

Resource Summary Report

Generated by [kravitz2](#) on Sep 5, 2026

Biopython

RRID:SCR_007173

Type: Tool

Proper Citation

Biopython (RRID:SCR_007173)

Resource Information

URL: <http://biopython.org>

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Description: Biopython is a set of freely available tools for biological computation written in Python by an international team of developers. It is a distributed collaborative effort to develop Python libraries and applications which address the needs of current and future work in bioinformatics. The source code is made available under the Biopython License, which is extremely liberal and compatible with almost every license in the world. It works along with the Open Bioinformatics Foundation, who generously host it's website, bug tracker, and mailing lists. Sponsor: This resource is supported by the Open Bioinformatics Foundation. Keywords: Tool, Software, Python, Biological, Computation, Bioinformatics,

Synonyms: Biopython

Resource Type: software application, software development tool, software resource

Defining Citation: [DOI:10.1093/bioinformatics/btp163](https://doi.org/10.1093/bioinformatics/btp163)

Resource Name: Biopython

Resource ID: SCR_007173

Alternate IDs: OMICS_04850, nif-0000-30202

Old URLs: <https://sources.debian.org/src/python-biopython-doc/>

Record Creation Time: 20220129T080240+0000

Record Last Update: 20260904T000418+0000

Ratings and Alerts

No rating or validation information has been found for Biopython.

No alerts have been found for Biopython.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2670 mentions in open access literature.

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

Dogra P, et al. (2026) Granular component sub-phases direct ribosome biogenesis in the nucleolus. *Molecular cell*.

Nickles GR, et al. (2026) Tracing the origins of crmA megasynthase through lichen genomes. *Current biology : CB*, 36(13), 3354.

Dombaxe CP, et al. (2026) Proteomic Signatures of Regeneration: Uncovering Extracellular Matrix-Associated Cues in Goldfish Spinal Cord Repair. *The Journal of comparative neurology*, 534(5), e70170.

Modlin SJ, et al. (2026) Pervasive genome structure heterogeneity in *Mycobacterium tuberculosis* constitutively generates subpopulations with distinct clinical phenotypes. *iScience*, 29(5), 115045.

Dong W, et al. (2026) PHR-Mediated Pi Starvation Response Mobile Messenger RNAs Represent Noncoding Transcripts in Recipient Tissues. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(4), e02911.

Lucas TN, et al. (2026) MMonitor for real-time monitoring of microbial communities using long reads. *Cell reports methods*, 6(1), 101266.

Thomas M, et al. (2026) Genomic and proteomic characterization of a newly isolated *Paenarthrobacter ilicis* strain and its plasmid-mediated xanthan degradation. *Microbiology spectrum*, 14(1), e0169025.

Burrows JT, et al. (2026) Structure of the *Enterobacter* pan-genome is revealed using machine learning. *Microbiology spectrum*, 14(2), e0192225.

P??verlein MC, et al. (2026) Protein-induced membrane strain drives supercomplex formation. *eLife*, 13.

Zhang X, et al. (2026) Evolutionary and Functional Characterization of an Auxin Methyltransferase (CslAMT) in Cucumber Reveals Its Role in Stress Adaptation and Development. *Ecology and evolution*, 16(3), e73178.

Mboowa G, et al. (2026) rMAP 2.0: a modular, reproducible, and scalable WDL-Cromwell-Docker workflow for genomic analysis of ESKAPEE pathogens. *Bioinformatics advances*, 6(1), vbag046.

Bastress C, et al. (2026) Extending Biopython to combine multiple sequence alignments with the same reference into a Multiple Sequence Alignment. *microPublication biology*, 2026.

Engin B, et al. (2026) Atlas of HIV cis-regulatory elements reveals extensive transcriptional variation across clades, isolates, and within individuals. *bioRxiv : the preprint server for biology*.

Villarreal DA, et al. (2026) Screening metatranscriptomes for ultrastable RNA secondary structures reveals hidden bacteriophages and novel capsid nanomaterials. *bioRxiv : the preprint server for biology*.

Jackson CR, et al. (2026) Defining a Midgestational Window for In Utero Genome Editing of the Fetal Murine Cortex. *bioRxiv : the preprint server for biology*.

Polunina PV, et al. (2026) VEFill: accurate and generalizable deep mutational scanning score imputation across protein domains. *Molecular systems biology*, 22(6), 979.

Arnaudi M, et al. (2026) MAVISp: A modular structure-based framework for protein variant effects. *Protein science : a publication of the Protein Society*, 35(5), e70548.

Rinke JL, et al. (2026) Comparative analysis of 163 ant genomes reveals recurrent horizontal gene transfer from bacteria to ants. *GigaScience*, 15.

Frank JA, et al. (2026) Systematic multi-reference vertebrate ACE2 sequence similarity analysis predicts species susceptibility to SARS-related sarbecoviruses. *Scientific reports*, 16(1).

Malik AJ, et al. (2026) Structome-AlignViewer: On Confidence Assessment in Structure-Aware Alignments. *Genome biology and evolution*, 18(1).