Resource Summary Report

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Kyoto Encyclopedia of Genes and Genomes Expression Database

RRID:SCR_001120
Type: Tool

Proper Citation

Kyoto Encyclopedia of Genes and Genomes Expression Database (RRID:SCR_001120)

Resource Information

URL: http://www.genome.jp/kegg/expression/

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Description: Database for mapping gene expression profiles to pathways and genomes. Repository of microarray gene expression profile data for Synechocystis PCC6803 (syn), Bacillus subtilis (bsu), Escherichia coli W3110 (ecj), Anabaena PCC7120 (ana), and other species contributed by the Japanese research community.

Abbreviations: KEGG Expression Database

Synonyms: Kyoto Encyclopedia of Genes and Genomes Expression Database

Resource Type: database, data repository, data or information resource, storage service resource, service resource

Defining Citation: PMID:9847135, PMID:10592173

Keywords: encyclopedia, endogenous, environment, enzyme, escherichia coli, exogenous, expression, family, functional, gene, genetic, anabaena, bacillus subtilis, biological system, biology, building block, cell, cellular, chemical, community, complex, genome, genomic, hierarchy, interaction, japanese, mapping, metabolic, metabolic pathway databases, microarray, molecular, molecular wiring, nomenclature, order, organism, ortholog, pathway, process, protein, reaction, research, sequence, specie, substance, synechocystis, FASEB list

Funding:

Availability: Free, Available for download, Freely available

Resource Name: Kyoto Encyclopedia of Genes and Genomes Expression Database

Resource ID: SCR_001120

Alternate IDs: nif-0000-21234

Record Creation Time: 20220129T080205+0000

Record Last Update: 20250417T065038+0000

Ratings and Alerts

No rating or validation information has been found for Kyoto Encyclopedia of Genes and Genomes Expression Database.

No alerts have been found for Kyoto Encyclopedia of Genes and Genomes Expression Database.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1269 mentions in open access literature.

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

Huang J, et al. (2024) BBOX1 mediates metabolic reprogramming driven by hypoxia and participates in the malignant progress of high-grade serous ovarian cancer. Biochimica et biophysica acta. Molecular cell research, 1871(8), 119830.

Tabachnick-Cherny S, et al. (2024) Characterization of Immunosuppressive Myeloid Cells in Merkel Cell Carcinoma: Correlation with Resistance to PD-1 Pathway Blockade. Clinical cancer research : an official journal of the American Association for Cancer Research, 30(6), 1189.

Roy TA, et al. (2024) Discovery and validation of genes driving drug-intake and related behavioral traits in mice. Genes, brain, and behavior, 23(1), e12875.

Wan S, et al. (2024) SPARC Stabilizes ApoE to Induce Cholesterol-Dependent Invasion and Sorafenib Resistance in Hepatocellular Carcinoma. Cancer research, 84(11), 1872.

Liang L, et al. (2024) Correlation between intestinal flora and GLP-1 receptor agonist dulaglutide in type 2 diabetes mellitus treatment-A preliminary longitudinal study. iScience, 27(5), 109784.

Roy TA, et al. (2023) DISCOVERY AND VALIDATION OF GENES DRIVING DRUG-INTAKE AND RELATED BEHAVIORAL TRAITS IN MICE. bioRxiv : the preprint server for biology.

Iqbal J, et al. (2023) Differential regulation of hippocampal transcriptome by circulating estrogen. Functional & integrative genomics, 23(4), 309.

Liu Y, et al. (2023) Immunogenetic Determinants of Susceptibility to Head and Neck Cancer in the Million Veteran Program Cohort. Cancer research, 83(3), 386.

Oljuskin T, et al. (2023) Leishmania major centrin knock-out parasites reprogram tryptophan metabolism to induce a pro-inflammatory response. iScience, 26(9), 107593.

Shen M, et al. (2022) The acetylome of adult mouse sciatic nerve. Journal of neurochemistry, 162(3), 262.

Millard RS, et al. (2022) Resistance to white spot syndrome virus in the European shore crab is associated with suppressed virion trafficking and heightened immune responses. Frontiers in immunology, 13, 1057421.

Jae Lee S, et al. (2021) Chromosomal assembly of the Antarctic toothfish (Dissostichus mawsoni) genome using third-generation DNA sequencing and Hi-C technology. Zoological research, 42(1), 124.

Rosenberg AM, et al. (2021) Quantitative mapping of human hair greying and reversal in relation to life stress. eLife, 10.

Kang SY, et al. (2021) Extracellular Vesicles Induce an Aggressive Phenotype in Luminal Breast Cancer Cells Via PKM2 Phosphorylation. Frontiers in oncology, 11, 785450.

Roccuzzo S, et al. (2020) Metabolic Insights Into Infochemicals Induced Colony Formation and Flocculation in Scenedesmus subspicatus Unraveled by Quantitative Proteomics. Frontiers in microbiology, 11, 792.

Wang J, et al. (2020) Construction of Pseudomolecules for the Chinese Chestnut (Castanea mollissima) Genome. G3 (Bethesda, Md.), 10(10), 3565.

Reitmeier S, et al. (2020) Comparing Circadian Rhythmicity in the Human Gut Microbiome. STAR protocols, 1(3), 100148.

Li Y, et al. (2020) Exosomal prostate-specific G-protein-coupled receptor induces osteoblast activity to promote the osteoblastic metastasis of prostate cancer. Translational cancer

research, 9(10), 5857.

Kim BM, et al. (2020) The Genome Assembly and Annotation of the Southern Elephant Seal Mirounga leonina. Genes, 11(2).

Michalovicz LT, et al. (2019) Astrocyte-specific transcriptome analysis using the ALDH1L1 bacTRAP mouse reveals novel biomarkers of astrogliosis in response to neurotoxicity. Journal of neurochemistry, 150(4), 420.