**Biopython**

RRID:SCR_007173  
Type: Tool

**Proper Citation**

Biopython (RRID:SCR_007173)

**Resource Information**

**URL:** [http://biopython.org](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 development tool, software resource, software application

**Defining Citation:** DOI: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:** 20240616T053506+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 1663 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [FDI Lab - SciCrunch.org](https://www.FDI-Lab.org).


Abdalfattah S, et al. (2024) Identification of Antagonistic Action of Pyrrolizidine Alkaloids in Muscarinic Acetylcholine Receptor M1 by Computational Target Prediction Analysis. Pharmaceuticals (Basel, Switzerland), 17(1).


Lim D, et al. (2024) Graphylo: A deep learning approach for predicting regulatory DNA and RNA sites from whole-genome multiple alignments. iScience, 27(2), 109002.


Kwon T, et al. (2024) Global characterization of biosynthetic gene clusters in non-model
eukaryotes using domain architectures. Scientific reports, 14(1), 1534.


Camara MB, et al. (2024) Visualizing a two-state conformational ensemble in stem-loop 3 of the transcriptional regulator 7SK RNA. Nucleic acids research, 52(2), 940.

