Resource Summary Report

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Robetta

RRID:SCR_018805
Type: Tool

Proper Citation

Robetta (RRID:SCR_018805)

Resource Information

URL: https://robetta.bakerlab.org/

Proper Citation: Robetta (RRID:SCR_018805)

Description: Web tool as protein structure prediction service. Provides automated structure prediction and analysis tools that can be used to infer protein structural information from genomic data. Produces model for entire protein sequence in presence or absence of sequence homology to protein of known structure.

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

Defining Citation: PMID:15215442

Keywords: Protein structure prediction, protein, structure prediction, prediction service, automated prediction, analysis tools, genomic data, protein sequence, protein model, bio.tools

Funding:

Availability: Restricted

Resource Name: Robetta

Resource ID: SCR_018805

Alternate IDs: biotools:robetta

Alternate URLs: https://bio.tools/robetta

Record Creation Time: 20220129T080342+0000

Record Last Update: 20250412T060240+0000

Ratings and Alerts

No rating or validation information has been found for Robetta.

No alerts have been found for Robetta.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 275 mentions in open access literature.

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

Chimienti R, et al. (2025) A WFS1 variant disrupting acceptor splice site uncovers the impact of alternative splicing on beta cell apoptosis in a patient with Wolfram syndrome. Diabetologia, 68(1), 128.

Knutson BA, et al. (2025) Evolutionary and Structural Insights into the RNA Polymerase I A34 Protein Family: A Focus on Intrinsic Disorder and Phase Separation. Genes, 16(1).

Ma L, et al. (2025) The Chlamydia pneumoniae inclusion membrane protein Cpn0308 interacts with host protein ACBD3. Journal of bacteriology, 207(1), e0027524.

Basmenj ER, et al. (2025) Computational epitope-based vaccine design with bioinformatics approach; a review. Heliyon, 11(1), e41714.

Ma S, et al. (2025) Development of a novel multi-epitope subunit mRNA vaccine candidate to combat Acinetobacter baumannii. Scientific reports, 15(1), 1410.

Zafar S, et al. (2025) Molecular dynamics simulation based prediction of T-cell epitopes for the production of effector molecules for liver cancer immunotherapy. PloS one, 20(1), e0309049.

Nahian M, et al. (2025) Development of a broad-spectrum epitope-based vaccine against Streptococcus pneumoniae. PloS one, 20(1), e0317216.

Guilvout I, et al. (2024) Membrane platform protein PulF of the Klebsiella type II secretion system forms a trimeric ion channel essential for endopilus assembly and protein secretion. mBio, 15(1), e0142323.

Sarvmeili J, et al. (2024) Immunoinformatics design of a structural proteins driven multi-epitope candidate vaccine against different SARS-CoV-2 variants based on fynomer. Scientific reports, 14(1), 10297.

Zhang JT, et al. (2024) Structural basis for phage-mediated activation and repression of bacterial DSR2 anti-phage defense system. Nature communications, 15(1), 2797.

Shi J, et al. (2024) In silico designed novel multi-epitope mRNA vaccines against Brucella by targeting extracellular protein BtuB and LptD. Scientific reports, 14(1), 7278.

Fronk AD, et al. (2024) Development and validation of AI/ML derived splice-switching oligonucleotides. Molecular systems biology, 20(6), 676.

Nath M, et al. (2024) Identification of potential inhibitor against Leishmania donovani mitochondrial DNA primase through in-silico and in vitro drug repurposing approaches. Scientific reports, 14(1), 3246.

Ali L, et al. (2024) In silico design of multi-epitope vaccines against the hantaviruses by integrated structural vaccinology and molecular modeling approaches. PloS one, 19(7), e0305417.

Li X, et al. (2024) Discovery, characterization and mechanism of a Microbacterium esterase for key d-biotin chiral intermediate synthesis. Bioresources and bioprocessing, 11(1), 59.

Farajzadeh-Dehkordi M, et al. (2024) Unraveling the function and structure impact of deleterious missense SNPs in the human OX1R receptor by computational analysis. Scientific reports, 14(1), 833.

Onele AO, et al. (2024) Role of Squalene Epoxidase Gene (SQE1) in the Response of the Lichen Lobaria pulmonaria to Temperature Stress. Journal of fungi (Basel, Switzerland), 10(10).

Cossio-Bayugar R, et al. (2024) Relationship between acaricide resistance and acetylcholinesterase gene polymorphisms in the cattle tick Rhipicephalus microplus. Parasite (Paris, France), 31, 3.

Wang J, et al. (2024) Mechanism of Mutation-Induced Effects on the Catalytic Function of TEV Protease: A Molecular Dynamics Study. Molecules (Basel, Switzerland), 29(5).

Das BK, et al. (2024) Molecular insights into STAT1a protein in rohu (Labeo rohita): unveiling expression profiles, SRC homology domain recognition, and protein-protein interactions triggered by poly I: C. Frontiers in immunology, 15, 1398955.