

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

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: 20260905T132842+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 487 mentions in open access literature.

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

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.

Schmieder SS, et al. (2026) Structure and function of a fungal AB toxin-like chimerolectin involved in anti-nematode defense. *The EMBO journal*, 45(13), 4766.

Ali A, et al. (2026) TZ1391: a computationally designed circular mRNA multi-epitope vaccine candidate against *Mycobacterium tuberculosis* via TLR3 immunomodulation. *BMC immunology*, 27(1).

Waleed Iqbal M, et al. (2026) Delving Into the Depths of AGTR2: In Silico Identification of Deleterious Nonsynonymous SNPs Associated With Cardiovascular Diseases. *Human mutation*, 2026, 9394808.

Hendgen-Cotta UB, et al. (2026) Reverse engineering of BNIP3 identifies a mitochondrial protective peptide. *Nature communications*, 17(1).

Lee MB, et al. (2026) Whitening fruit by CRISPR/Cas9-mediated homoeolog-specific gene editing of MYB10-1B in strawberry (*F. ?? ananassa*). *Horticulture research*, 13(1), uhaf272.

Zhang Y, et al. (2026) Multi-omics and functional analyses in *Aesculus wilsonii* elucidate the biosynthetic pathways of moretane- and oleanane-type triterpenoids. *Plant communications*, 7(4), 101715.

Zhu Z, et al. (2026) Identification of HSF gene family and functional analysis of two HSFA1 genes with tandem repeat features in *Fritillaria cirrhosa* D.Don. *BMC genomics*, 27(1).

Li L, et al. (2026) Immunoinformatics based designing of a broad-spectrum multi-epitope vaccine against co-infection of human metapneumovirus, respiratory syncytial virus, and influenza A virus. *Scientific reports*, 16(1).

Rahimi-Farsi N, et al. (2026) Immunoinformatic-driven design of a multi-epitope vaccine against *Helicobacter pylori*. *Biochemistry and biophysics reports*, 45, 102498.

Zheng N, et al. (2026) In silico design of a novel multi-epitope mRNA vaccine candidate for BtHKU5-CoV-2 using immunoinformatics. *PLoS neglected tropical diseases*, 20(4), e0013517.

Ma J, et al. (2026) The alkylation of AIM2 by itaconate mediates macrophage PANoptosis during sepsis. *Cellular & molecular immunology*, 23(6), 619.

Kolla HB, et al. (2026) Unleashing the immune arsenal: development of broad spectrum multiepitope bluetongue vaccine targeting conserved T cell epitopes of structural proteins. *BMC genomics*, 27(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.

Ali S, et al. (2026) Immunoinformatics-guided design of a universal chimeric multi-epitope subunit vaccine against Marburg virus disease and Ravn virus co-infection. *Scientific reports*, 16(1), 6984.

Nam KH, et al. (2026) Evaluation of AI-Predicted GH11 Xylanase Models Against a Previously Unreported Experimental Structure: Implications for Conformational Accuracy and Ligand Binding. *International journal of molecular sciences*, 27(3).

Shuvo MN, et al. (2026) Computational and immunoinformatics approaches for designing phytocompound-based drugs and a multi-epitope vaccine targeting FemA, a cell wall protein of *Staphylococcus aureus*. *PloS one*, 21(4), e0346271.

Shi WO, et al. (2026) A lipid-binding protein in black-legged tick saliva selectively recognizes *Borrelia burgdorferi* lipids. *bioRxiv* : the preprint server for biology.

Duncan M, et al. (2026) Learning the Structural Diversity of Olfactory Receptors: A Genomic Case Study in Two Longhorn Beetles (Cerambycidae: Lamiinae). *Insects*, 17(6).

Ponniah C, et al. (2026) Zika NS2B Protein: In Vitro Formation of Large Multimeric Networks. *International journal of molecular sciences*, 27(3).