

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

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

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: 20260728T043550+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 330 mentions in open access literature.

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

Parnandi VA, et al. (2026) A small *Candida glabrata* protein promotes hyphal growth in *C. albicans* during mixed-species invasive candidiasis. *Current biology* : CB, 36(1), 1.

Khan A, et al. (2026) HMPV-TherResDB: Comprehensive human metapneumovirus (HMPV) database for sequence-structure annotations, vaccine resources, and therapeutics research. *Virus research*, 363, 199665.

Nobari MB, et al. (2025) The Lpp-OmpA-BtaE fusion protein causes a protective immune response against *Brucella melitensis* in mice. *Scientific reports*, 15(1), 27210.

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.

Zhou C, et al. (2025) tRNA selectivity during ribosome-associated quality control regulates the critical sterility-inducing temperature in two-line hybrid rice. *Proceedings of the National Academy of Sciences of the United States of America*, 122(6), e2417526122.

Nahian M, et al. (2025) Immunoinformatic strategy for developing multi-epitope subunit vaccine against *Helicobacter pylori*. *PloS one*, 20(2), e0318750.

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).

Zheng Y, et al. (2025) Functional evolution of thyrotropin-releasing hormone neuropeptides: Insights from an echinoderm. *Zoological research*, 46(1), 236.

Becker JT, et al. (2025) Mammalian antiviral proteins ZAP and KHNYN can independently restrict CpG-enriched avian viruses. *PLoS biology*, 23(10), e3003471.

Antoni??to ACC, et al. (2025) Rme1: Unveiling a Novel Repressor in the Cellulolytic Pathway of *Trichoderma reesei*. *Journal of fungi (Basel, Switzerland)*, 11(9).

Weiblen C, et al. (2025) Diverse bacteriohemerythrin genes of *Methylobacter denitrificans* FJG1 provide insight into the survival and activity of methanotrophs in low oxygen ecosystems. *mBio*, 16(11), e0153325.

Suneesh NS, et al. (2025) Reverse vaccinology-based design of multivalent multiepitope mRNA vaccines targeting key viral proteins of Herpes Simplex Virus type-2. *Frontiers in immunology*, 16, 1586271.

Iannucci A, et al. (2025) The PYRIN domain is required for TLR4-mediated inflammation by PYHIN family members. *iScience*, 28(5), 112413.

Ramos L, et al. (2025) Novel non-synonymous and synonymous gene variants of SRD5A2 in patients with 46,XY-DSD and DSD-free subjects. *PloS one*, 20(3), e0316497.

Sheikhi A, et al. (2025) Novel sACE2-Anti-CD16VHH Fusion Protein Surreptitiously Inhibits SARS-CoV-2 Variant Spike Proteins and Macrophage Cytokines, and Activates Natural Killer Cell Cytotoxicity. *Vaccines*, 13(2).

Souod N, et al. (2025) In silico design and evaluation of a multiepitope vaccine against *Bordetella pertussis*: structural, immunological, and biological properties. *Genomics & informatics*, 23(1), 16.

Naderian R, et al. (2025) Rational design of multi-epitope vaccine for Chandipura virus using an immunoinformatics approach. *PloS one*, 20(10), e0335147.

Li C, et al. (2025) Design of a multi-epitope recombinant BCG vaccine targeting *Brucella* OMP31, LptE and VirB2 in immunoinformatics approaches. *PloS one*, 20(11), e0334843.

Liang X, et al. (2025) Advances in semi-rational design of terpene synthases and their modifying enzymes. *AMB Express*, 15(1), 178.

Khan S, et al. (2025) Immunoinformatics-based strategies for developing DNA and mRNA vaccines against monkeypox virus (MPXV). *Virology journal*, 22(1), 377.