Resource Summary Report

Generated by NIF on May 7, 2025

JAMM

RRID:SCR_017049
Type: Tool

Proper Citation

JAMM (RRID:SCR_017049)

Resource Information

URL: https://github.com/mahmoudibrahim/JAMM

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Description: Software tool as peak finder for joint analysis of NGS replicates. Used for peak finding in next generation sequencing broad and narrow datasets like ChIP-Seq, ATAC-Seq, DNase-Seq. Can integrate information from biological replicates and assign peak boundaries accurately.

Synonyms: J oint A nalysis of NGS replicates via M ixture M odel clustering, Joint Analysis of NGS replicates via Mixture Model clustering

Resource Type: software application, software resource, data analysis software, data processing software

Defining Citation: PMID:25223640

Keywords: peak, finder, sequencing, dataset, integrate, replicate, boundary, accurately, bio.tools

Funding: Max-Delbrück-Center/New York University Exchange Program.

Availability: Free, Available for download, Freely available

Resource Name: JAMM

Resource ID: SCR_017049

Alternate IDs: biotools:jamm

Alternate URLs: https://bio.tools/jamm

License: GNU GPL v3.0

Record Creation Time: 20220129T080333+0000

Record Last Update: 20250506T061549+0000

Ratings and Alerts

No rating or validation information has been found for JAMM.

No alerts have been found for JAMM.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 2 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Ivanyi-Nagy R, et al. (2018) The RNA interactome of human telomerase RNA reveals a coding-independent role for a histone mRNA in telomere homeostasis. eLife, 7.

Behjati Ardakani F, et al. (2018) Predicting transcription factor binding using ensemble random forest models. F1000Research, 7, 1603.