte Carlo simulation, free modeling,

Funding:

Availability: Restricted

Resource Name: QUARK

Resource ID: SCR_018777

Record Creation Time: 20220129T080341+0000

Record Last Update: 20250330T061804+0000

Ratings and Alerts

No rating or validation information has been found for QUARK.

No alerts have been found for QUARK.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 22 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Dogaru CB, et al. (2023) "Alphabet" Selenoproteins: Their Characteristics and Physiological Roles. International journal of molecular sciences, 24(21).

Bartas M, et al. (2022) Unheeded SARS-CoV-2 proteins? A deep look into negative-sense RNA. Briefings in bioinformatics, 23(3).

Westman J, et al. (2022) Calcium-dependent ESCRT recruitment and lysosome exocytosis maintain epithelial integrity during Candida albicans invasion. Cell reports, 38(1), 110187.

Philip J, et al. (2022) Cdc6 is sequentially regulated by PP2A-Cdc55, Cdc14, and Sic1 for origin licensing in S. cerevisiae. eLife, 11.

Xu X, et al. (2022) Rare hypomagnesemia, seizures, and mental retardation in a 4-month-old patient caused by novel CNNM2 mutation Tyr189Cys: Genetic analysis and review. Molecular genetics & genomic medicine, 10(4), e1898.

Fouillen A, et al. (2021) A proline rich protein from the gingival seal around teeth exhibits antimicrobial properties against Porphyromonas gingivalis. Scientific reports, 11(1), 2353.

Lange A, et al. (2021) Structural and functional characterization of a putative de novo gene in Drosophila. Nature communications, 12(1), 1667.

Ali NF, et al. (2021) In silico evaluation of molecular virus-virus interactions taking place between Cotton leaf curl Kokhran virus- Burewala strain and Tomato leaf curl New Delhi virus. PeerJ, 9, e12018.

Barazesh M, et al. (2021) Design and characterization of a recombinant immunotoxin for targeted therapy of breast cancer cells: In vitro and in silico analyses. Life sciences, 265, 118866.

Xiao S, et al. (2021) Fisetin inhibits tau aggregation by interacting with the protein and preventing the formation of ?-strands. International journal of biological macromolecules, 178, 381.

Strokach A, et al. (2021) Computational generation of proteins with predetermined three-dimensional shapes using ProteinSolver. STAR protocols, 2(2), 100505.

Gong Y, et al. (2021) Identification and functional characterization of AP-2 complex subunit mu-A as a new member of antimicrobial protein. Developmental and comparative immunology, 121, 104099.

Kim SI, et al. (2021) Overexpression of Rice OsS1Fa1 Gene Confers Drought Tolerance in Arabidopsis. Plants (Basel, Switzerland), 10(10).

De Smet J, et al. (2021) The bacteriophage LUZ24 "Igy" peptide inhibits the Pseudomonas DNA gyrase. Cell reports, 36(8), 109567.

González García M, et al. (2020) New Antibacterial Peptides from the Freshwater Mollusk Pomacea poeyana (Pilsbry, 1927). Biomolecules, 10(11).

Mobini S, et al. (2020) Computational Design of a Novel VLP-Based Vaccine for Hepatitis B Virus. Frontiers in immunology, 11, 2074.

Miao X, et al. (2020) Enhanced cell selectivity of hybrid peptides with potential antimicrobial activity and immunomodulatory effect. Biochimica et biophysica acta. General subjects, 1864(4), 129532.

Strokach A, et al. (2020) Fast and Flexible Protein Design Using Deep Graph Neural Networks. Cell systems, 11(4), 402.

Vermot A, et al. (2020) Interdomain Flexibility within NADPH Oxidase Suggested by SANS Using LMNG Stealth Carrier. Biophysical journal, 119(3), 605.

Hernández-Segura T, et al. (2020) Identification of an ?-MoRF in the Intrinsically Disordered Region of the Escargot Transcription Factor. ACS omega, 5(29), 18331.