Resource Summary Report

Generated by RRID on May 21, 2025

RosettaDock

RRID:SCR_013393
Type: Tool

Proper Citation

RosettaDock (RRID:SCR_013393)

Resource Information

URL: http://graylab.jhu.edu/docking/rosetta/

Proper Citation: RosettaDock (RRID:SCR_013393)

Description: Predicts the structure of a protein-protein complex from the individual structures of the monomer components.

Abbreviations: RosettaDock

Resource Type: software resource

Funding:

Resource Name: RosettaDock

Resource ID: SCR_013393

Alternate IDs: OMICS_01604

Record Creation Time: 20220129T080315+0000

Record Last Update: 20250519T203807+0000

Ratings and Alerts

No rating or validation information has been found for RosettaDock.

No alerts have been found for RosettaDock.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 101 mentions in open access literature.

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

Abba Moussa D, et al. (2025) Discovery of a pan anti-SARS-CoV-2 monoclonal antibody with highly efficient infected cell killing capacity for novel immunotherapeutic approaches. Emerging microbes & infections, 14(1), 2432345.

Kantheti U, et al. (2025) PD-L1-CD80 interactions are required for intracellular signaling necessary for dendritic cell migration. Science advances, 11(5), eadt3044.

Shirali A, et al. (2025) A comprehensive survey of scoring functions for protein docking models. BMC bioinformatics, 26(1), 25.

Paik H, et al. (2024) ELiAH: the atlas of E3 ligases in human tissues for targeted protein degradation with reduced off-target effect. Database : the journal of biological databases and curation, 2024.

Tang D, et al. (2024) Streptolysin O accelerates the conversion of plasminogen to plasmin. Nature communications, 15(1), 10212.

Yan Z, et al. (2024) Evolution shapes interaction patterns for epistasis and specific protein binding in a two-component signaling system. Communications chemistry, 7(1), 13.

Karagöl A, et al. (2024) Inhibitory Potential of the Truncated Isoforms on Glutamate Transporter Oligomerization Identified by Computational Analysis of Gene-Centric Isoform Maps. Pharmaceutical research, 41(11), 2173.

Zheng H, et al. (2024) Aurora-A condensation mediated by BuGZ aids its mitotic centrosome functions. iScience, 27(5), 109785.

Ngo K, et al. (2024) Elucidating molecular mechanisms of protoxin-II state-specific binding to the human NaV1.7 channel. The Journal of general physiology, 156(2).

Marson NA, et al. (2024) In silico prediction of heme binding in proteins. The Journal of biological chemistry, 300(5), 107250.

Hsiao MH, et al. (2024) Molecular Display of the Animal Meta-Venome for Discovery of Novel Therapeutic Peptides. bioRxiv : the preprint server for biology.

Lu Z, et al. (2024) An osteosarcoma-on-a-chip model for studying osteosarcoma matrix-cell interactions and drug responses. Bioactive materials, 34, 1.

Wilson J, et al. (2024) Programable Albumin-Hitchhiking Nanobodies Enhance the Delivery of STING Agonists to Potentiate Cancer Immunotherapy. Research square.

Ahn T, et al. (2024) Non-invasive strategy: Developing a topical IL-4R?-specific nanobody for the treatment of allergic airway diseases. Materials today. Bio, 27, 101148.

Zheng F, et al. (2024) Systematic investigation of machine learning on limited data: A study on predicting protein-protein binding strength. Computational and structural biotechnology journal, 23, 460.

Kannoth S, et al. (2023) Transcriptome analysis of Corvus splendens reveals a repertoire of antimicrobial peptides. Scientific reports, 13(1), 18728.

Tam C, et al. (2023) Targeting Ras-binding domain of ELMO1 by computational nanobody design. Communications biology, 6(1), 284.

Gogar RK, et al. (2023) The ?-latch structural element of the SufS cysteine desulfurase mediates active site accessibility and SufE transpersulfurase positioning. The Journal of biological chemistry, 299(3), 102966.

Wydorski PM, et al. (2023) Dual domain recognition determines SARS-CoV-2 PLpro selectivity for human ISG15 and K48-linked di-ubiquitin. bioRxiv : the preprint server for biology.

Weng G, et al. (2023) PROTAC-DB 2.0: an updated database of PROTACs. Nucleic acids research, 51(D1), D1367.