

Resource Summary Report

Generated by [dkNET](#) on Aug 20, 2026

GSEAPy

RRID:SCR_025803

Type: Tool

Proper Citation

GSEAPy (RRID:SCR_025803)

Resource Information

URL: <https://gseapy.readthedocs.io/en/latest/>

Proper Citation: GSEAPy (RRID:SCR_025803)

Description: Software Python package for performing gene set enrichment analysis. Used for characterizing gene expression changes by analysis of large single-cell datasets.

Synonyms: Gene Set Enrichment Analysis python

Resource Type: software toolkit, source code, software resource

Defining Citation: [PMID:36426870](#)

Keywords: gene set enrichment analysis, characterizing gene expression changes, large single-cell datasets,

Funding: NIDA 5U01DA04439902

Availability: Free, Available for download, Freely available

Resource Name: GSEAPy

Resource ID: SCR_025803

Alternate URLs: <https://github.com/zqfang/GSEAPy>

License: BSD-3-Clause license

Record Creation Time: 20240927T053302+0000

Record Last Update: 20260820T055053+0000

Ratings and Alerts

No rating or validation information has been found for GSEApv.

No alerts have been found for GSEApv.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 185 mentions in open access literature.

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

Ishiguro S, et al. (2026) A multi-kingdom genetic barcoding system for precise clone isolation. *Nature biotechnology*, 44(4), 616.

Zhang M, et al. (2026) A self-adaptive and versatile tool for eliminating multiple undesirable variations from large-scale transcriptomes. *Nature biomedical engineering*, 10(3), 413.

Jiménez-Sánchez A, et al. (2026) Transcriptomic Plasticity Is a Hallmark of Metastatic Pancreatic Cancer. *Cancer research*, 86(7), 1769.

Bradford B, et al. (2026) Nickel exposure disrupts epigenetic repression of developmental genes in mouse embryonic stem cells. *Toxicology and applied pharmacology*, 511, 117810.

Maravall-López J, et al. (2026) Ancient DNA reveals that natural selection has upregulated the immune system over the last 10,000 years. *bioRxiv : the preprint server for biology*.

Whittle J, et al. (2026) Single-cell atlas of AML reveals age-related gene regulatory networks in t(8;21) AML. *eLife*, 14.

He C, et al. (2026) Multimodal framework for the joint analysis of single-cell RNA and T cell receptor sequencing data predicts T cell response to cancer immunotherapy. *Nature communications*, 17(1).

Ko H, et al. (2026) Commensal microbe-derived butyrate enhances T follicular helper cell function to boost mucosal vaccine efficacy. *Microbiome*, 14(1), 37.

Alsugair Z, et al. (2026) Insights From Mutational and Transcriptomic Profiles in Epithelial-myoepithelial Carcinoma. *The American journal of surgical pathology*, 50(7), 716.

Chhabra NF, et al. (2026) High-quality acinar cell isolation enables single-cell analysis of healthy and injured pancreas. *Cell reports methods*, 6(5), 101415.

Nwizu C, et al. (2026) Scalable nonparametric clustering with unified marker gene selection for single-cell RNA-seq data. *Cell reports methods*, 6(3), 101329.

He Q, et al. (2026) Single-cell omics data-driven decoding of tumor clonal evolution through reinforcement learning. *Genome medicine*, 18(1).

Kawazu M, et al. (2026) Genomic and Transcriptomic Analysis of High-Grade Endometrial Carcinoma Reveals Biological Heterogeneity and Molecular Classification Challenges. *Cancer research communications*, 6(4), 961.

Stefanska M, et al. (2026) Cardiac Macrophages Exhibit Dynamic Heterogeneity and Functional Specialization During Experimental Autoimmune Myocarditis. *Cells*, 15(12).

Paroni M, et al. (2026) Pro-inflammatory intestinal Th17-cells are tissue-resident, accumulate in the epithelia in Crohn's disease, and predict unresponsiveness to vedolizumab. *Journal of Crohn's & colitis*, 20(6).

Yu ZM, et al. (2026) scVMAP: a comprehensive platform for integrating single-cell chromatin accessibility regions with causal variants. *Nucleic acids research*, 54(D1), D1270.

Lundgren P, et al. (2026) Proteomic Profile in Retinopathy of Prematurity: A Secondary Analysis of the Mega Donna Mega Randomized Clinical Trial. *JAMA ophthalmology*, 144(2), 174.

Yuki R, et al. (2026) Targeting the splicing factor CWC22 induces mitotic slippage through repression of BubR1 expression and CDK1 activity in cancer cells. *The Journal of biological chemistry*, 111148.

Stier MT, et al. (2026) Metabolic adaptations rewire CD4+ T cells in a subset-specific manner in human critical illness with and without sepsis. *Nature immunology*, 27(2), 236.

Anderson BJ, et al. (2026) Proteomic and Lipidomic Atlas of Gut-Associated Lymph and Venous Depots in Female Piglets. *Arteriosclerosis, thrombosis, and vascular biology*, 46(3), e323883.