

Resource Summary Report

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Gene Expression Profiling Interactive Analysis 2

RRID:SCR_026154

Type: Tool

Proper Citation

Gene Expression Profiling Interactive Analysis 2 (RRID:SCR_026154)

Resource Information

URL: <http://gepia2.cancer-pku.cn/#index>

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Description: Enhanced web server for large-scale expression profiling and interactive analysis. GEPIA2 is updated and enhanced version of GEPIA, offering more functionalities, higher resolution data analysis, and additional features like ability to analyze specific cancer subtypes, quantify gene signatures based on single-cell sequencing studies, and allow users to upload their own RNA-seq data for comparison with the TCGA and GTEx datasets; essentially providing more comprehensive and advanced platform for gene expression analysis compared to the original GEPIA version.

Synonyms: Gene Expression Profiling Interactive Analysis 2

Resource Type: software resource, data access protocol, web service

Defining Citation: [PMID:31114875](#)

Keywords: gene expression analysis, large-scale expression profiling, interactive analysis, quantify gene signatures,

Funding: National Natural Science Foundation of China ;
Peking University

Availability: Free, Freely available

Resource Name: Gene Expression Profiling Interactive Analysis 2

Resource ID: SCR_026154

Alternate IDs: GEPIA2

Alternate URLs: <http://gepia2.cancer-pku.cn/>

Record Creation Time: 20241210T053256+0000

Record Last Update: 20260801T042941+0000

Ratings and Alerts

No rating or validation information has been found for Gene Expression Profiling Interactive Analysis 2.

No alerts have been found for Gene Expression Profiling Interactive Analysis 2.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 545 mentions in open access literature.

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

Pan K, et al. (2026) Lysine methylation-mediated SMYD2 degradation by casticin sensitizes non-small-cell lung cancer cells to osimertinib therapy. *Biochemical pharmacology*, 243(Pt 2), 117562.

Li H, et al. (2026) PDZRN4 suppresses lung adenocarcinoma progression via inhibiting ubiquitin-mediated HIF-1A degradation. *Oncogene*, 45(4), 577.

Cao H, et al. (2026) TDP2 drives immune evasion and metastatic progression in prostate cancer. *PloS one*, 21(1), e0339607.

Hu X, et al. (2026) Pan-cancer bone metastasis atlas at single-cell resolution identifies a distinct tumor-associated macrophage subset for mediating Denosumab-induced immunosensitization in lung cancer bone metastasis. *International journal of biological sciences*, 22(1), 365.

Gulbey O, et al. (2026) Integrated Bioinformatics and Experimental Analysis of Argonaute Family Members in Pancreatic Adenocarcinoma. *In vivo (Athens, Greece)*, 40(1), 123.

Wen J, et al. (2026) Fibrotic scar formation after cerebral ischemic stroke: Targeting the Sonic hedgehog signaling pathway for scar reduction. *Neural regeneration research*, 21(2), 756.

Luan R, et al. (2026) Pan-cancer multi-omics reveals DCAF7 as an immune-modulating prognostic driver and Wnt/?-catenin activator in hepatocellular carcinoma. *Clinical and translational medicine*, 16(1), e70572.

Yang YF, et al. (2026) Integrative analysis identifies PIGK as an oncogenic glycosylphosphatidylinositol transamidase subunit with prognostic, immunological, and therapeutic relevance in head and neck cancer. *International journal of medical sciences*,

23(1), 161.

Chen K, et al. (2026) Liquid-liquid phase separation of PHLDB2 promotes oral squamous cell carcinoma metastasis through regulating epithelial mesenchymal transition and PIK3CA expression. *Molecular medicine reports*, 33(1).

Hayashi M, et al. (2026) PDGFR γ governs multiple cellular signals and plays a protective role in tumor progression. *Neoplasia (New York, N.Y.)*, 71, 101248.

Chen L, et al. (2026) RNF39 promotes colorectal cancer progression by driving RINT1 degradation and suppressing ER stress-induced apoptosis. *Clinical and translational medicine*, 16(1), e70577.

Rodrigues-Junior DM, et al. (2026) Loss of ErbB3 redirects Integrin α 1 from early endosomal recycling to secretion in extracellular vesicles. *The Journal of cell biology*, 225(1).

Dorstyn L, et al. (2026) Caspase-2 deficiency drives pathogenic liver polyploidy and increases age-associated hepatocellular carcinoma in mice. *Science advances*, 12(1), eaeb2571.

Jin SK, et al. (2026) Deubiquitomic and bioinformatic analyses in cisplatin-treated lung cancer cells. *International journal of medical sciences*, 23(1), 1.

Zhong L, et al. (2026) Loss of FAT1 drives cyclophosphamide resistance in breast cancer via the Wnt/ β -Catenin pathway. *International journal of biological sciences*, 22(1), 447.

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).

Luo Y, et al. (2025) Single-cell clonal lineage tracing identifies the transcriptional program controlling the cell fate decisions by neoantigen-specific CD8 + T cells. *bioRxiv : the preprint server for biology*.

Lahusen A, et al. (2025) An immune responsive tumor microenvironment imprints into PBMCs and predicts outcome in advanced pancreatic cancer: lessons from the PREDICT trial. *Molecular cancer*, 24(1), 202.

Liu S, et al. (2025) AEnet: a practical tool to construct the splicing-associated phenotype atlas at a single cell level. *GigaScience*, 14.

Digomann D, et al. (2025) Soluble TIM-3 and galectin-9 predict survival in gastric and gastroesophageal junction cancer. *iScience*, 28(11), 113871.