

Resource Summary Report

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ChrAccR

RRID:SCR_024397

Type: Tool

Proper Citation

ChrAccR (RRID:SCR_024397)

Resource Information

URL: <https://github.com/GreenleafLab/ChrAccR>

Proper Citation: ChrAccR (RRID:SCR_024397)

Description: Software R package for comprehensive analysis chromatin accessibility data. Analyzing chromatin accessibility data in R. Used for data quality control, exploratory analyses including unsupervised methods for dimension reduction, clustering and quantifying transcription factor activities, and identification and characterization of differentially accessible regions. Used for analysis of large bulk datasets comprising hundreds of samples as well as for single cell datasets.

Synonyms: Chromatin Accessibility data in R

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

Keywords: analysis chromatin accessibility data, data quality control, identification and characterization of differentially accessible regions, clustering and quantifying transcription factor activities,

Availability: Free, Available for download, Freely available

Resource Name: ChrAccR

Resource ID: SCR_024397

Alternate URLs: <https://greenleaflab.github.io/ChrAccR/>

License: GPL v2

Record Creation Time: 20230902T050213+0000

Record Last Update: 20260919T195543+0000

Ratings and Alerts

No rating or validation information has been found for ChrAccR.

No alerts have been found for ChrAccR.

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 [dkNET](#) .

Liu BB, et al. (2025) An automated ATAC-seq method reveals sequence determinants of transcription factor dose response in the open chromatin. bioRxiv : the preprint server for biology.

Doughty BR, et al. (2024) Single-molecule chromatin configurations link transcription factor binding to expression in human cells. bioRxiv : the preprint server for biology.