Biopython
RRID:SCR_007173
Type: Tool

Proper Citation

Biopython (RRID:SCR_007173)

Resource Information

URL: http://biopython.org

Proper Citation: Biopython (RRID:SCR_007173)

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 resource, software application, software development tool

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: 20240701T053502+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.


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.


Høie MH, et al. (2024) DiscoTope-3.0: improved B-cell epitope prediction using inverse
folding latent representations. Frontiers in immunology, 15, 1322712.


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.

