

Resource Summary Report

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GeneSwitches

RRID:SCR_022826

Type: Tool

Proper Citation

GeneSwitches (RRID:SCR_022826)

Resource Information

URL: <https://geneswitches.ddnetbio.com/>

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Description: Software tool to discover order of gene expression and functional events during cell state transitions at single cell resolution. Works on any single cell trajectory or pseudo time ordering of cells to discover genes that act as on/off switches between cell states and ordering at which these switches take place. Takes any single-cell pseudo-time trajectory and determines precise order of gene expression and functional event changes over time.

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

Defining Citation: [PMID:32058565](#)

Keywords: Ordering gene expression and functional events, single cell experiments, cell state transitions at single cell resolution, discover genes switches between cell states

Funding: Singapore National Research Foundation

Availability: Free, Available for download, Freely available

Resource Name: GeneSwitches

Resource ID: SCR_022826

Alternate URLs: <https://github.com/SGDDNB/GeneSwitches>

Record Creation Time: 20221006T194909+0000

Record Last Update: 20260818T043716+0000

Ratings and Alerts

No rating or validation information has been found for GeneSwitches.

No alerts have been found for GeneSwitches.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 11 mentions in open access literature.

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

Tong Z, et al. (2026) SLC25A37 as a novel therapeutic target for benign prostatic hyperplasia: integrative analyses of single-cell RNA sequencing and genome-wide association studies. Open medicine (Warsaw, Poland), 21(1), 20251371.

Zhu G, et al. (2026) Deciphering CD4+ Naive T cell-mediated divergent pathogenic links between type 2 diabetes and pathologic scarring via an integrated multi-omics approach. International journal of surgery (London, England), 112(4), 9378.

Wang X, et al. (2026) Integrating Single-Cell Transcriptomics and Mendelian Randomization to Identify RAC1 as a Causal Metabolic Driver of Pericyte Dysfunction in Systemic Sclerosis. Mediators of inflammation, 2026(1), e6166654.

Yu Q, et al. (2025) Causal genes identification of giant cell arteritis in CD4+???Memory t cells: an integration of multi-omics and expression quantitative trait locus analysis. Inflammation research : official journal of the European Histamine Research Society ... [et al.], 74(1), 3.

Lusby R, et al. (2025) Pan-cancer drivers of metastasis. Molecular cancer, 24(1), 2.

Li B, et al. (2025) From Invaginating Site to Deep Lesion: Spatial Transcriptomics Unravels Ectopic Endometrial Penetration Features in Adenomyosis. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(20), e2411752.

Wang K, et al. (2025) Exploring the Role of Ccn3 in Type III Cell of Mice Taste Buds. Journal of neurochemistry, 169(1), e16291.

Vercauteren Drubbel A, et al. (2023) Single-cell transcriptomics uncovers the differentiation of a subset of murine esophageal progenitors into taste buds in vivo. Science advances, 9(10), eadd9135.

Xia Y, et al. (2023) Spatial single cell analysis of tumor microenvironment remodeling pattern in primary central nervous system lymphoma. Leukemia, 37(7), 1499.

Quah HS, et al. (2023) Single cell analysis in head and neck cancer reveals potential immune evasion mechanisms during early metastasis. Nature communications, 14(1), 1680.

Hu H, et al. (2022) Dental niche cells directly contribute to tooth reconstitution and morphogenesis. *Cell reports*, 41(10), 111737.