Resource Summary Report

Generated by RRID on May 21, 2025

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

Funding:

Resource Name: MolBioLib

Resource ID: SCR_005372

Alternate IDs: OMICS_01145

Record Creation Time: 20220129T080229+0000

Record Last Update: 20250519T203357+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.