

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

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: 20260805T044416+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 149 mentions in open access literature.

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

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.

Nicolás-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.

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.

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.

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.

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.

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.

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).

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.

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

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).

Faysal MA, et al. (2024) In Silico Driven Multi-Epitope Subunit Candidate Vaccine against Bovine Tuberculosis. *Transboundary and emerging diseases*, 2024, 5534041.

Elshafei SO, et al. (2024) Immunoinformatics, molecular docking and dynamics simulation approaches unveil a multi epitope-based potent peptide vaccine candidate against avian leukosis virus. *Scientific reports*, 14(1), 2870.

Maekawa T, et al. (2023) Dying in self-defence: a comparative overview of immunogenic cell death signalling in animals and plants. *Cell death and differentiation*, 30(2), 258.

Wang XC, et al. (2023) A novel missense mutation in SPAST causes hereditary spastic paraplegia in male members of a family: A case report. *Molecular medicine reports*, 27(4).

Akter S, et al. (2023) Spike protein mutations and structural insights of pangolin lineage B.1.1.25 with implications for viral pathogenicity and ACE2 binding affinity. *Scientific reports*, 13(1), 13146.

Vainonen JP, et al. (2023) Poly(ADP-ribose)-binding protein RCD1 is a plant PARylation reader regulated by Photoregulatory Protein Kinases. *Communications biology*, 6(1), 429.

Grochowska KM, et al. (2023) Jacob-induced transcriptional inactivation of CREB promotes A β -induced synapse loss in Alzheimer's disease. *The EMBO journal*, 42(4), e112453.

Keshri AK, et al. (2023) Designing and development of multi-epitope chimeric vaccine against *Helicobacter pylori* by exploring its entire immunogenic epitopes: an immunoinformatic approach. *BMC bioinformatics*, 24(1), 358.