

Resource Summary Report

Generated by T1D on Jul 29, 2026

GSEAPy

RRID:SCR_025803

Type: Tool

Proper Citation

GSEAPy (RRID:SCR_025803)

Resource Information

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

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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: source code, software toolkit, 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: 20260729T044629+0000

Ratings and Alerts

No rating or validation information has been found for GSEAPy.

No alerts have been found for GSEAPy.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 127 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Carver S, et al. (2026) Discovery of disease-associated cellular states using ResidPCA in single-cell RNA and ATAC sequencing data. HGG advances, 7(1), 100538.

Kim JS, et al. (2025) Male preference for TERT alterations and HBV integration in young-age HBV-related HCC: implications for sex disparity. Clinical and molecular hepatology, 31(2), 509.

Yi W, et al. (2025) In silico characterization of defense system hotspots in Acinetobacter spp. Communications biology, 8(1), 39.

Zhang M, et al. (2025) Identification of Critical Phosphorylation Sites Enhancing Kinase Activity With a Bimodal Fusion Framework. Molecular & cellular proteomics : MCP, 24(1), 100889.

Sato T, et al. (2025) Sustained inhibition of CSF1R signaling augments antitumor immunity through inhibiting tumor-associated macrophages. JCI insight, 10(1).

Tan B, et al. (2025) CeiTEA: Adaptive Hierarchy of Single Cells with Topological Entropy. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(26), e2503539.

Wang Y, et al. (2025) FmH2ST: foundation model-based spatial transcriptomics generation from histological images. Nucleic acids research, 53(17).

Shneyderman A, et al. (2025) Evaluation of (Z)-endoxifen as a potential therapy for glioblastoma multiforme through computational and experimental analyses. Scientific reports, 15(1), 38225.

Case AG, et al. (2025) Low-dose interleukin-2 induces clonal expansion of BACH2-repressed effector regulatory T cells following acute coronary syndrome. Nature cardiovascular research, 4(6), 727.

Cangkrama M, et al. (2025) MIRO2-mediated mitochondrial transfer from cancer cells induces cancer-associated fibroblast differentiation. Nature cancer, 6(10), 1714.

Lin MY, et al. (2025) Unveiling chromatin dynamics with virtual epigenome. Nature communications, 16(1), 3491.

Onat B, et al. (2025) Cell Storage Conditions Impact Single-Cell Proteomic Landscapes. *Journal of proteome research*, 24(4), 1586.

Kabatnik S, et al. (2025) Deep visual proteomics reveals DNA replication stress as a hallmark of signet ring cell carcinoma. *NPJ precision oncology*, 9(1), 37.

Ogden S, et al. (2025) Phenotypic heterogeneity and plasticity in colorectal cancer metastasis. *Cell genomics*, 5(7), 100881.

Tai H, et al. (2025) Computational tracking of cell origins using CellSexID from single-cell transcriptomes. *Cell reports methods*, 101181.

Munquad S, et al. (2025) Biologically explainable multi-omics feature demonstrates greater learning potential by identifying tissue of origin, stages, and subtypes for pan-cancer classification. *Scientific reports*, 15(1), 40627.

Ji P, et al. (2025) Single-cell delineation of the microbiota-gut-brain axis: Probiotic intervention in Chd8 haploinsufficient mice. *Cell genomics*, 5(2), 100768.

Ng CW, et al. (2025) Spatial transcriptome reveals histology-correlated immune signature learnt by deep learning attention mechanism on H&E-stained images for ovarian cancer prognosis. *Journal of translational medicine*, 23(1), 113.

Watson BR, et al. (2025) Spatial transcriptomics of healthy and fibrotic human liver at single-cell resolution. *Nature communications*, 16(1), 319.

Manda SS, et al. (2025) Overcoming intra-tumoral heterogeneity for biomarker discovery in the high-grade serous ovarian cancer proteome. *NPJ precision oncology*, 9(1), 172.