

Resource Summary Report

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Cell Ranger ARC

RRID:SCR_023897

Type: Tool

Proper Citation

Cell Ranger ARC (RRID:SCR_023897)

Resource Information

URL: <https://support.10xgenomics.com/single-cell-multiome-atac-gex/software/pipelines/latest/what-is-cell-ranger-arc>

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Description: Software analysis pipelines that process Chromium Single Cell Multiome ATAC + Gene Expression sequencing data to generate variety of analyses pertaining to gene expression , chromatin accessibility, and their linkage. Used to perform analyses that link chromatin accessibility and GEX.

Synonyms: 10x Genomics Cell Ranger ARC

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

Keywords: Chromium Single Cell Multiome ATAC, Gene Expression, sequencing data, processing sequencing data, gene expression analysis, chromatin accessibility analysis,

Availability: Restricted

Resource Name: Cell Ranger ARC

Resource ID: SCR_023897

License URLs: <https://support.10xgenomics.com/single-cell-multiome-atac-gex/software/downloads/latest>

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Ratings and Alerts

No rating or validation information has been found for Cell Ranger ARC .

No alerts have been found for Cell Ranger ARC .

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 23 mentions in open access literature.

Listed below are recent publications. The full list is available at [RRID](#) .

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

Huerga Encabo H, et al. (2026) Human TET2-Mutant Clonal Hematopoiesis Expansion Is Driven by Distinct Inflammatory Signaling Responses in Stem Cells Versus Myeloid Progeny. *Blood cancer discovery*, 7(2), 287.

Herbrich S, et al. (2026) TET2-mutant clonal hematopoiesis enhances macrophage antigen presentation and improves immune checkpoint therapy in solid tumors. *Cancer cell*, 44(1), 187.

Kim SK, et al. (2026) Human-specific features of the cerebellum and ZP2-regulated synapse development. *Cell*, 189(6), 1802.

Hilgart E, et al. (2026) DNA Methylation Stochasticity Is Linked to Transcriptional Variability and Convergent Epigenetic Disruption across Genetic Subtypes of Acute Myeloid Leukemia. *Cancer research*, 86(13), 3325.

Weber PAA, et al. (2026) Tobemstomig, a Novel Bispecific Antibody, Preferentially Blocks PD-1 and LAG-3 on CD8 TILs to Expand Stem-like T Cells for Sustained Tumor Control. *Cancer research communications*, 6(7), 1619.

Wang BS, et al. (2026) Single-cell multiomic approaches define a gradual, spatially regulated epigenetic and transcriptional transition from embryonic to adult neural stem cells. *Stem cell reports*, 21(7), 102967.

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

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

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

Montuori G, et al. (2025) Extrachromosomal DNA-Driven Oncogene Dosage Heterogeneity Promotes Rapid Adaptation to Therapy in MYCN-Amplified Cancers. *Cancer discovery*, 15(10), 2054.

Wu Y, et al. (2025) Neurodevelopmental hijacking of oligodendrocyte lineage programs drives glioblastoma infiltration. *Developmental cell*.

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

Garnica J, et al. (2024) T-follicular helper cells are epigenetically poised to transdifferentiate into T-regulatory type 1 cells. *eLife*, 13.

Montaño J, et al. (2024) Transcriptional re-programming of liver-resident iNKT cells into T-regulatory type-1-like liver iNKT cells involves extensive gene de-methylation. *Frontiers in immunology*, 15, 1454314.

Sharma A, et al. (2024) Enhanced analysis of tabular data through Multi-representation DeeplInsight. *Scientific reports*, 14(1), 12851.

Littleton SH, et al. (2024) Variant-to-function analysis of the childhood obesity chr12q13 locus implicates rs7132908 as a causal variant within the 3' UTR of FAIM2. *Cell genomics*, 4(5), 100556.

Jessa S, et al. (2024) FOXR2 targets LHX6+/DLX+ neural lineages to drive CNS neuroblastoma. *Cancer research*.

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

Liu SJ, et al. (2024) Epigenetic reprogramming shapes the cellular landscape of schwannoma. *Nature communications*, 15(1), 476.