Resource Summary Report

Generated by T1D on Sep 19, 2026

rDock

RRID:SCR_002838
Type: Tool

Proper Citation

rDock (RRID:SCR_002838)

Resource Information

URL: http://rdock.sourceforge.net/

Proper Citation: rDock (RRID:SCR_002838)

Description: A fast and versatile Open Source docking software program that can be used to dock small molecules against proteins and nucleic acids.

Resource Type: software resource

Defining Citation: PMID:24722481

Keywords: standalone software

Availability: Free, Freely available, Available for download

Resource Name: rDock

Resource ID: SCR_002838

Alternate IDs: OMICS_03835

Record Creation Time: 20220129T080215+0000

Record Last Update: 20260919T195006+0000

Ratings and Alerts

No rating or validation information has been found for rDock.

No alerts have been found for rDock.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 122 mentions in open access literature.

Listed below are recent publications. The full list is available at T1D .

Vila IK, et al. (2026) DNA-PK interacts with cyclic dinucleotides and inhibits type I interferon responses. The Journal of experimental medicine, 223(5).

Matralis AN, et al. (2026) An aerosolized dual-action autotaxin inhibitor-PPAR? agonist for the treatment of pulmonary fibrosis. Cell reports. Medicine, 7(5), 102778.

Cabot-March J, et al. (2026) SAFR: Enabling Fragment-Based Drug Discovery with a Synthetic Binding Pose Data Set. Journal of chemical information and modeling, 66(8), 4848.

Han F, et al. (2026) An mRNA-encoded scFv antibody targeting the helix-?3 of HPV18 E7 oncoprotein as a novel antiviral strategy. mBio, 17(3), e0262725.

Peyrat G, et al. (2026) Frags2Drugs: A Novel In Silico Fragment-Based Approach to the Discovery of Kinase Inhibitors. Pharmaceuticals (Basel, Switzerland), 19(2).

Wang Y, et al. (2026) Novel Small Molecule DZ-865B Effectively Degrades BCL6, Promotes Apoptosis and Reduces Proliferation of Diffuse Large B-Cell Lymphoma Cells. Oncology research, 34(3), 23.

Aguti R, et al. (2026) Critical Assessment of a Structure-Based Pipeline for Targeting the Long Noncoding RNA MALAT1. Journal of chemical information and modeling, 66(7), 4187.

Carvajal-Patiño JG, et al. (2025) RNAmigos2: accelerated structure-based RNA virtual screening with deep graph learning. Nature communications, 16(1), 2799.

Wang X, et al. (2025) A novel approach for target deconvolution from phenotype-based screening using knowledge graph. Scientific reports, 15(1), 2414.

Ferla MP, et al. (2025) Fragmenstein: predicting protein-ligand structures of compounds derived from known crystallographic fragment hits using a strict conserved-binding-based methodology. Journal of cheminformatics, 17(1), 4.

Wang B, et al. (2025) Tenascin-R aggravates A? production in the perforant pathway by regulating Nav1.6 activity in APP/PS1 mice. Alzheimer's & dementia : the journal of the Alzheimer's Association, 21(9), e70633.

Gao S, et al. (2025) Activation of PI3K-AKT pathway prevents steroid-induced osteonecrosis of the femoral head via inhibiting Cuproptosis. Scientific reports, 15(1), 8950.

Greer RA, et al. (2025) TREM2-apoE3 interactions and Alzheimer's disease: Molecular and structural insights and effects of TREM2 R47H and apoE4 variants. Alzheimer's & dementia : the journal of the Alzheimer's Association, 21(10), e70729.

Cheng X, et al. (2025) The quantitative detection method employing a combination of high-affinity antibodies targeting PCT. Biochemistry and biophysics reports, 43, 102091.

Matsoukas MT, et al. (2025) Design of Small Non-Peptidic Ligands That Alter Heteromerization between Cannabinoid CB1 and Serotonin 5HT2A Receptors. Journal of medicinal chemistry, 68(1), 261.

Yin D, et al. (2025) Adipocytes-induced ANGPTL4/KLF4 axis drives glycolysis and metastasis in triple-negative breast cancer. Journal of experimental & clinical cancer research : CR, 44(1), 192.

Natsumoto B, et al. (2025) Identification of Potential Therapeutic Agents for Type I Interferonopathy Using iPSC-Based Disease Modeling. Journal of clinical immunology, 45(1), 140.

Ergün Ö, et al. (2025) Characterization of Ligand Binding in Human Serum Albumin from Atomistic Energy Transfer Simulations. Small methods, 9(12), e01820.

Debnath A, et al. (2025) Identification of novel cyclin-dependent kinase 4/6 inhibitors from marine natural products. PloS one, 20(1), e0313830.

Martínez-Cartró M, et al. (2025) Discovering Uncharted Binding Pockets on E3 Ligases Leads to the Identification of FBW7 Allosteric Modulators. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(39), e06068.