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: web application, software resource

Defining Citation: DOI: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

Funding:

Availability: Free, Freely available

Resource Name: Azimuth

Resource ID: SCR_021084

Record Creation Time: 20220129T080353+0000

Record Last Update: 20250412T060313+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 36 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

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.

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

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.

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.

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

Xie J, et al. (2024) Cytosolic DNA sensors in neurodegenerative diseases: from physiological defenders to pathological culprits. EMBO molecular medicine, 16(4), 678.

Guerrero-Murillo M, et al. (2024) Integrative single-cell multi-omics of CD19-CARpos and CARneg T cells suggest drivers of immunotherapy response in B cell neoplasias. Cell reports. Medicine, 5(11), 101803.

Lamba R, et al. (2024) MatriCom: a scRNA-Seq data mining tool to infer ECM-ECM and cell-ECM communication systems. bioRxiv : the preprint server for biology.

Liu A, et al. (2024) Discovery of optimal cell type classification marker genes from single cell RNA sequencing data. bioRxiv : the preprint server for biology.

Börner K, et al. (2024) Human BioMolecular Atlas Program (HuBMAP): 3D Human Reference Atlas Construction and Usage. bioRxiv : the preprint server for biology.

Subedi S, et al. (2024) A scalable approach to topic modelling in single-cell data by approximate pseudobulk projection. Life science alliance, 7(10).

Hou W, et al. (2024) Assessing GPT-4 for cell type annotation in single-cell RNA-seq analysis. Nature methods, 21(8), 1462.

Vu Manh TP, et al. (2024) SARS-CoV2 infection in whole lung primarily targets macrophages that display subset-specific responses. Cellular and molecular life sciences : CMLS, 81(1), 351.

Nicholls K, et al. (2024) Bayesian clustering with uncertain data. PLoS computational biology, 20(9), e1012301.

D'Angelo SP, et al. (2024) Biomarker Analyses Investigating Disease Biology and Associations with Outcomes in the JAVELIN Merkel 200 Trial of Avelumab in Metastatic Merkel Cell Carcinoma. Clinical cancer research : an official journal of the American Association for Cancer Research, 30(19), 4352.

Hwang JY, et al. (2024) Exploring the Expression and Function of T Cell Surface Markers Identified through Cellular Indexing of Transcriptomes and Epitopes by Sequencing. Yonsei medical journal, 65(9), 544.

Sikkema L, et al. (2023) An integrated cell atlas of the lung in health and disease. Nature medicine, 29(6), 1563.

Lake BB, et al. (2023) An atlas of healthy and injured cell states and niches in the human kidney. Nature, 619(7970), 585.

Missarova A, et al. (2023) Sensitive cluster-free differential expression testing. bioRxiv : the preprint server for biology.

Madissoon E, et al. (2023) A spatially resolved atlas of the human lung characterizes a gland-associated immune niche. Nature genetics, 55(1), 66.