

Resource Summary Report

Generated by [dkNET](#) on Aug 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 resource, software development tool

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: 20260805T044147+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 2371 mentions in open access literature.

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

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.

Khan A, et al. (2026) HMPV-TherResDB: Comprehensive human metapneumovirus (HMPV) database for sequence-structure annotations, vaccine resources, and therapeutics research. *Virus research*, 363, 199665.

Guellil M, et al. (2026) Tracing 2500 years of human betaherpesvirus 6A and 6B diversity through ancient DNA. *Science advances*, 12(1), eadx5460.

Vinogradov-Talyah E, et al. (2026) Human clearance systems have a layered architecture across tissues and cell types that supports varied proteome compositions. *Autophagy*, 22(1), 145.

Farias FM, et al. (2026) Streptocyclin BTW is a novel member of a diverse family of circular bacteriocins in the genus *Streptococcus*. *Molecular nutrition & food research*, 70(1), e70290.

Ramasamy P, et al. (2026) Assessing the relation between protein phosphorylation, AlphaFold3 models, and conformational variability. *Protein science : a publication of the Protein Society*, 35(1), e70376.

van Hooff JJE, et al. (2025) Repeated duplications and losses shaped SMC complex evolution from archaeal ancestors to modern eukaryotes. *Cell reports*, 44(7), 115855.

Kennard AS, et al. (2025) Tubulin sequence divergence is associated with the use of distinct microtubule regulators. *Current biology : CB*, 35(2), 233.

Zhong S, et al. (2025) Modular DNA barcoding of nanobodies enables multiplexed in situ protein imaging and high-throughput biomolecule detection. *eLife*, 14.

Krüger T, et al. (2025) Toxin data quality: a critical examination of bacterial exotoxins and animal toxins. *BMC research notes*, 18(1), 418.

Starcevic A, et al. (2025) Long-read metagenomic sequencing negates inferred loss of cytosine methylation in Myxosporea (Cnidaria: Myxozoa). *GigaScience*, 14.

Lee KS, et al. (2025) Functional assessment of all ATM SNVs using prime editing and deep learning. *Cell*, 188(18), 5081.

Blanco Mendana J, et al. (2025) Deterministic genetic barcoding for multiplexed behavioral and single-cell transcriptomic studies. *eLife*, 12.

Proença M, et al. (2025) Prophage dynamics in gastric and enterohepatic environments: unraveling ecological barriers and adaptive transitions. *ISME communications*, 5(1), ycaf017.

Priego-Cubero S, et al. (2025) Subfunctionalization and epigenetic regulation of a biosynthetic gene cluster in Solanaceae. *Proceedings of the National Academy of Sciences of the United States of America*, 122(8), e2420164122.

Baty SM, et al. (2025) Strong Signatures of Selection on Candidate Genes Underlying Core Speciation Mechanisms in Desert Tortoises. *Molecular ecology resources*, 25(6), e14098.

Cirincione A, et al. (2025) A benchmarked, high-efficiency prime editing platform for multiplexed dropout screening. *Nature methods*, 22(1), 92.

Danner M, et al. (2025) Mutational constraint analysis workflow for overlapping short open reading frames and genomic neighbors. *BMC genomics*, 26(1), 254.

Iida N, et al. (2025) Systematically developing a registry of splice-site creating variants utilizing massive publicly available transcriptome sequence data. *Nature communications*, 16(1), 426.

Xie P, et al. (2025) A fiducial-assisted strategy compatible with resolving small MFS transporter structures in multiple conformations using cryo-EM. *Nature communications*, 16(1), 7.