

Resource Summary Report

Generated by SPARC SAWG on Sep 17, 2026

Jackal

RRID:SCR_008665

Type: Tool

Proper Citation

Jackal (RRID:SCR_008665)

Resource Information

URL: http://wiki.c2b2.columbia.edu/honiglab_public/index.php/Software:Jackal

Proper Citation: Jackal (RRID:SCR_008665)

Description: Jackal is a collection of programs designed for the modeling and analysis of protein structures. Its core program is a versatile homology modeling package. It contains twelve individual programs, each with their own function.

Resource Type: software resource

Keywords: software, software repository, modeling, analysis, protein structure

Funding: NSF DBI-9904841;
NIGMS 5 R37 GM30518

Availability: Public, Free

Resource Name: Jackal

Resource ID: SCR_008665

Alternate IDs: nif-0000-33373

Record Creation Time: 20220129T080248+0000

Record Last Update: 20260912T195707+0000

Ratings and Alerts

No rating or validation information has been found for Jackal.

No alerts have been found for Jackal.

Data and Source Information

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Chen J, et al. (2022) Mathematical artificial intelligence design of mutation-proof COVID-19 monoclonal antibodies. ArXiv.

Gavira JA, et al. (2020) How Bacterial Chemoreceptors Evolve Novel Ligand Specificities. mBio, 11(1).

Hajdú I, et al. (2020) Ligand-induced conformational rearrangements regulate the switch between membrane-proximal and distal functions of Rho kinase 2. Communications biology, 3(1), 721.

Wu B, et al. (2019) Novel Genetic Markers for Early Detection of Elevated Breast Cancer Risk in Women. International journal of molecular sciences, 20(19).

Horitani M, et al. (2017) ¹³C ENDOR Spectroscopy of Lipoxygenase-Substrate Complexes Reveals the Structural Basis for C-H Activation by Tunneling. Journal of the American Chemical Society, 139(5), 1984.

Copie G, et al. (2016) On the ability of molecular dynamics simulation and continuum electrostatics to treat interfacial water molecules in protein-protein complexes. Scientific reports, 6, 38259.

Getov I, et al. (2016) SAAFEC: Predicting the Effect of Single Point Mutations on Protein Folding Free Energy Using a Knowledge-Modified MM/PBSA Approach. International journal of molecular sciences, 17(4), 512.

Zheng F, et al. (2016) The Ascaris suum nicotinic receptor, ACR-16, as a drug target: Four novel negative allosteric modulators from virtual screening. International journal for parasitology. Drugs and drug resistance, 6(1), 60.

Petukh M, et al. (2015) Predicting Binding Free Energy Change Caused by Point Mutations with Knowledge-Modified MM/PBSA Method. PLoS computational biology, 11(7), e1004276.

May M, et al. (2015) ZC4H2, an XLID gene, is required for the generation of a specific subset of CNS interneurons. Human molecular genetics, 24(17), 4848.

Mageroy MH, et al. (2015) Expression of the β -glucosidase gene Pg β glu-1 underpins natural resistance of white spruce against spruce budworm. The Plant journal : for cell and molecular biology, 81(1), 68.

Nishi H, et al. (2015) Crosstalk between signaling pathways provided by single and multiple protein phosphorylation sites. Journal of molecular biology, 427(2), 511.

Buonocore F, et al. (2008) A CD4 homologue in sea bass (*Dicentrarchus labrax*): molecular characterization and structural analysis. *Molecular immunology*, 45(11), 3168.

Guo H, et al. (2007) Computational studies for the structure and function of mRPE65. *Journal of theoretical biology*, 245(2), 312.