Resource Summary Report

Generated by RRID on Apr 28, 2025

PatchDock

RRID:SCR_017589
Type: Tool

Proper Citation

PatchDock (RRID:SCR_017589)

Resource Information

URL: https://bioinfo3d.cs.tau.ac.il/PatchDock/

Proper Citation: PatchDock (RRID:SCR_017589)

Description: Web server for molecular docking. Performs structure prediction of protein–protein and protein–small molecule complexes. Molecular docking algorithm based on shape complementarity principles.

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

Defining Citation: PMID:15980490

Keywords: Molecular, docking, structure, prediction, protein, molecule, shape, complex, bio.tools

Funding: Israel Science Foundation ;
Hermann Minkowski-Minerva Center for Geometry at Tel Aviv University ;
Israeli Ministry of Science ;
National Cancer Institute ;
NIH

Availability: Free, Freely available

Resource Name: PatchDock

Resource ID: SCR_017589

Alternate IDs: biotools:patchdock

Alternate URLs: https://bio.tools/patchdock

Record Creation Time: 20220129T080336+0000

Record Last Update: 20250428T054055+0000

Ratings and Alerts

No rating or validation information has been found for PatchDock.

No alerts have been found for PatchDock.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 82 mentions in open access literature.

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

Siddiki AZ, et al. (2025) Development of a multi-epitope chimeric vaccine in silico against Babesia bovis, Theileria annulata, and Anaplasma marginale using computational biology tools and reverse vaccinology approach. PloS one, 20(1), e0312262.

Mishra A, et al. (2024) HRAMS Proteomics Insights on the Anti-Filarial Effect of Ocimum sanctum: Implications in Phytochemical-Based Drug-Targeting and Designing. Proteomes, 13(1).

Lee JR, et al. (2024) Advancing Breast Cancer Therapeutics: Targeted Gene Delivery Systems Unveiling the Potential of Estrogen Receptor-Targeting Ligands. Biomaterials research, 28, 0087.

Das S, et al. (2024) Encapsulation of Apium graveolens essential oil into chitosan nanobiopolymer for protection of stored rice against Fusarium verticillioides and fumonisins contamination. Heliyon, 10(9), e29954.

Heidari Horestani M, et al. (2024) The clock gene BHLHE40 and atypical CCNG2 control androgen-induced cellular senescence as a novel tumor suppressive pathway in prostate cancer. Journal of experimental & clinical cancer research : CR, 43(1), 174.

Cui J, et al. (2023) Glycosylated and Succinylated Macrocyclic Lactones with Amyloid-?-Aggregation-Regulating Activity from a Marine Bacillus sp. Marine drugs, 21(2).

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.

Motamedi H, et al. (2023) In silico designing and immunoinformatics analysis of a novel peptide vaccine against metallo-beta-lactamase (VIM and IMP) variants. PloS one, 18(7), e0275237.

Ruiz-Ciancio D, et al. (2023) Selection of a novel cell-internalizing RNA aptamer specific for CD22 antigen in B cell acute lymphoblastic leukemia. Molecular therapy. Nucleic acids, 33, 698.

Kandhavelu J, et al. (2023) A novel EGFR Inhibitor, HNPMI regulates apoptosis and oncogenesis by modulating BCL-2/BAX and p53 in colon cancer. British journal of pharmacology.

Elmetwalli A, et al. (2023) Diarylheptanoids/sorafenib as a potential anticancer combination against hepatocellular carcinoma: the p53/MMP9 axis of action. Naunyn-Schmiedeberg's archives of pharmacology, 396(10), 2501.

Rahmani A, et al. (2022) Applying high throughput and comprehensive immunoinformatics approaches to design a trivalent subunit vaccine for induction of immune response against emerging human coronaviruses SARS-CoV, MERS-CoV and SARS-CoV-2. Journal of biomolecular structure & dynamics, 40(13), 6097.

Jabin D, et al. (2022) T-cell epitope-based vaccine prediction against Aspergillus fumigatus: a harmful causative agent of aspergillosis. Journal, genetic engineering & biotechnology, 20(1), 72.

Bondarchuk TV, et al. (2022) Quaternary organization of the human eEF1B complex reveals unique multi-GEF domain assembly. Nucleic acids research, 50(16), 9490.

Kausar MA, et al. (2022) In Silico Comparative Exploration of Allergens of Periplaneta americana, Blattella germanica and Phoenix dactylifera for the Diagnosis of Patients Suffering from IgE-Mediated Allergic Respiratory Diseases. Molecules (Basel, Switzerland), 27(24).

Baughman HER, et al. (2022) An intrinsically disordered transcription activation domain increases the DNA binding affinity and reduces the specificity of NF?B p50/RelA. The Journal of biological chemistry, 298(9), 102349.

Kadam US, et al. (2022) Identification and structural analysis of novel malathion-specific DNA aptameric sensors designed for food testing. Biomaterials, 287, 121617.

Srivastava S, et al. (2022) Computationally validated SARS-CoV-2 CTL and HTL Multi-Patch vaccines, designed by reverse epitomics approach, show potential to cover large ethnically distributed human population worldwide. Journal of biomolecular structure & dynamics, 40(5), 2369.

Mazor RD, et al. (2022) Tumor-reactive antibodies evolve from non-binding and autoreactive precursors. Cell, 185(7), 1208.

Korona B, et al. (2022) CCR6 activation links innate immune responses to mucosa-associated lymphoid tissue lymphoma development. Haematologica, 107(6), 1384.