

Resource Summary Report

Generated by [RRID](#) on Aug 2, 2026

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

Resource Name: RosettaDock

Resource ID: SCR_013393

Alternate IDs: OMICS_01604

Record Creation Time: 20220129T080315+0000

Record Last Update: 20260801T190448+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 118 mentions in open access literature.

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

Li C, et al. (2025) Mapk7 enhances osteogenesis and suppresses adipogenesis by activating Lrp6/ β -catenin signaling axis in mesenchymal stem cells. *Communications biology*, 8(1), 310.

Fan S, et al. (2025) Pyridoxine dehydrogenase SePdx regulates photosynthesis via an association with the phycobilisome in a cyanobacterium. *The Plant journal : for cell and molecular biology*, 121(6), e70055.

Richard AC, et al. (2025) Using Short Molecular Dynamics Simulations to Determine the Important Features of Interactions in Antibody-Protein Complexes. *Proteins*, 93(4), 812.

An D, et al. (2025) Resolving the APN controversy in PEDV infection: Comparative kinetic characterization through single-virus tracking. *PLoS pathogens*, 21(6), e1013317.

Osmakov DI, et al. (2025) Two Amino Acid Substitutions Improve the Pharmacological Profile of the Snake Venom Peptide Mambalgins. *Toxins*, 17(3).

Chang R, et al. (2025) A new type of Caspase-1 upon recognizing bacteria inhibits GSDME-dependent histone modification and NF- κ B signaling. *Communications biology*, 8(1), 827.

Jeon J, et al. (2025) Blockade of the vaspin-AP-1 axis inhibits arthritis development. *Experimental & molecular medicine*, 57(3), 628.

Lian S, et al. (2025) Conjugated Lithocholic Acid Activates Hepatic TGR5 to Promote Lipotoxicity and MASLD-MASH Transition by Disrupting Carnitine Biosynthesis. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 12(20), e2410602.

Juraszek J, et al. (2025) De novo design of D-peptide ligands: Application to influenza virus hemagglutinin. *Proceedings of the National Academy of Sciences of the United States of America*, 122(26), e2426554122.

Ugurlu SY, et al. (2025) MEGA PROTAC, MEGA DOCK-based PROTAC mediated ternary complex formation pipeline with sequential filtering and rank aggregation. *Scientific reports*, 15(1), 5545.

Hsiao MH, et al. (2025) Molecular Display of the Animal Meta-Venome for Discovery of Novel Therapeutic Peptides. *Molecular & cellular proteomics : MCP*, 24(2), 100901.

Duan Z, et al. (2025) Artificial intelligence-driven framework for discovering synthetic binding protein-like scaffolds from the entire protein universe. *Briefings in bioinformatics*, 26(5).

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.

Tang M, et al. (2025) A positive feedback loop between SMAD3 and PINK1 in regulation of mitophagy. *Cell discovery*, 11(1), 22.

Kimmel BR, et al. (2025) Potentiating cancer immunotherapies with modular albumin-hitchhiking nanobody-STING agonist conjugates. *Nature biomedical engineering*, 9(10), 1719.

Alisaraie L, et al. (2025) Application of temperature replica exchange molecular dynamics: Structure of mitotic spindle-associated protein SHE1 and its binding to dynein. *Computational and structural biotechnology journal*, 27, 2359.

Tran MH, et al. (2025) RosettaHDX: Predicting antibody-antigen interaction from hydrogen-deuterium exchange mass spectrometry data. *Journal of structural biology*, 217(1), 108166.

Chen Q, et al. (2025) A moonlighting function of tumoral interleukin-1 β precursor promotes metastasis via RACK1-mediated actin remodeling. *Nature communications*, 16(1), 10148.