

Resource Summary Report

Generated by SPARC SAWG on Sep 16, 2026

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: 20260912T200036+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 75 mentions in open access literature.

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

Börner K, et al. (2026) SenNet Portal: Build, Optimization and Usage. bioRxiv : the preprint server for biology.

Shi H, et al. (2026) Chemotherapy-induced reactive myelopoiesis promotes expansion of immunosuppressive neutrophil-like monocytes in mice and humans. JCI insight, 11(10).

Sonthalia S, et al. (2026) NeMO Analytics: a compendium of transcriptomic data for the exploration of neocortical development. Nature neuroscience, 29(4), 978.

Xu J, et al. (2026) A deep adversarial network model for multi-task analysis of single-cell omics data. Briefings in bioinformatics, 27(2).

Altendorf L, et al. (2026) Molecular changes during AT/RT progression associated with epithelial-mesenchymal transition and extracellular matrix changes. Acta neuropathologica, 152(1).

Rosenbaum E, et al. (2026) Tumor and Immune Dynamics Following Sequential CDK4/6 and PD-1 Inhibition: Results from a Phase 2 Study in Dedifferentiated Liposarcoma. Cancer research communications, 6(2), 437.

Foster KA, et al. (2026) Tumour-intrinsic features shape T cell differentiation through precursor to symptomatic multiple myeloma. Nature communications, 17(1).

Randolph HE, et al. (2026) Widespread gene-environment interactions shape the immune response to SARS-CoV-2 infection in hospitalized COVID-19 patients. Nature communications, 17(1).

Farsi Z, et al. (2026) Aberrant mRNA splicing and impaired hippocampal neurogenesis in Grin2b mutant mice. iScience, 29(2), 114700.

Leu JS, et al. (2026) Combined inhibition of S100A4 and TIGIT suppresses late-stage breast cancer metastasis. Cancer letters, 649, 218491.

Luquez T, et al. (2025) Cell type-specific associations with Alzheimer's Disease conserved across racial and ethnic groups. bioRxiv : the preprint server for biology.

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.

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

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

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.

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*.

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.

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.

Ahooyi TM, et al. (2025) The Data Distillery: A Graph Framework for Semantic Integration and Querying of Biomedical Data. *bioRxiv : the preprint server for biology*.