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

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

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: data processing software, software resource, software application

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

Record Last Update: 20250416T063640+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 FDI Lab - SciCrunch.org.

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.

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.

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).

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.

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

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

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 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.

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

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.

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

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.

Porrello A, et al. (2018) Factor XIIIA-expressing inflammatory monocytes promote lung squamous cancer through fibrin cross-linking. Nature communications, 9(1), 1988.

Seo SW, et al. (2018) TLR4-mediated activation of the ERK pathway following UVA irradiation contributes to increased cytokine and MMP expression in senescent human dermal fibroblasts. PloS one, 13(8), e0202323.