

Resource Summary Report

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Rosetta

RRID:SCR_015701

Type: Tool

Proper Citation

Rosetta (RRID:SCR_015701)

Resource Information

URL: <https://www.rosettacommons.org/home>

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Description: Molecular modeling software package for 3D structure prediction and high resolution design of proteins, nucleic acids, and non natural polymers. Used in computational biology, including de novo protein design, enzyme design, ligand docking, and structure prediction of biological macromolecules and macromolecular complexes.

Synonyms: Rosetta modeling software

Resource Type: software resource, software application, software toolkit, simulation software

Defining Citation: [PMID:28430426](#), [PMID:21829626](#), [PMID:18442991](#)

Keywords: Molecular modeling, structure prediction, computational modeling, protein analysis, enzyme design, macromolecular complexes

Funding: Hertz Foundation Fellowship ;
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NIGMS GM078221;
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NIGMS GM111819;
NSF BMAT 1507736;
NCI F32 CA189246;
NIGMS GM092802;
NIGMS GM110089;
NIGMS GM117189

Availability: Restricted

Resource Name: Rosetta

Resource ID: SCR_015701

Record Creation Time: 20220129T080327+0000

Record Last Update: 20260801T190519+0000

Ratings and Alerts

No rating or validation information has been found for Rosetta.

No alerts have been found for Rosetta.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 212 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Huang J, et al. (2026) Cryo-EM structures of antibodies elicited by germline-targeting HIV MPER epitope scaffolds. Cell reports, 45(1), 116818.

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.

Smith AM, et al. (2025) The HIV-1 nuclear export complex reveals the role of RNA in CRM1 cargo recognition. Molecular cell, 85(16), 3108.

Wicke D, et al. (2024) The previously uncharacterized RnpM (YlxR) protein modulates the activity of ribonuclease P in Bacillus subtilis in vitro. Nucleic acids research, 52(3), 1404.

Yang R, et al. (2024) Structural basis for nuclear import of hepatitis B virus (HBV) nucleocapsid core. Science advances, 10(2), eadi7606.

Au CW, et al. (2024) The Mutagenic Plasticity of the Cholera Toxin B-Subunit Surface Residues: Stability and Affinity. Toxins, 16(3).

Lolicato F, et al. (2024) Disulfide bridge-dependent dimerization triggers FGF2 membrane translocation into the extracellular space. eLife, 12.

Eirich P, et al. (2024) The release of host-derived antibodies bound to the variant surface glycoprotein (VSG) of Trypanosoma brucei cannot be explained by pH-dependent conformational changes of the VSG dimer. Open research Europe, 4, 87.

Bursch KL, et al. (2024) Cancer-associated polybromo-1 bromodomain 4 missense variants variably impact bromodomain ligand binding and cell growth suppression. *The Journal of biological chemistry*, 300(4), 107146.

Pandey A, et al. (2024) Therapeutic Targeting and Structural Characterization of a Sotorasib-Modified KRAS G12C-MHC I complex Demonstrates the Antitumor Efficacy of Hapten-Based Strategies. *Cancer research*.

Ray R, et al. (2024) Eliciting a single amino acid change by vaccination generates antibody protection against group 1 and group 2 influenza A viruses. *Immunity*, 57(5), 1141.

Braxton JR, et al. (2023) The p97/VCP adaptor UBXD1 drives AAA+ remodeling and ring opening through multi-domain tethered interactions. *Nature structural & molecular biology*, 30(12), 2009.

Song J, et al. (2023) Noncovalent antibody catenation on a target surface greatly increases the antigen-binding avidity. *eLife*, 12.

Han Y, et al. (2023) Elucidation of a dynamic interplay between a beta-2 adrenergic receptor, its agonist, and stimulatory G protein. *Proceedings of the National Academy of Sciences of the United States of America*, 120(10), e2215916120.

Dickey TH, et al. (2023) Design of a stabilized RBD enables potently neutralizing SARS-CoV-2 single-component nanoparticle vaccines. *Cell reports*, 42(3), 112266.

Wang X, et al. (2023) Structural insights into dimerization and activation of the mGlu2-mGlu3 and mGlu2-mGlu4 heterodimers. *Cell research*, 33(10), 762.

Krebs AS, et al. (2023) Molecular architecture and conservation of an immature human endogenous retrovirus. *Nature communications*, 14(1), 5149.

Reimer JM, et al. (2023) Structure of LRRK1 and mechanisms of autoinhibition and activation. *Nature structural & molecular biology*, 30(11), 1735.

Sawade K, et al. (2023) Combining molecular dynamics simulations and scoring method to computationally model ubiquitylated linker histones in chromatosomes. *PLoS computational biology*, 19(8), e1010531.

Goswami A, et al. (2023) De novo design of anti-variant COVID-19 vaccine. *Biology methods & protocols*, 8(1), bpad021.