

Resource Summary Report

Generated by [RRID](#) on Aug 12, 2026

FASTGenomics

RRID:SCR_022898

Type: Tool

Proper Citation

FASTGenomics (RRID:SCR_022898)

Resource Information

URL: <https://www.fastgenomics.org/>

Proper Citation: FASTGenomics (RRID:SCR_022898)

Description: Open online platform for single cell RNA-seq. Provides data management and analytics. Used to analyze public and private datasets and you can choose between several best practices workflows and browse existing analyses.

Resource Type: service resource, analysis service resource, data analysis service, production service resource

Keywords: single cell RNA-seq, data management, data analytics, analyze public and private datasets, best practices workflows

Funding: German Federal Ministry of Economic Affairs and Energy

Availability: Free, Freely available

Resource Name: FASTGenomics

Resource ID: SCR_022898

Alternate URLs: <https://github.com/FASTGenomics>

Record Creation Time: 20221019T050203+0000

Record Last Update: 20260812T044430+0000

Ratings and Alerts

No rating or validation information has been found for FASTGenomics.

No alerts have been found for FASTGenomics.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 9 mentions in open access literature.

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

Toner YC, et al. (2025) Targeting mTOR in myeloid cells prevents infection-associated inflammation. *iScience*, 28(4), 112163.

Aksu MD, et al. (2024) Regulation of plasma soluble receptors of TNF and IL-1 in patients with COVID-19 differs from that observed in sepsis. *The Journal of infection*, 89(6), 106300.

Arora JK, et al. (2024) Single-cell RNA sequencing reveals the expansion of circulating tissue-homing B cell subsets in secondary acute dengue viral infection. *Heliyon*, 10(10), e30314.

Siewert A, et al. (2023) Analysis of candidate genes for cleft lip ± cleft palate using murine single-cell expression data. *Frontiers in cell and developmental biology*, 11, 1091666.

Hackney JA, et al. (2023) A myeloid program associated with COVID-19 severity is decreased by therapeutic blockade of IL-6 signaling. *iScience*, 26(10), 107813.

Arora JK, et al. (2023) Computational workflow for investigating highly variable genes in single-cell RNA-seq across multiple time points and cell types. *STAR protocols*, 4(3), 102387.

Baßler K, et al. (2022) Alveolar macrophages in early stage COPD show functional deviations with properties of impaired immune activation. *Frontiers in immunology*, 13, 917232.

Marongiu L, et al. (2022) Maturation signatures of conventional dendritic cell subtypes in COVID-19 suggest direct viral sensing. *European journal of immunology*, 52(1), 109.

Guo C, et al. (2022) Single-cell transcriptomics reveal a unique memory-like NK cell subset that accumulates with ageing and correlates with disease severity in COVID-19. *Genome medicine*, 14(1), 46.