Resource Summary Report

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Epigenomics Workflow on Galaxy and Jupyter

RRID:SCR_017544
Type: Tool

Proper Citation

Epigenomics Workflow on Galaxy and Jupyter (RRID:SCR_017544)

Resource Information

URL: https://github.com/wilkinsonlab/epigenomics_pipeline

Proper Citation: Epigenomics Workflow on Galaxy and Jupyter (RRID:SCR_017544)

Description: Software tool as epigenomics analysis pipeline for analysis of ChIP-Seq and RNA-Seq data using Docker images containing Galaxy and Jupyter.

Synonyms: REA pipeline

Resource Type: data analysis software, training material, software application, narrative resource, software resource, data processing software, workflow, data or information resource

Keywords: Epigenomic, analysis, pipeline, ChIP-Seq, RNA-Seq, data, Galaxy, Jupyter, bio.tools

Funding: Agencia Estatal de Investigación of Spain SEV-2016-0672 (2017-2021)

Availability: Free, Available for download, Freely available

Resource Name: Epigenomics Workflow on Galaxy and Jupyter

Resource ID: SCR_017544

Alternate IDs: biotools:Epigenomics_Workflow_on_Galaxy_and_Jupyter

Alternate URLs: https://zenodo.org/record/3298029,
https://bio.tools/Epigenomics_Workflow_on_Galaxy_and_Jupyter

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Ratings and Alerts

No rating or validation information has been found for Epigenomics Workflow on Galaxy and Jupyter.

No alerts have been found for Epigenomics Workflow on Galaxy and Jupyter.

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 FDI Lab - SciCrunch.org.

Payá-Milans M, et al. (2019) Genome-wide analysis of the H3K27me3 epigenome and transcriptome in Brassica rapa. GigaScience, 8(12).

Denaxas S, et al. (2017) Methods for enhancing the reproducibility of biomedical research findings using electronic health records. BioData mining, 10, 31.