Resource Summary Report

Generated by NIF on Apr 16, 2025

RaptorX

RRID:SCR_018118
Type: Tool

Proper Citation

RaptorX (RRID:SCR_018118)

Resource Information

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

Proper Citation: RaptorX (RRID:SCR_018118)

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

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: 20250416T063834+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 142 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

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.

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

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.

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).

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

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.

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

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.

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.

La Paglia L, et al. (2023) Bioactive Molecules from the Innate Immunity of Ascidians and Innovative Methods of Drug Discovery: A Computational Approach Based on Artificial Intelligence. Marine drugs, 22(1).

Banerjee A, et al. (2023) Emergence of a unique SARS-CoV-2 Delta sub-cluster harboring a constellation of co-appearing non-Spike mutations. Journal of medical virology, 95(1), e28413.

Kupani M, et al. (2023) Prediction of an immunogenic peptide ensemble and multi-subunit vaccine for Visceral leishmaniasis using bioinformatics approaches. Heliyon, 9(12), e22121.

Prieto-Ruiz F, et al. (2023) Divergence of cytokinesis and dimorphism control by myosin II regulatory light chain in fission yeasts. iScience, 26(9), 107611.

Alam R, et al. (2023) In silico formulation of a next-generation multiepitope vaccine for use as a prophylactic candidate against Crimean-Congo hemorrhagic fever. BMC medicine, 21(1), 36.

Debroy R, et al. (2023) Translational protein RpsE as an alternative target for novel nucleoside analogues to treat MDR Enterobacter cloacae ATCC 13047: network analysis and molecular dynamics study. World journal of microbiology & biotechnology, 39(7), 187.

Subramanian A, et al. (2023) A Legionella toxin exhibits tRNA mimicry and glycosyl transferase activity to target the translation machinery and trigger a ribotoxic stress response. Nature cell biology, 25(11), 1600.