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

Proper Citation: Gene Expression Profiling Interactive Analysis 2 (RRID:SCR_026154)

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: data access protocol, software resource, 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: 20260821T194320+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 1694 mentions in open access literature.

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

Tao H, et al. (2026) NSD1-Mediated PPAR? Methylation Enhances PTEN Activity to Suppress Glycolysis and Tumor Progression in Endometrial Cancer. Cancer research, 86(10), 2464.

Ratnawati H, et al. (2026) The ubiquitin-proteasome system is an important driver of EBV-associated nasopharyngeal carcinoma progression: a meta-analysis of transcriptomic data. Scientific reports, 16(1).

Loh D, et al. (2026) Multiaxial Biophysical Control of Oncogenic Phase Separation by Indoleamines: A Proof-of-Concept Synthesis of Landscape-Level Regulation. Journal of pineal research, 78(4), e70156.

Ma Z, et al. (2026) Elevated PTK6 expression is associated with tumor immune microenvironment remodeling and predicts poor prognosis in endometrial carcinoma. Frontiers in medicine, 13, 1842564.

Monteagudo-García Ó, et al. (2026) ZC3H13 Loss Drives Cancer Metastatic Progression by Disrupting m6A RNA Methylation. Cancer research, 86(3), 622.

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

Zhao C, et al. (2026) Progranulin promotes glioma progression via interaction with cathepsin D and serves as a diagnostic and prognostic biomarker. Discover oncology, 17(1), 336.

Li J, et al. (2026) FNDC4 Drives Metastasis and Immune Evasion in Pancreatic Cancer. Cancer research, 86(2), 349.

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.

Anderko RR, et al. (2026) Pancreatic Cancer Organoids Recapitulate Chemotherapy Response and Identify a Potent Cytotoxic T-Cell Population. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(3), 596.

Quatannens D, et al. (2026) Protein-level profiling of TIGIT axis components in human PDAC reveals immune-suppressive expression patterns. Cancer immunology, immunotherapy : CII, 75(4).

Solernó LM, et al. (2026) Combined treatment using repurposed synthetic peptide desmopressin and bevacizumab as a potential antiangiogenic strategy in osteosarcoma. Frontiers in medicine, 13, 1864843.

Yoo J, et al. (2026) Spatial Transcriptomic Landscape of Brain Metastases from Triple-Negative Breast Cancer: Comparison of Primary Tumor and Brain Metastases Using Spatial Analysis. Cancer research and treatment, 58(1), 182.

Wei Z, et al. (2026) IER3 Promotes Malignant Progression of Colorectal Cancer Through the NF-?B Pathway. International journal of genomics, 2026, 8379666.

Tang Q, et al. (2026) PTEN-AKT2 Regulates Mixed Lineage Liver Cancer Development and Sensitizes Cancer Cells to TGF? Treatment. Research square.

Wang Q, et al. (2026) Comprehensive bioinformatics analysis and clinical validation of PPP1R13L in rectal adenocarcinoma. BMC cancer, 26(1).

Chakraborty D, et al. (2026) Protumorigenic Responses of CEACAM6 in Helicobacter pylori-Infected Gastric Cancer Cells. Journal of cellular and molecular medicine, 30(2), e70869.

Chen X, et al. (2026) Helicobacter pylori promotes gastric cancer progression via UPP1-mediated uridine bypass of glycolysis. Cancer cell international, 26(1), 91.

Hsieh MS, et al. (2026) APOBEC3B/ASF1B-TGF-? signaling axis promotes epithelial-mesenchymal transition in HPV-positive oropharyngeal cancer. Journal of dental sciences, 21(1), 562.

Lu L, et al. (2026) The pseudouridine synthase PUS7 is associated with stemness and represents a potential therapeutic target in triple-negative breast cancer cells. Scientific reports, 16(1), 2411.