

Resource Summary Report

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Gene Set Enrichment Analysis

RRID:SCR_003199

Type: Tool

Proper Citation

Gene Set Enrichment Analysis (RRID:SCR_003199)

Resource Information

URL: <http://www.broadinstitute.org/gsea/>

Proper Citation: Gene Set Enrichment Analysis (RRID:SCR_003199)

Description: Software package for interpreting gene expression data. Used for interpretation of a large-scale experiment by identifying pathways and processes.

Abbreviations: GSEA

Synonyms: GSEA, Gene Set Enrichment Analysis, Gene Set Enrichment Analysis (GSEA)

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

Defining Citation: [PMID:16199517](#)

Keywords: gene, expression, profile, pathway, data, set, phenotype, genome, enrichment, RNA, analysis, bio.tools, bio.tools

Funding: NCI ;
NIGMS ;
NIH

Availability: Free, Freely available

Resource Name: Gene Set Enrichment Analysis

Resource ID: SCR_003199

Alternate IDs: SCR_016882, nif-0000-30629, biotools:gsea, OMICS_02279

Alternate URLs: <http://www.broad.mit.edu/gsea>, <https://bio.tools/gsea>

License: BSD license

Record Creation Time: 20220129T080217+0000

Record Last Update: 20260905T132459+0000

Ratings and Alerts

No rating or validation information has been found for Gene Set Enrichment Analysis.

No alerts have been found for Gene Set Enrichment Analysis.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 20985 mentions in open access literature.

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

Takahashi J, et al. (2026) Spatial Multiomic Analyses Reveal Carcinogenic Pathways in End-Stage Renal Disease. Cancer discovery, 16(3), 478.

Prasad M, et al. (2026) Genomic Enrichment and Functional Impact of TP53 and CYLD Alterations in Recurrent and Metastatic HPV-Associated Head and Neck Cancer. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(9), 1809.

Cappadona C, et al. (2026) Multi-omics identifies oxidative stress, prothrombotic pathways, and lactoperoxidase variants as key factors in COVID-19 severity. EBioMedicine, 123, 106111.

Sato K, et al. (2026) Aberrant Hippo-YAP/TEAD Signaling Drives Malignant Transcriptional Reprogramming in External Auditory Canal Squamous Cell Carcinoma. Cancer research communications, 6(2), 260.

Ye J, et al. (2026) Baseline Tumor Features and Systemic Immune Dynamics Underlying Efficacy in MSS Metastatic Colorectal Cancer Treated with Regorafenib, Ipilimumab, and Nivolumab. Cancer immunology research, 14(4), 585.

Li H, et al. (2026) Tumor Extracellular Vesicles IncOSLMT Drives Lung Inflammatory Premetastatic Niche Formation in Osteosarcoma via m6A-Dependent hnRNPA2B1/COX-2 Axis. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 13(17), e19490.

Ding C, et al. (2026) MYO1G Facilitates Caveolin 1-Mediated Endocytosis of the N-Terminal Fragments of Gasdermin E to Restrain Pyroptosis and Chemotherapy Efficacy. Cancer research, 86(15), 3741.

Ben-Shalom N, et al. (2026) Decoy antibodies block extracellular HSP70, prevent self-signaling, and inhibit melanoma cell survival. *Cell reports*, 45(5), 117300.

Gui S, et al. (2026) Multiomics Profiling Reveals Distinct Immunosuppression and Metabolic Dysregulation in Aggressive Subtypes of Thyroid Cancer. *Molecular & cellular proteomics : MCP*, 25(3), 101513.

Sekiguchi N, et al. (2026)

Circ72309 modulates gemcitabine metabolism and gemcitabine sensitivity in pancreatic cancer: Serum Circ72309 levels as a potential predictor of treatment response

. *International journal of oncology*, 68(3).

Bloomfield M, et al. (2026) Cell and Nuclear Size Is Associated with Chromosomal Instability and Tumorigenicity in Cancer Cells That Undergo Whole Genome Doubling. *Cancer research*, 86(9), 2126.

Lan L, et al. (2026) A Jagged1-regulated hybrid-EMT state identifies pancreatic cancer stem cells. *Cell reports*, 45(2), 116909.

Ji Y, et al. (2026) Serotonin Modulates Lineage Plasticity in Neuroendocrine Prostate Cancer via Epigenetic Reprogramming. *Cancer discovery*, 16(4), 760.

Muppirala AN, et al. (2026) Tachykinin signaling defines distinct populations of glia in the enteric nervous system. *Neuron*.

Wu X, et al. (2026) Locus-Specific Human Endogenous Retrovirus ERVK18 Expression Indicates an Inflamed Microenvironment and Favorable Immunotherapy Outcome in Small Cell Lung Cancer. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(11), 2214.

Yan C, et al. (2026) RAS/MEK/PI3K pathway inhibition augments response to CD40 agonism by targeting CD11b+ Bregs thereby overcoming melanoma PD1-resistance. *Nature communications*, 17(1), 162.

Tao Y, et al. (2026) TENT5A Maintains MYC mRNA Stability to Enhance Osteosarcoma Stemness. *Cancer research*, 86(9), 2161.

Molotkova A, et al. (2026) ROME, an Ancient Gene with a Novel Function in Vertebrates, Is a Key Modulator of Embryonal Development and Cancer Metastasis. *Cancer research communications*, 6(3), 477.

Sun W, et al. (2026) Reconstruction of T cell infiltration in an osteosarcoma PDX-organoid interactive biobank for personalized immunotherapy. *Cell reports. Medicine*, 7(3), 102644.

Fukumura K, et al. (2026) Ionizing Radiation Enhances Prognostically Significant Cellular Immunity Programs in the Brain Metastasis Microenvironment. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(11), 2305.