

Resource Summary Report

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

[popscle](#)

RRID:SCR_026707

Type: Tool

Proper Citation

popscle (RRID:SCR_026707)

Resource Information

URL: <https://github.com/statgen/popscle>

Proper Citation: popscle (RRID:SCR_026707)

Description: Software suite of population scale analysis tools for single-cell genomics data.

Resource Type: software toolkit, software resource

Keywords: population scale analysis tools, single-cell genomics data,

Availability: Free, Available for download, Freely available

Resource Name: popscle

Resource ID: SCR_026707

License: Apache-2.0 license

Record Creation Time: 20250407T215450+0000

Record Last Update: 20260810T040917+0000

Ratings and Alerts

No rating or validation information has been found for popscle.

No alerts have been found for popscle.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 17 mentions in open access literature.

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

Sasaki T, et al. (2026) A CD57+CD8+ T cell subset links T cell cytotoxicity to fibrotic lung disease in systemic sclerosis. *The Journal of clinical investigation*, 136(9).

Zhang Y, et al. (2026) Dynamic heterogeneity towards drug resistance in AML cells is primarily driven by epigenomic mechanism unveiled by multi-omics analysis. *Journal of advanced research*, 80, 487.

Espinosa-Jaime A, et al. (2026) SiteCELL enables on-site PBMCs purification and cryopreservation for immune single-cell profiling of underrepresented ancestries. *iScience*, 29(6), 115961.

Patop IL, et al. (2025) Remote and partial clocks expand the circadian neuronal network, driving widespread molecular rhythmicity in *Drosophila*. *bioRxiv : the preprint server for biology*.

Elison W, et al. (2025) Single cell multiomics reveals drivers of metabolic dysfunction-associated steatohepatitis. *medRxiv : the preprint server for health sciences*.

Wilson AM, et al. (2025) Transcriptional impacts of substance use disorder and HIV on human ventral midbrain neurons and microglia. *Nature communications*, 16(1), 9123.

Hennick K, et al. (2025) Sex differences in the developing human cortex intersect with genetic risk of neurodevelopmental disorders. *bioRxiv : the preprint server for biology*.

Alvarez M, et al. (2025) Integrated ambient modeling and genetic demultiplexing of single-cell RNA+ATAC multiome experiments with Ambimux. *bioRxiv : the preprint server for biology*.

Neely J, et al. (2025) Discovery of tissue-specific proteomic signatures in juvenile dermatomyositis highlights pathways reflecting persistent disease activity, clinical heterogeneity, and myositis-specific autoantibody subtype. *Annals of the rheumatic diseases*, 84(11), 1836.

Mummey HM, et al. (2025) Single cell and spatial characterization of the human pancreas reveals drivers of beta cell dysfunction in cystic fibrosis. *bioRxiv : the preprint server for biology*.

Masrori P, et al. (2025) C9orf72 hexanucleotide repeat expansions impair microglial response in ALS. *Nature neuroscience*, 28(11), 2217.

Dombrovski M, et al. (2025) Molecular gradients shape synaptic specificity of a visuomotor transformation. *Nature*, 644(8076), 453.

Bonanno SL, et al. (2023) Transcriptional changes in specific subsets of *Drosophila* neurons following inhibition of the serotonin transporter. *Research square*.

Liu J, et al. (2022) Combined Single Cell Transcriptome and Surface Epitope Profiling Identifies Potential Biomarkers of Psoriatic Arthritis and Facilitates Diagnosis via Machine Learning. *Frontiers in immunology*, 13, 835760.

Neely J, et al. (2022) Multi-Modal Single-Cell Sequencing Identifies Cellular Immunophenotypes Associated With Juvenile Dermatomyositis Disease Activity. *Frontiers in immunology*, 13, 902232.

Alber S, et al. (2022) Single Cell Transcriptome and Surface Epitope Analysis of Ankylosing Spondylitis Facilitates Disease Classification by Machine Learning. *Frontiers in immunology*, 13, 838636.

Mylka V, et al. (2022) Comparative analysis of antibody-??and lipid-based multiplexing methods for single-cell RNA-seq. *Genome biology*, 23(1), 55.