

Resource Summary Report

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RaptorX

RRID:SCR_018118

Type: Tool

Proper Citation

RaptorX (RRID:SCR_018118)

Resource Information

URL: <http://raptorx.uchicago.edu/>

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Description: Software package and web server for protein structure and function prediction. Used for predicting 3D structures for protein sequences without close homologs in Protein Data Bank. Given input sequence, predicts its secondary and tertiary structures, contacts, solvent accessibility, disordered regions and binding sites. Assigns some confidence scores to indicate quality of predicted 3D model.

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

Defining Citation: [PMID:21987485](#)

Keywords: Protein structure predictor, 3D structure, protein sequence, secondary and tertiary structure, binding site, solvent accessibility, disordered region, bio.tools

Funding: NIGMS R01 GM089753;
NSF DBI 0960390

Availability: Restricted

Resource Name: RaptorX

Resource ID: SCR_018118

Alternate IDs: biotools:raptorx

Alternate URLs: <https://bio.tools/raptorx>

Record Creation Time: 20220129T080338+0000

Record Last Update: 20260905T132831+0000

Ratings and Alerts

No rating or validation information has been found for RaptorX.

No alerts have been found for RaptorX.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 198 mentions in open access literature.

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

Abebe MA, et al. (2026) In silico Design and Analysis of Engineered Proteins Containing Multi-Epitope and Immunodominant Domains Derived From Rickettsia prowazekii Antigens. Bioinformatics and biology insights, 20, 11779322261461934.

Elrashedy A, et al. (2026) Immunoinformatics-based design of artificial chimeric proteins as universal vaccine candidates against foot-and-mouth disease virus serotypes A, O, and SAT2. Scientific reports, 16(1).

Bonardi CM, et al. (2026) Biallelic variants in CELSR1 cause brain malformations, neurodevelopmental disorders and epilepsy in humans. Nature communications, 17(1), 862.

Zhang Y, et al. (2026) Nuclear Localization of Effector BPE159: A Pivotal Mechanism for Intracellular Persistence of Brucella by Hampering Host Autophagy. Microorganisms, 14(3).

Aali F, et al. (2025) Bioinformatics analysis of innovative multi-epitope vaccine utilizing MAGE-A, MAM-A, and Gal-3 for breast cancer management. Scientific reports, 15(1), 19774.

Nicol??s-Morales ML, et al. (2025) The administration of passive and active immunotherapy against Syntenin-1 decreased the tumoral growth and pulmonary metastasis in a murine model of triple-negative breast cancer. Scientific reports, 15(1), 32134.

Shabbir MA, et al. (2025) Immunoinformatics-driven design of a multi-epitope vaccine against nipah virus: A promising approach for global health protection. Journal, genetic engineering & biotechnology, 23(2), 100482.

Albocher-Kedem N, et al. (2025) Uncovering the mechanism for polar sequestration of the major bacterial sugar regulator by high-throughput screens and 3D interaction modeling. Cell reports, 44(3), 115436.

Wang G, et al. (2025) Functional study of FleQ reveals the co-regulation of flgG by rpoN2vemRfleQ operon members in *Xanthomonas citri* subsp. *citri*. *iScience*, 28(7), 112960.

Ling Z, et al. (2025) Optimizing a Subunit Vaccine of *Mycobacterium tuberculosis* Using In-Silico and In-Vitro Approaches. *Iranian journal of public health*, 54(9), 1938.

Aseel DG, et al. (2025) Prediction of single nucleotide polymorphisms of RNA dependent RNA polymerase for the potato leafroll virus using computational and experimental approaches. *Scientific reports*, 15(1), 30121.

Evangelista GCL, et al. (2025) Apoptosis Inhibitor of Macrophages in Cats: A Potential Link Between an Exon 3 Variant Allele and Progression of Naturally Occurring Chronic Kidney Disease. *Journal of veterinary internal medicine*, 39(4), e70136.

Zhou QX, et al. (2025) Ubiquitin-activating enzyme1 (TgUAE1) acts as a key regulator of *Toxoplasma gondii* lytic cycle and homeostasis. *Communications biology*, 8(1), 728.

Nebangwa DN, et al. (2024) Predictive immunoinformatics reveal promising safety and anti-onchocerciasis protective immune response profiles to vaccine candidates (Ov-RAL-2 and Ov-103) in anticipation of phase I clinical trials. *PloS one*, 19(10), e0312315.

Ossowski MS, et al. (2024) Characterization of Novel *Trypanosoma cruzi*-Specific Antigen with Potential Use in the Diagnosis of Chagas Disease. *International journal of molecular sciences*, 25(2).

Moran BM, et al. (2024) A lethal mitonuclear incompatibility in complex I of natural hybrids. *Nature*, 626(7997), 119.

da Silva OLT, et al. (2024) Advancing molecular modeling and reverse vaccinology in broad-spectrum yellow fever virus vaccine development. *Scientific reports*, 14(1), 10842.

Rozano L, et al. (2024) Template-Based Modelling of the Structure of Fungal Effector Proteins. *Molecular biotechnology*, 66(4), 784.

Wu W, et al. (2024) *Ralstonia solanacearum* type III effector RipAF1 mediates plant resistance signaling by ADP-ribosylation of host FBN1. *Horticulture research*, 11(8), uhae162.

Shang G, et al. (2024) Structural Basis of Nucleic Acid Recognition and 6mA Demethylation by *Caenorhabditis elegans* NMAD-1A. *International journal of molecular sciences*, 25(2).