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: web service, data access protocol, software resource

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: 20250527T060046+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 80 mentions in open access literature.

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

Jia Y, et al. (2025) RUNX1 promotes proliferation of cervical cancer through TGFB2-MAPK pathway. Scientific reports, 15(1), 497.

Wu L, et al. (2025) Comprehensive investigation of matrix metalloproteinases in skin cutaneous melanoma: diagnostic, prognostic, and therapeutic insights. Scientific reports, 15(1), 2152.

Mi S, et al. (2025) m1A-regulated DIAPH3 promotes the invasiveness of colorectal cancer via stabilization of KRT19. Clinical & experimental metastasis, 42(2), 10.

Wang X, et al. (2025) Alternative splicing of EZH2 regulated by SNRPB mediates hepatocellular carcinoma progression via BMP2 signaling pathway. iScience, 28(1), 111626.

Yao HF, et al. (2025) CASC8 activates the pentose phosphate pathway to inhibit disulfidptosis in pancreatic ductal adenocarcinoma though the c-Myc-GLUT1 axis. Journal of experimental & clinical cancer research : CR, 44(1), 26.

Rambaldelli G, et al. (2025) From Flies to Humans: Conserved Roles of CEBPZ, NOC2L, and NOC3L in rRNA Processing and Tumorigenesis. bioRxiv : the preprint server for biology.

Zou YP, et al. (2025) Systematic identification of pathological mechanisms, prognostic

biomarkers and therapeutic targets by integrating lncRNA expression variation in salivary gland mucoepidermoid carcinoma. Scientific reports, 15(1), 1573.

Zhao Y, et al. (2025) A novel machine learning-based immune prognostic signature for improving clinical outcomes and guiding therapy in colorectal cancer: an integrated bioinformatics and experimental study. BMC cancer, 25(1), 65.

Koch S, et al. (2025) The transcription factor FOXQ1 in cancer. Cancer metastasis reviews, 44(1), 22.

Heidari R, et al. (2025) The miRNA-mRNA Regulatory Network in Human Hepatocellular Carcinoma by Transcriptomic Analysis From GEO. Cancer reports (Hoboken, N.J.), 8(1), e70098.

Chen G, et al. (2025) Expression and prognostic value of ferritinophagy-related NCOA4 gene in low-grade glioma: integration of bioinformatics and experimental validation. BMC neurology, 25(1), 26.

Zhang X, et al. (2025) Tumour heterogeneity and personalized treatment screening based on single-cell transcriptomics. Computational and structural biotechnology journal, 27, 307.

Tang L, et al. (2025) CXCL14 in prostate cancer: complex interactions in the tumor microenvironment and future prospects. Journal of translational medicine, 23(1), 9.

Luo Z, et al. (2025) Targeted Degradation of SOS1 Exhibits Potent Anticancer Activity and Overcomes Resistance in KRAS-Mutant Tumors and BCR-ABL-Positive Leukemia. Cancer research, 85(1), 101.

Liao F, et al. (2025) The role of FOXK2-FBXO32 in breast cancer tumorigenesis: Insights into ribosome-associated pathways. Thoracic cancer, 16(1), e15482.

Li Z, et al. (2025) Transcription factor TCF7L1 targeting HSPB6 is involved in EMT and PI3K/AKT/mTOR pathways in bladder cancer. The Journal of biological chemistry, 301(1), 108024.

Song L, et al. (2025) Integrin ?8 Facilitates Macrophage Infiltration and Polarization by Regulating CCL5 to Promote LUAD Progression. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(2), e2406865.

Tang Y, et al. (2025) FLT3 is associated with dendritic cell infiltration, tertiary lymphoid structure construction, and predict response to checkpoint inhibitors immunotherapy in solid cancers. Scientific reports, 15(1), 2477.

Li D, et al. (2025) Integrative pan-cancer analysis and experiment validation identified GLS as a biomarker in tumor progression, prognosis, immune microenvironment, and immunotherapy. Scientific reports, 15(1), 525.

Chen S, et al. (2025) RNA binding protein ILF3 increases CEP55 mRNA stability to enhance malignant potential of breast cancer cells and suppress ferroptosis. Hereditas, 162(1), 10.