

Resource Summary Report

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[MolBioLib](#)

RRID:SCR_005372

Type: Tool

Proper Citation

MolBioLib (RRID:SCR_005372)

Resource Information

URL: <http://sourceforge.net/projects/molbiolib/>

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Description: A compact, portable, and extensively tested C++11 software framework and set of applications tailored to the demands of next-generation sequencing data and applicable to many other applications. It is designed to work with common file formats and data types used both in genomic analysis and general data analysis. A central relational-database-like Table class is a flexible and powerful object to intuitively represent and work with a wide variety of tabular datasets, ranging from alignment data to annotations. MolBioLib includes programs to perform a wide variety of analysis tasks such as computing read coverage, annotating genomic intervals, and novel peak calling with a wavelet algorithm. This package assumes fluency in both UNIX and C++.

Abbreviations: MolBioLib

Synonyms: MolBioLib: C++11 framework for rapid develop and deploy of bioinformatic tasks

Resource Type: software resource

Defining Citation: [PMID:22815363](#)

Keywords: c++, next-generation sequencing, genomic, analysis, genome

Resource Name: MolBioLib

Resource ID: SCR_005372

Alternate IDs: OMICS_01145

Record Creation Time: 20220129T080229+0000

Record Last Update: 20260905T132534+0000

Ratings and Alerts

No rating or validation information has been found for MolBioLib.

No alerts have been found for MolBioLib.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.