

Resource Summary Report

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Gene Expression Profile Analysis Suite

RRID:SCR_008341

Type: Tool

Proper Citation

Gene Expression Profile Analysis Suite (RRID:SCR_008341)

Resource Information

URL: <http://www.gepas.org/>

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Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on May 12,2023. An integrated packages of tools for microarray data analysis. GEPAS provides a web-based interface that offers diverse analysis options from the early step of preprocessing (normalization of Affymetrix and two-color microarray experiments and other preprocessing options), to the final step of the functional profiling of the experiment (using Gene Ontology, pathways, PubMed abstracts etc.), which include different possibilities for clustering, gene selection, class prediction and array-comparative genomic hybridization management.

Synonyms: Gepas

Resource Type: software resource, software application, data processing software

Keywords: expression, gene, analysis, genomic, microarray, microarray platform, prediction, data set

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Gene Expression Profile Analysis Suite

Resource ID: SCR_008341

Alternate IDs: nif-0000-25201

Record Creation Time: 20220129T080246+0000

Record Last Update: 20260731T042747+0000

Ratings and Alerts

No rating or validation information has been found for Gene Expression Profile Analysis Suite.

No alerts have been found for Gene Expression Profile Analysis Suite.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 20 mentions in open access literature.

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

Ambrosio MR, et al. (2014) The Epstein Barr-encoded BART-6-3p microRNA affects regulation of cell growth and immuno response in Burkitt lymphoma. Infectious agents and cancer, 9, 12.

Hampson P, et al. (2014) Up-regulation of anti-apoptotic genes confers resistance to the novel anti-leukaemic compound PEP005 in primary AML cells. Oncoscience, 1(8), 529.

Balbás-Martínez C, et al. (2013) ARID1A alterations are associated with FGFR3-wild type, poor-prognosis, urothelial bladder tumors. PloS one, 8(5), e62483.

López V, et al. (2013) Identification of prefoldin amplification (1q23.3-q24.1) in bladder cancer using comparative genomic hybridization (CGH) arrays of urinary DNA. Journal of translational medicine, 11, 182.

Menzel R, et al. (2012) The Nematode *Caenorhabditis elegans*, Stress and Aging: Identifying the Complex Interplay of Genetic Pathways Following the Treatment with Humic Substances. Frontiers in genetics, 3, 50.

Pietsch K, et al. (2012) Meta-Analysis of Global Transcriptomics Suggests that Conserved Genetic Pathways are Responsible for Quercetin and Tannic Acid Mediated Longevity in *C. elegans*. Frontiers in genetics, 3, 48.

Trevino V, et al. (2011) Analysis of normal-tumour tissue interaction in tumours: prediction of prostate cancer features from the molecular profile of adjacent normal cells. PloS one, 6(3), e16492.

He J, et al. (2011) Proteomic-based biosignatures in breast cancer classification and prediction of therapeutic response. International journal of proteomics, 2011, 896476.

Castells-Roca L, et al. (2011) Heat shock response in yeast involves changes in both transcription rates and mRNA stabilities. PloS one, 6(2), e17272.

López E, et al. (2011) Gene expression profiling in lungs of chronic asthmatic mice treated with galectin-3: downregulation of inflammatory and regulatory genes. Mediators of inflammation, 2011, 823279.

Zhao C, et al. (2010) The CD14(+/-)CD16(+) monocyte subset is more susceptible to spontaneous and oxidant-induced apoptosis than the CD14(+)CD16(-) subset. *Cell death & disease*, 1(11), e95.

López-García B, et al. (2010) A genomic approach highlights common and diverse effects and determinants of susceptibility on the yeast *Saccharomyces cerevisiae* exposed to distinct antimicrobial peptides. *BMC microbiology*, 10, 289.

Karimpour-Fard A, et al. (2010) A survey of analysis software for array-comparative genomic hybridisation studies to detect copy number variation. *Human genomics*, 4(6), 421.

Rodríguez-Acebes S, et al. (2010) Gene expression profiling of subcutaneous adipose tissue in morbid obesity using a focused microarray: distinct expression of cell-cycle- and differentiation-related genes. *BMC medical genomics*, 3, 61.

Mishra A, et al. (2010) Cancer biomarkers: are we ready for the prime time? *Cancers*, 2(1), 190.

Martín-Pérez D, et al. (2010) Deregulated expression of the polycomb-group protein SUZ12 target genes characterizes mantle cell lymphoma. *The American journal of pathology*, 177(2), 930.

Frias-Lopez J, et al. (2009) Use of stable isotope-labelled cells to identify active grazers of picocyanobacteria in ocean surface waters. *Environmental microbiology*, 11(2), 512.

van Heerden JH, et al. (2009) Parallel changes in gene expression in peripheral blood mononuclear cells and the brain after maternal separation in the mouse. *BMC research notes*, 2, 195.

McHale CM, et al. (2009) Changes in the peripheral blood transcriptome associated with occupational benzene exposure identified by cross-comparison on two microarray platforms. *Genomics*, 93(4), 343.

Fox JA, et al. (2005) The Bioinformatics Links Directory: a compilation of molecular biology web servers. *Nucleic acids research*, 33(Web Server issue), W3.