

# Resource Summary Report

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## Gene Expression Profiling Interactive Analysis

RRID:SCR\_018294

Type: Tool

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### Proper Citation

Gene Expression Profiling Interactive Analysis (RRID:SCR\_018294)

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### Resource Information

**URL:** <http://gepia.cancer-pku.cn>

**Proper Citation:** Gene Expression Profiling Interactive Analysis (RRID:SCR\_018294)

**Description:** Web server for cancer and normal gene expression profiling and interactive analyses. Interactive web server for analyzing RNA sequencing expression data of tumors and normal samples from TCGA and GTEx projects, using standard processing pipeline. Provides customizable functions such as tumor or normal differential expression analysis, profiling according to cancer types or pathological stages, patient survival analysis, similar gene detection, correlation analysis and dimensionality reduction analysis.

**Abbreviations:** GEPIA

**Resource Type:** service resource, web service, analysis service resource, software resource, production service resource, data access protocol

**Defining Citation:** [PMID:28407145](#)

**Keywords:** Cancer gene expression, normal gene expression, analysis, RNA sequencing, expression data, TCGA project, GTEx project, patient survival analysis, correlation analysis

**Related Condition:** Cancer

**Funding:** Peking University ;  
National Natural Science Foundation of China

**Availability:** Free, Freely available

**Resource Name:** Gene Expression Profiling Interactive Analysis

**Resource ID:** SCR\_018294

**Record Creation Time:** 20220129T080339+0000

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## Ratings and Alerts

No rating or validation information has been found for Gene Expression Profiling Interactive Analysis.

No alerts have been found for Gene Expression Profiling Interactive Analysis.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 5635 mentions in open access literature.

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

Cao Z, et al. (2026) Study on the mechanism of PSENEN in modulating cisplatin resistance in NSCLC through stromal cell interactions. International immunopharmacology, 169, 116037.

Liu S, et al. (2026) Clinical significance and molecular mechanism of CDX2-CBX3 regulatory axis in lung adenocarcinoma progression. Translational oncology, 63, 102590.

Munyembaraga V, et al. (2026) MiR-493-3p suppresses the DPY-30 histone methyltransferase complex regulatory subunit to attenuate gefitinib resistance in lung cancer. Translational oncology, 63, 102570.

Ding D, et al. (2026) Ephrin?B2 promotes gastric cancer growth by inhibiting apoptosis and regulating the cell cycle via the Wnt/??catenin signaling pathway. International journal of oncology, 68(1).

Meng Y, et al. (2026) c?Myc?regulated RPLP0 via the ROS?mediated JAK2/STAT3 positive feedback loop facilitates hepatocellular carcinoma malignancy progression. International journal of oncology, 68(1).

Liao X, et al. (2026) S100B drives glioblastoma invasion and migration through TGF??2? mediated epithelial?mesenchymal transition. Oncology reports, 55(1).

Egea-Rodriguez S, et al. (2025) RECQL4 affects MHC class II-mediated signalling and favours an immune-evasive signature that limits response to immune checkpoint inhibitor therapy in patients with malignant melanoma. Clinical and translational medicine, 15(1), e70094.

Qiu SQ, et al. (2025) GLUT1 as a generic biomarker enables near-infrared fluorescence molecular imaging guided precise intraoperative tumor detection in breast cancer. European journal of nuclear medicine and molecular imaging, 52(6), 2171.

Zampieri C, et al. (2025) The urokinase receptor/uPAR is a major effector of p53 gain-of-function mutations in gemcitabine-treated pancreatic ductal adenocarcinoma. *The Journal of biological chemistry*, 301(9), 110561.

Hiltunen J, et al. (2025) Androgen receptor-mediated assisted loading of the glucocorticoid receptor modulates transcriptional responses in prostate cancer cells. *Genome research*, 35(8), 1717.

Yu J, et al. (2025) Resilience and vulnerabilities of tumor cells under purine shortage stress. *Clinical cancer research : an official journal of the American Association for Cancer Research*.

Xiao G, et al. (2025) Single-cell RNA-sequencing and spatial transcriptomic analysis reveal a distinct population of APOE- cells yielding pathological lymph node metastasis in papillary thyroid cancer. *Clinical and translational medicine*, 15(1), e70172.

Li X, et al. (2025) SLC4A11 is a targetable marker correlated with therapeutic responses in ovarian cancer. *Journal of ovarian research*, 18(1), 167.

Mu H, et al. (2025) Methionine intervention induces PD-L1 expression to enhance the immune checkpoint therapy response in MTAP-deleted osteosarcoma. *Cell reports. Medicine*, 6(3), 101977.

Xiaoxia F, et al. (2025) CD147 regulates the Rap1 signaling pathway to promote proliferation, migration, and invasion, and inhibit apoptosis in colorectal cancer cells. *Scientific reports*, 15(1), 13647.

Tang X, et al. (2025) Inhibition of autotaxin activity with IOA-289 decreases fibrosis in mouse E0771 breast tumors. *International journal of cancer*, 157(6), 1205.

Shang K, et al. (2025) CD97-directed CAR-T cells with enhanced persistence eradicate acute myeloid leukemia in diverse xenograft models. *Cell reports. Medicine*, 6(6), 102148.

Wang W, et al. (2025) FBXW5 Promotes Epithelial-Mesenchymal Transition in Lung Adenocarcinoma Through the KLF13/TROAP Signaling Pathway. *Molecular carcinogenesis*.

Kong F, et al. (2025) MEF2D regulates T-cell function via CD70-CD27 signaling and promotes immune evasion in hepatocellular carcinoma. *Journal of immunology (Baltimore, Md. : 1950)*, 214(11), 3162.

Ruckert MT, et al. (2025) DUSP6 is upregulated in metastasis and influences migration and metabolism in pancreatic cancer cells. *Scientific reports*, 15(1), 33996.