

Resource Summary Report

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bio3d

RRID:SCR_024266

Type: Tool

Proper Citation

bio3d (RRID:SCR_024266)

Resource Information

URL: <https://cran.r-project.org/web/packages/bio3d/index.html>

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Description: Softwar R package for comparative analysis of protein structures. Used to process, organize and explore protein structure, sequence and dynamics data. Used to read and write structure, sequence and dynamic trajectory data, perform sequence and structure database searches, data summaries, atom selection, alignment, superposition, rigid core identification, clustering, torsion analysis, distance matrix analysis, structure and sequence conservation analysis, normal mode analysis, principal component analysis of heterogeneous structure data, and correlation network analysis from normal mode and molecular dynamics data. Enables statistical and graphical power of R environment to work with biological sequence and structural data.

Synonyms: r-cran-bio3d, bio3d: Biological Structure Analysis

Resource Type: software resource, software toolkit

Defining Citation: [PMID:16940322](#)

Keywords: comparative analysis of protein structures, process protein structure, organize and explore protein structure, sequence and dynamics data,

Funding:

Availability: Free, Available for download, Freely available,

Resource Name: bio3d

Resource ID: SCR_024266

Alternate IDs: OMICS_12577

Alternate URLs: <https://sources.debian.org/src/r-cran-bio3d/>

License: GPL-2 | GPL-3 [expanded from: GPL (? 2)]

Record Creation Time: 20230830T050217+0000

Record Last Update: 20250525T032137+0000

Ratings and Alerts

No rating or validation information has been found for bio3d.

No alerts have been found for bio3d.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 273 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Lee YT, et al. (2025) The conformational space of RNase P RNA in solution. Nature, 637(8048), 1244.

Buric F, et al. (2025) Amino acid sequence encodes protein abundance shaped by protein stability at reduced synthesis cost. Protein science : a publication of the Protein Society, 34(1), e5239.

Guiré R, et al. (2025) The inhibitory activities of two compounds from Securidaca longepedunculata Fresen on the acetylcholinesterase from wheat pest Schizaphis graminum Rondani: in silico analysis. Plant signaling & behavior, 20(1), 2444311.

Scott CE, et al. (2025) Impact of Intracellular Proteins on μ -Opioid Receptor Structure and Ligand Binding. The journal of physical chemistry. B, 129(1), 71.

Bouزيد A, et al. (2025) Whole exome sequencing identifies ABHD14A and MRNIP as novel candidate genes for developmental language disorder. Scientific reports, 15(1), 367.

Root J, et al. (2024) Granulins rescue inflammation, lysosome dysfunction, lipofuscin, and

neuropathology in a mouse model of progranulin deficiency. *Cell reports*, 43(12), 114985.

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.

Ray P, et al. (2024) Bioinformatics and computational studies of chabamide F and chabamide G for breast cancer and their probable mechanisms of action. *Scientific reports*, 14(1), 19893.

Negi H, et al. (2024) Plasticity of the proteasome-targeting signal Fat10 enhances substrate degradation. *eLife*, 13.

Khachatryan H, et al. (2024) Computational evaluation and benchmark study of 342 crystallographic holo-structures of SARS-CoV-2 Mpro enzyme. *Scientific reports*, 14(1), 14255.

Trinidad DD, et al. (2024) Deep mutational scanning of EccD3 reveals the molecular basis of its essentiality in the mycobacterium ESX secretion system. *bioRxiv : the preprint server for biology*.

Karagöl A, et al. (2024) Molecular Dynamic Simulations Reveal that Water-Soluble QTY-Variants of Glutamate Transporters EAA1, EAA2 and EAA3 Retain the Conformational Characteristics of Native Transporters. *Pharmaceutical research*, 41(10), 1965.

Jung J, et al. (2024) MYH1 deficiency disrupts outer hair cell electromotility, resulting in hearing loss. *Experimental & molecular medicine*, 56(11), 2423.

Ruiz-Serra V, et al. (2024) 3Dmapper: a command line tool for BioBank-scale mapping of variants to protein structures. *Bioinformatics (Oxford, England)*, 40(4).

Alharbi YTM, et al. (2024) Investigation of phytochemicals isolated from selected Saudi medicinal plants as natural inhibitors of SARS CoV-2 main protease: In vitro, molecular docking and simulation analysis. *Saudi pharmaceutical journal : SPJ : the official publication of the Saudi Pharmaceutical Society*, 32(5), 102023.

Martins NF, et al. (2024) Fungi Tryptophan Synthases: What Is the Role of the Linker Connecting the ? and ? Structural Domains in *Hemileia vastatrix* TRPS? A Molecular Dynamics Investigation. *Molecules (Basel, Switzerland)*, 29(4).

Ahmad B, et al. (2024) Investigating Potential Cancer Therapeutics: Insight into Histone Deacetylases (HDACs) Inhibitions. *Pharmaceuticals (Basel, Switzerland)*, 17(4).

Rani NA, et al. (2024) Development of multi epitope subunit vaccines against emerging carp viruses Cyprinid herpesvirus 1 and 3 using immunoinformatics approach. *Scientific reports*, 14(1), 11783.

Spiteri VA, et al. (2024) Using atomistic solution scattering modelling to elucidate the role of the Fc glycans in human IgG4. PloS one, 19(4), e0300964.

Han X, et al. (2024) Pharmacophore-based virtual screening of commercial databases against γ -secretase 1 for drug development against Alzheimer's disease. Frontiers in chemistry, 12, 1412349.