Resource Summary Report

Generated by NIF on Sep 18, 2026

chromvar

RRID:SCR_026570
Type: Tool

Proper Citation

chromvar (RRID:SCR_026570)

Resource Information

URL: https://github.com/GreenleafLab/chromVAR

Proper Citation: chromvar (RRID:SCR_026570)

Description: Software R package for analyzing sparse chromatin-accessibility data by estimating gain or loss of accessibility within peaks sharing the same motif or annotation while controlling for technical biases. Enables accurate clustering of scATAC-seq profiles and characterization of known and de novo sequence motifs associated with variation in chromatin accessibility. Used for analysis of sparse chromatin accessibility data from single cell or bulk ATAC or DNAse-seq data.

Synonyms: chromatin Variability Across Regions

Resource Type: data analysis software, data processing software, software application, software resource, software toolkit, source code

Defining Citation: PMID:28825706

Keywords: analyzing sparse chromatin-accessibility data, analysis of sparse chromatin accessibility data, single cell, bulk ATAC, DNAse-seq data,

Funding: Broad Institute Fellowship ;
Harvard Society of Fellows ;
NHGRI P50HG007735;
NIAID U19AI057266;
Rita Allen Foundation

Availability: Free, Available for download, Freely available

Resource Name: chromvar

Resource ID: SCR_026570

Record Creation Time: 20250313T060330+0000

Record Last Update: 20260912T200507+0000

Ratings and Alerts

No rating or validation information has been found for chromvar.

No alerts have been found for chromvar.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 15 mentions in open access literature.

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

López-Fuentes E, et al. (2026) Epigenetic and Transcriptional Programs Define Osteosarcoma Subtypes and Establish Targetable Vulnerabilities. Cancer discovery, 16(2), 296.

Al Souz J, et al. (2026) Organ injury in systemic autoimmunity is mediated by stem-like CD8+ T cells arising from tissue-draining lymph nodes. Immunity, 59(6), 1667.

Roger E, et al. (2026) ATM Deficiency Induces TGF?-Mediated Stromal Programming in Pancreatic Cancer. Cancer research, 86(14), 3412.

Yang Y, et al. (2025) Cross-modal contrastive learning decodes developmental regulatory features through chromatin potential analysis. GigaScience, 14.

You T, et al. (2025) Role of progesterone action in inguinal hernia formation via skeletal muscle fibrosis and atrophy. JCI insight, 10(14).

Mout L, et al. (2025) Genetic and Epigenetic Reprogramming of Transposable Elements Drives ecDNA-Mediated Metastatic Prostate Cancer. bioRxiv : the preprint server for biology.

Krauter D, et al. (2025) Spatial organization, chromatin accessibility and gene-regulatory programs defining mouse sensory neurons. Communications biology, 8(1), 908.

Chen M, et al. (2025) SMOPCA: spatially aware dimension reduction integrating multi-omics improves the efficiency of spatial domain detection. Genome biology, 26(1), 135.

Ver Heul AM, et al. (2025) RAG suppresses group 2 innate lymphoid cells. eLife, 13.

Daman AW, et al. (2025) Microbial cancer immunotherapy reprograms hematopoiesis to enhance myeloid-driven anti-tumor immunity. Cancer cell, 43(8), 1442.

Gao Y, et al. (2025) Multimodal analyses reveal genes driving electrophysiological maturation of neurons in the primate prefrontal cortex. Neuron, 113(15), 2490.

Valenzi E, et al. (2024) Altered AP-1, RUNX and EGR chromatin dynamics drive fibrotic lung disease. bioRxiv : the preprint server for biology.

Travisano SI, et al. (2024) Protocol for the isolation and single-nuclei multiomic analyses of the human fetal epicardium. STAR protocols, 5(2), 102973.

Li J, et al. (2022) Aberrant DNA hydroxymethylation reshapes transcription factor binding in myeloid neoplasms. Clinical epigenetics, 14(1), 81.

Chung CY, et al. (2019) Single-Cell Chromatin Analysis of Mammary Gland Development Reveals Cell-State Transcriptional Regulators and Lineage Relationships. Cell reports, 29(2), 495.