Resource Summary Report

Generated by NIF on Apr 29, 2025

BioJava Project

RRID:SCR_007180
Type: Tool

Proper Citation

BioJava Project (RRID:SCR_007180)

Resource Information

URL: http://www.biojava.org

Proper Citation: BioJava Project (RRID:SCR_007180)

Description: Project dedicated to providing Java framework for processing biological data. It provides analytical and statistical routines, parsers for common file formats and allows the manipulation of sequences and 3D structures. The goal of the biojava project is to facilitate rapid application development for bioinformatics. Sponsor: BioJava is not formally funded by any grants. Through the OBF they have received sponsorship from Sun Microsystems, Apple Computers and NESCent. The initial development of the phylogenetics module was undertaken as a Google Summer of Code 2007 project in collaboration with NESCent.

Abbreviations: BioJava

Synonyms: The BioJava Project, BioJava Project

Resource Type: data processing software, software resource, software application

Keywords: biojava, framework, biological, data, analytical, statistical, file, manipulation, 3d structure, application, bioinformatics

Funding:

Resource Name: BioJava Project

Resource ID: SCR_007180

Alternate IDs: OMICS_04848, nif-0000-30181

Alternate URLs: https://sources.debian.org/src/libbiojava4-java/

Record Creation Time: 20220129T080240+0000

Record Last Update: 20250429T055132+0000

Ratings and Alerts

No rating or validation information has been found for BioJava Project.

No alerts have been found for BioJava Project.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 84 mentions in open access literature.

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

Angles R, et al. (2024) An optimized relational database for querying structural patterns in proteins. Database : the journal of biological databases and curation, 2024.

Planas-Iglesias J, et al. (2024) AggreProt: a web server for predicting and engineering aggregation prone regions in proteins. Nucleic acids research, 52(W1), W159.

van Kempen M, et al. (2024) Fast and accurate protein structure search with Foldseek. Nature biotechnology, 42(2), 243.

Scheepbouwer C, et al. (2024) Full-length tRNAs lacking a functional CCA tail are selectively sorted into the lumen of extracellular vesicles. bioRxiv : the preprint server for biology.

Wishart DS, et al. (2023) PlasMapper 3.0-a web server for generating, editing, annotating and visualizing publication quality plasmid maps. Nucleic acids research, 51(W1), W459.

Ammar A, et al. (2023) PSnpBind-ML: predicting the effect of binding site mutations on protein-ligand binding affinity. Journal of cheminformatics, 15(1), 31.

Scheepbouwer C, et al. (2023) ALL-tRNAseq enables robust tRNA profiling in tissue samples. Genes & development, 37(5-6), 243.

Tanramluk D, et al. (2022) MANORAA: A machine learning platform to guide protein-ligand design by anchors and influential distances. Structure (London, England : 1993), 30(1), 181.

Cauchy P, et al. (2019) 2HybridTools, a handy software to facilitate clone identification and mutation mapping from yeast two-hybrid screening. PeerJ, 7, e7245.

Bliven SE, et al. (2019) Analyzing the symmetrical arrangement of structural repeats in proteins with CE-Symm. PLoS computational biology, 15(4), e1006842.

Lafita A, et al. (2019) BioJava 5: A community driven open-source bioinformatics library. PLoS computational biology, 15(2), e1006791.

Fukasawa Y, et al. (2019) Accurate Classification of Biological and non-Biological Interfaces in Protein Crystal Structures using Subtle Covariation Signals. Scientific reports, 9(1), 12603.

Bliven S, et al. (2018) Automated evaluation of quaternary structures from protein crystals. PLoS computational biology, 14(4), e1006104.

Korkmaz S, et al. (2018) Investigation of protein quaternary structure via stoichiometry and symmetry information. PloS one, 13(6), e0197176.

Nakamura T, et al. (2018) Template-based quaternary structure prediction of proteins using enhanced profile-profile alignments. Proteins, 86 Suppl 1(Suppl Suppl 1), 274.

Zeng C, et al. (2018) SDADB: a functional annotation database of protein structural domains. Database : the journal of biological databases and curation, 2018.

Bittrich S, et al. (2018) Characterizing the relation of functional and Early Folding Residues in protein structures using the example of aminoacyl-tRNA synthetases. PloS one, 13(10), e0206369.

Bonnici V, et al. (2018) Arena-Idb: a platform to build human non-coding RNA interaction networks. BMC bioinformatics, 19(Suppl 10), 350.

Gao J, et al. (2017) BioJava-ModFinder: identification of protein modifications in 3D structures from the Protein Data Bank. Bioinformatics (Oxford, England), 33(13), 2047.

Gao J, et al. (2017) 3D clusters of somatic mutations in cancer reveal numerous rare mutations as functional targets. Genome medicine, 9(1), 4.