

Resource Summary Report

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Azimuth

RRID:SCR_021084

Type: Tool

Proper Citation

Azimuth (RRID:SCR_021084)

Resource Information

URL: <https://azimuth.hubmapconsortium.org/>

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Description: Web application that uses annotated reference dataset to automate processing, analysis, and interpretation of new single cell RNA-seq experiment. Azimuth leverages reference based mapping, pipeline that inputs counts matrix of gene expression in single cells, and performs normalization, visualization, cell annotation, and differential expression. All results can be explored within the app, and easily downloaded for additional downstream analysis.

Resource Type: software resource, web application

Defining Citation: [DOI:10.1101/2020.10.12.335331](https://doi.org/10.1101/2020.10.12.335331)

Keywords: HubMap, BICCN, biomarker discovery, molecular reference maps, annotated reference dataset, automate processing, automate analysis, new single cell RNA-seq experiment interpretation

Availability: Free, Freely available

Resource Name: Azimuth

Resource ID: SCR_021084

Record Creation Time: 20220129T080353+0000

Record Last Update: 20260731T043051+0000

Ratings and Alerts

No rating or validation information has been found for Azimuth.

No alerts have been found for Azimuth.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 52 mentions in open access literature.

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

Xiao T, et al. (2025) Benchmarking large language models for cell typing in single-cell RNA-Seq. *Briefings in bioinformatics*, 26(6).

Krossa S, et al. (2025) Spatial multi-omics identifies aggressive prostate cancer signatures highlighting pro-inflammatory chemokine activity in the tumor microenvironment. *Nature communications*, 16(1), 10160.

Svobodová B, et al. (2025) Collagen VII Is Associated with Airway Remodeling, Honeycombing, and Fibroblast Foci in Usual Interstitial Pneumonia/Idiopathic Pulmonary Fibrosis. *The American journal of pathology*, 195(8), 1467.

Lamba R, et al. (2025) MatriCom, a single-cell RNA-sequencing data mining tool to infer cell-extracellular matrix interactions. *Journal of cell science*, 138(13).

Bhattacharya N, et al. (2025) Artificial intelligence approaches for tumor phenotype stratification from single-cell transcriptomic data. *eLife*, 13.

Chen J, et al. (2025) CellTypeAgent: Trustworthy cell type annotation with Large Language Models. *ArXiv*.

Chockalingam SP, et al. (2025) SCEMENT: scalable and memory efficient integration of large-scale single-cell RNA-sequencing data. *Bioinformatics (Oxford, England)*, 41(2).

Park SY, et al. (2025) Cathepsin L as a dual-target to mitigate muscle wasting while enhancing anti-tumor efficacy of anti-PD-L1. *Nature communications*, 16(1), 10706.

Marchand V, et al. (2025) Monocytes generated by interleukin-6-treated human hematopoietic stem and progenitor cells secrete calprotectin that inhibits erythropoiesis. *iScience*, 28(1), 111522.

Bojovi? I, et al. (2025) Sketching T cell atlases in the single-cell era: challenges and recommendations. *Immunology and cell biology*, 103(7), 723.

Uhl DP, et al. (2025) A single-cell transcriptomic atlas of peripheral blood immune cells spanning progressive canine leishmaniosis. *bioRxiv : the preprint server for biology*.

Gur ER, et al. (2025) scATAC-seq generates more accurate and complete regulatory maps than bulk ATAC-seq. *Scientific reports*, 15(1), 3665.

Börner K, et al. (2025) Human BioMolecular Atlas Program (HuBMAP): 3D Human Reference Atlas construction and usage. *Nature methods*, 22(4), 845.

Yata T, et al. (2025) Contribution of germline and somatic mutations to risk of neuromyelitis optica spectrum disorder. *Cell genomics*, 5(3), 100776.

Lee-Ferris RE, et al. (2025) Prolonged airway explant culture enables study of health, disease, and viral pathogenesis. *Science advances*, 11(17), eadp0451.

Santiago-Carvalho I, et al. (2025) Sensing of extracellular ATP via P2RX7 drives lung tumor growth through regulatory T cell suppressive function. *bioRxiv : the preprint server for biology*.

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

Yasumizu Y, et al. (2024) Single-cell transcriptome landscape of circulating CD4+ T cell populations in autoimmune diseases. *Cell genomics*, 4(2), 100473.

Perez-Bermejo JA, et al. (2024) Functional screening in human HSPCs identifies optimized protein-based enhancers of Homology Directed Repair. *Nature communications*, 15(1), 2625.

Solovyeva AI, et al. (2024) Dysregulation of Transposon Transcription Profiles in Cancer Cells Resembles That of Embryonic Stem Cells. *Current issues in molecular biology*, 46(8), 8576.