

Resource Summary Report

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EASE: the Expression Analysis Systematic Explorer

RRID:SCR_013361

Type: Tool

Proper Citation

EASE: the Expression Analysis Systematic Explorer (RRID:SCR_013361)

Resource Information

URL: <http://david.abcc.ncifcrf.gov/content.jsp?file=/ease/ease1.htm&type=1>

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Description: Windows(c) desktop software application, customizable and standalone, that facilitates the biological interpretation of gene lists derived from the results of microarray, proteomic, and SAGE experiments. Provides statistical methods for discovering enriched biological themes within gene lists, generates gene annotation tables, and enables automated linking to online analysis tools. Offers statistical models to deal with multi-test comparison problem. Platform: Windows compatible

Abbreviations: EASE

Synonyms: Expression Analysis Systematic Explorer

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

Defining Citation: [PMID:12734009](#), [PMID:19131956](#), [PMID:19033363](#)

Keywords: gene, microarray, genome, gene ontology, statistical analysis, enrichment analysis, FASEB list

Funding: NIAID

Availability: Free for academic use

Resource Name: EASE: the Expression Analysis Systematic Explorer

Resource ID: SCR_013361

Alternate IDs: nlx_149218

Record Creation Time: 20220129T080315+0000

Ratings and Alerts

No rating or validation information has been found for EASE: the Expression Analysis Systematic Explorer.

No alerts have been found for EASE: the Expression Analysis Systematic Explorer.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 94 mentions in open access literature.

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

Xu-Monette ZY, et al. (2023) Tumor-Infiltrating Normal B Cells Revealed by Immunoglobulin Repertoire Clonotype Analysis Are Highly Prognostic and Crucial for Antitumor Immune Responses in DLBCL. Clinical cancer research : an official journal of the American Association for Cancer Research, 29(23), 4808.

Singh A, et al. (2021) Cultural adaptation of a scalable psychological intervention for Burundian refugee adolescents in Tanzania: a qualitative study. Conflict and health, 15(1), 73.

Dodla P, et al. (2020) Gene expression analysis of human prostate cell lines with and without tumor metastasis suppressor CD82. BMC cancer, 20(1), 1211.

Pan ZG, et al. (2019) Optimal pathways involved in the treatment of sevoflurane or propofol for patients undergoing coronary artery bypass graft surgery. Experimental and therapeutic medicine, 17(5), 3637.

Sheu CC, et al. (2019) Gene Expression Changes Associated with Nintedanib Treatment in Idiopathic Pulmonary Fibrosis Fibroblasts: A Next-Generation Sequencing and Bioinformatics Study. Journal of clinical medicine, 8(3).

Chen YJ, et al. (2019) Identification of Novel Genes in Osteoarthritic Fibroblast-Like Synoviocytes Using Next-Generation Sequencing and Bioinformatics Approaches. International journal of medical sciences, 16(8), 1057.

Li G, et al. (2019) An integrative module analysis of DNA methylation landscape in aging. Experimental and therapeutic medicine, 17(5), 3411.

Schafer ST, et al. (2019) Pathological priming causes developmental gene network heterochronicity in autistic subject-derived neurons. Nature neuroscience, 22(2), 243.

Sheu CC, et al. (2019) Bioinformatic analysis of next-generation sequencing data to identify dysregulated genes in fibroblasts of idiopathic pulmonary fibrosis. *International journal of molecular medicine*, 43(4), 1643.

Guo SZ, et al. (2019) Constructing differential co-expression network to predict key pathways for myocardial infarction. *Experimental and therapeutic medicine*, 17(4), 3029.

Guo W, et al. (2019) Integrating Network Pharmacology and Pharmacological Evaluation for Deciphering the Action Mechanism of Herbal Formula Zuojin Pill in Suppressing Hepatocellular Carcinoma. *Frontiers in pharmacology*, 10, 1185.

Ungard RG, et al. (2019) xCT knockdown in human breast cancer cells delays onset of cancer-induced bone pain. *Molecular pain*, 15, 1744806918822185.

Li H, et al. (2018) Gene Expression Profiling Confirms the Dosage-Dependent Additive Neuroprotective Effects of Jasminoidin in a Mouse Model of Ischemia-Reperfusion Injury. *BioMed research international*, 2018, 2785636.

Brouwers B, et al. (2018) Elevated Nicotinamide Phosphoribosyl Transferase in Skeletal Muscle Augments Exercise Performance and Mitochondrial Respiratory Capacity Following Exercise Training. *Frontiers in physiology*, 9, 704.

Yumnam S, et al. (2018) Identification of a novel biomarker in tangeretin-induced cell death in AGS human gastric cancer cells. *Oncology reports*, 40(6), 3249.

Jeong H, et al. (2018) Gene Network Dysregulation in the Trigeminal Ganglia and Nucleus Accumbens of a Model of Chronic Migraine-Associated Hyperalgesia. *Frontiers in systems neuroscience*, 12, 63.

Gao X, et al. (2018) MicroRNA-142-3p Promotes Cellular Invasion of Colorectal Cancer Cells by Activation of RAC1. *Technology in cancer research & treatment*, 17, 1533033818790508.

Ripoll VM, et al. (2018) Gene expression profiling identifies distinct molecular signatures in thrombotic and obstetric antiphospholipid syndrome. *Journal of autoimmunity*, 93, 114.

Reddy KE, et al. (2018) Effects of deoxynivalenol- and zearalenone-contaminated feed on the gene expression profiles in the kidneys of piglets. *Asian-Australasian journal of animal sciences*, 31(1), 138.

Reddy KE, et al. (2018) Deoxynivalenol- and zearalenone-contaminated feeds alter gene expression profiles in the livers of piglets. *Asian-Australasian journal of animal sciences*, 31(4), 595.