# Resource Summary Report

Generated by NIF on May 25, 2025

## Gene Expression Profiling Interactive Analysis

RRID:SCR_018294
Type: Tool

### Proper Citation

Gene Expression Profiling Interactive Analysis (RRID:SCR_018294)

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

**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

**Record Last Update:** 20250525T031546+0000

## 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.

## Data and Source Information

**Source:** SciCrunch Registry

## Usage and Citation Metrics

We found 5025 mentions in open access literature.

**Listed below are recent publications.** The full list is available at NIF.

Li H, et al. (2025) Integrated multi-omics demonstrates enhanced antitumor efficacy of donafenib combined with FADS2 inhibition in hepatocellular carcinoma. Translational oncology, 51, 102142.

Elhinnawi MA, et al. (2025) GPNMB is a novel binding partner of FGFR1 that affects tumorigenic potential through AKT phosphorylation in TNBC. Cancer science, 116(2), 432.

Huang Y, et al. (2025) OSBPL10-CNBP axis mediates hypoxia-induced pancreatic cancer development. BioFactors (Oxford, England), 51(1), e2124.

Chen J, et al. (2025) Comprehensive Analysis Identifies THEMIS2 as a Potential Prognostic and Immunological Biomarker in Glioblastoma. Cells, 14(2).

Tang C, et al. (2025) GPR137-RAB8A activation promotes ovarian cancer development via the Hedgehog pathway. Journal of experimental & clinical cancer research : CR, 44(1), 22.

Deng M, et al. (2025) Temozolomide-Promoted MGMT Transcription Contributes to Chemoresistance by Activating the ERK Signalling Pathway in Malignant Melanoma. Journal of cellular and molecular medicine, 29(3), e70380.

Tian Y, et al. (2025) CCR5 and IL-12 co-expression in CAR T cells improves antitumor efficacy by reprogramming tumor microenvironment in solid tumors. Cancer immunology, immunotherapy : CII, 74(2), 55.

Zhu Q, et al. (2025) NVP-2, in combination with Orlistat, represents a promising therapeutic strategy for acute myeloid leukemia. Cancer biology & therapy, 26(1), 2450859.

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.

Koo H, et al. (2025) Anti-proteolytic regulation of KRAS by USP9X/NDRG3 in KRAS-driven cancer development. Nature communications, 16(1), 628.

Liao S, et al. (2025) Exploration of metastasis-related signatures in osteosarcoma based on tumor microenvironment by integrated bioinformatic analysis. Heliyon, 11(1), e41358.

Lin YH, et al. (2025) ANGPTL3 overcomes sorafenib resistance via suppression of SNAI1 and CPT1A in liver cancer. Translational oncology, 52, 102250.

Shang L, et al. (2025) Statistical identification of cell type-specific spatially variable genes in spatial transcriptomics. Nature communications, 16(1), 1059.

Wan L, et al. (2025) Dissecting macrophage heterogeneity and kaempferol in lung adenocarcinoma: a single-cell transcriptomic approach and network pharmacology. Discover oncology, 16(1), 104.

Li Y, et al. (2025) PARP4 deficiency enhances sensitivity to ATM inhibitor by impairing DNA damage repair in melanoma. Cell death discovery, 11(1), 35.

Xu H, et al. (2025) CREB3L1 facilitates pancreatic tumor progression and reprograms intratumoral tumor-associated macrophages to shape an immunotherapy-resistance microenvironment. Journal for immunotherapy of cancer, 13(1).

Ahmadi M, et al. (2025) Bioinformatics analysis of mitochondrial metabolism-related genes demonstrates their importance in renal cell carcinoma. Discover oncology, 16(1), 28.

Zhang L, et al. (2025) Comprehensive analysis pinpoints CCNA2 as a prognostic and immunological biomarker in non-small cell lung cancer. BMC pulmonary medicine, 25(1), 14.

Ju Y, et al. (2025) Inactivation of glutathione S-transferase alpha 4 blocks Enterococcus faecalis-induced bystander effect by promoting macrophage ferroptosis. Gut microbes, 17(1), 2451090.

Chaharlashkar Z, et al. (2025) Metastatic melanoma: An integrated analysis to identify critical regulators associated with prognosis, pathogenesis and targeted therapies. PloS one, 20(1), e0312754.