

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 16, 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: 20260912T195802+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 125 mentions in open access literature.

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

Bai Q, et al. (2026) PCK2-Mediated PQBP1 Lactylation Promotes Asthmatic Inflammation through PRMT5 Inhibition. *Research* (Washington, D.C.), 9, 1321.

Ali S, et al. (2026) Butyrophilin 2A2 promotes T cell immunoregulation via CD45 phosphatase activation and protects against murine autoimmune glomerulonephritis and pregnancy loss. *Nature communications*, 17(1), 1325.

Casasampere M, et al. (2026) Expanding the targeted protein degradation approach with small molecule chimeras directed to the 26S proteasome. *Nature communications*, 17(1).

Zuo S, et al. (2026) ENY2 transcription and export complex 2 subunit deficiency induces nucleolar stress to inhibit tumor progression through NPM1/MDM2/p53-dependent and - independent responses. *Cellular oncology* (Dordrecht, Netherlands), 49(1), 41.

Yasuda Y, et al. (2026) Observation of redistribution for local conformational dynamics in cross-reactive antibody design. *Journal of biochemistry*, 179(4), 259.

Kim H, et al. (2026) Advanced immunodiagnostics for periodontal disease: Targeted detection of Kgp and RgpB using A7 and G1 antibody set. *Journal of advanced research*, 85, 495.

Zhang W, et al. (2026) Cyclin-E/A/CDK1/2 Kinetic Landscapes Drive Cell Cycle Phase-Specific Progression and Guide Cyclin-E Degradation Strategy. *Journal of chemical information and modeling*, 66(6), 3188.

Li C, et al. (2025) Mapk7 enhances osteogenesis and suppresses adipogenesis by activating Lrp6/?-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.

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

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.

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

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