

Resource Summary Report

Generated by [RRID](#) on Aug 2, 2026

[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>

Proper Citation: bio3d (RRID:SCR_024266)

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,

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: 20260801T190900+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 311 mentions in open access literature.

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

Castillo MB, et al. (2025) Identification of immunogenic KIF5B-RET fusion neopeptides driving immune stimulation in tumor specific CD8+ T cells. *Frontiers in immunology*, 16, 1635810.

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

Siddiquee NH, et al. (2025) Molecular activity of bioactive phytochemicals for inhibiting host cell attachment and membrane fusion interacting with West Nile Virus envelope glycoprotein. *PloS one*, 20(4), e0321902.

Tamta AK, et al. (2025) SIRT2 attenuates stress-induced skeletal muscle atrophy by inhibiting glucocorticoid receptor signalling. *bioRxiv : the preprint server for biology*.

Ahamed MS, et al. (2025) Bioinformatics-driven identification of pathogenic missense nsSNPs in the human proto-oncogene SRC and cancer susceptibility. *Journal, genetic engineering & biotechnology*, 23(4), 100618.

Masum MHU, et al. (2025) Bioactive fungal metabolites as SIRT2 antagonists: A computational quest for cancer treatment. *PloS one*, 20(12), e0339474.

Ahmed WS, et al. (2025) Coevolving residues distant from the ligand binding site are involved in GAF domain function. *Communications chemistry*, 8(1), 107.

Guir?? 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.

Islam MT, et al. (2025) In silico screening of naturally derived dietary compounds as potential butyrylcholinesterase inhibitors for Alzheimer's disease treatment. *Scientific*

reports, 15(1), 17134.

Quaranta M, et al. (2025) Structural Analysis of the SARS-CoV-2 Spike N-Terminal Domain Across Wild-Type and Recent Variants: A Comparative Study. *Proteins*, 93(11), 1891.

Shred M, et al. (2025) Conformational flexibility of tubulin dimers regulates the transitions of microtubule dynamic instability. *bioRxiv : the preprint server for biology*.

Islam KMT, et al. (2025) In silico approaches unveil the mechanism of action of *Eclipta prostrata* against acute myeloid leukemia. *Scientific reports*, 15(1), 33267.

Magill DJ, et al. (2025) ProFlex as a linguistic bridge for decoding protein dynamics in normal mode analysis. *Nature communications*, 16(1), 9074.

Perkins-Jechow BH, et al. (2025) Challenging AlphaFold in predicting proteins with large-scale allosteric transitions. *Communications chemistry*, 8(1), 378.

Alshahrani M, et al. (2025) Ensemble-Based Binding Free Energy Profiling and Network Analysis of the KRAS Interactions with DARPin Proteins Targeting Distinct Binding Sites: Revealing Molecular Determinants and Universal Architecture of Regulatory Hotspots and Allosteric Binding. *Biomolecules*, 15(6).

Wallmann A, et al. (2025) Structural and evolutionary determinants of Argonaute function. *Nucleic acids research*, 53(18).

Zhang W, et al. (2025) Distinct allosteric networks in CDK4 and CDK6 in the cell cycle and in drug resistance. *bioRxiv : the preprint server for biology*.

Adeleke MA, et al. (2025) Computational Development of Transmission-Blocking Vaccine Candidates Based on Fused Antigens of Pre- and Post-fertilization Gametocytes Against *Plasmodium falciparum*. *Bioinformatics and biology insights*, 19, 11779322241306215.

Gao B, et al. (2025) Molecular dynamics simulations reveal key roles of the LIF receptor in the assembly of human LIF signaling complex. *Computational and structural biotechnology journal*, 27, 585.

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.