Resource Summary Report

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PubMatrix

RRID:SCR_008236
Type: Tool

Proper Citation

PubMatrix (RRID:SCR_008236)

Resource Information

URL: http://pubmatrix.grc.nia.nih.gov/

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Description: PubMatrix is a web-based tool that allows simple text based mining of the NCBI literature search service PubMed using any two lists of keywords terms, resulting in a frequency matrix of term co-occurrence. PubMatrix is a simple way to rapidly and systematically compare any list of terms against any other list of terms in PubMed. It reports back the frequency of co-occurrence between all pairwise comparisons between the two lists as a matrix table. Lists of terms can be anything; gene names, diseases, gene functions, authors, etc. The user can then quickly sort or browse the frequency matrix table to do individual searches independently. This allows the user to build up tables of word relationships in PubMed in the context of your experiments or your scientific interests. This is useful for analyzing combinatorial datasets, as found with multiplex experimental systems, such as cDNA microarrays, genomic, proteomic, or other multiplex comparisons. The PubMatrix database is an archive of previous searches on many topics. Sponsors: PubMatrix is supported by the National Institutes of Health.

Synonyms: PubMatrix

Resource Type: software resource, software application, text-mining software

Keywords: experiment, function, gene, author, cdna, combinatorial, comparison, dataset, disease, genomic, keyword, literature, matrix, medline interfaces, microarray, ncbi, proteomic, pubmed, scientific, system, term, text mining, FASEB list

Funding:

Resource Name: PubMatrix

Resource ID: SCR_008236

Alternate IDs: nif-0000-21348

Record Creation Time: 20220129T080246+0000

Record Last Update: 20250421T053636+0000

Ratings and Alerts

No rating or validation information has been found for PubMatrix.

No alerts have been found for PubMatrix.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 35 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Zhang X, et al. (2023) Information-incorporated sparse convex clustering for disease subtyping. Bioinformatics (Oxford, England), 39(7).

Au NPB, et al. (2022) Clinically relevant small-molecule promotes nerve repair and visual function recovery. NPJ Regenerative medicine, 7(1), 50.

Kim SW, et al. (2021) Dysregulation of the Acrosome Formation Network by 8-oxoguanine (8-oxoG) in Infertile Sperm: A Case Report with Advanced Techniques. International journal of molecular sciences, 22(11).

Bravatà V, et al. (2021) Hypoxia Transcriptomic Modifications Induced by Proton Irradiation in U87 Glioblastoma Multiforme Cell Line. Journal of personalized medicine, 11(4).

Tubau-Juni N, et al. (2020) Identification of new regulatory genes through expression pattern analysis of a global RNA-seq dataset from a Helicobacter pylori co-culture system. Scientific reports, 10(1), 11506.

Choi K, et al. (2020) No excessive mutations in transcription activator-like effector nuclease-mediated ?-1,3-galactosyltransferase knockout Yucatan miniature pigs. Asian-Australasian journal of animal sciences, 33(2), 360.

Cammarata FP, et al. (2020) Molecular Investigation on a Triple Negative Breast Cancer Xenograft Model Exposed to Proton Beams. International journal of molecular sciences, 21(17).

Bravatà V, et al. (2019) Proton-irradiated breast cells: molecular points of view. Journal of radiation research, 60(4), 451.

Grilli A, et al. (2018) Transcriptional profiling of human bronchial epithelial cell BEAS-2B exposed to diesel and biomass ultrafine particles. BMC genomics, 19(1), 302.

Kim BY, et al. (2017) Therapeutic properties of Scutellaria baicalensis in db/db mice evaluated using Connectivity Map and network pharmacology. Scientific reports, 7, 41711.

Yang M, et al. (2017) Novel Genetic Variants Associated with Child Refractory Esophageal Stricture with Food Allergy by Exome Sequencing. Nutrients, 9(4).

Kleinstreuer NC, et al. (2017) Development and Validation of a Computational Model for Androgen Receptor Activity. Chemical research in toxicology, 30(4), 946.

Chandran V, et al. (2017) Inducible and reversible phenotypes in a novel mouse model of Friedreich's Ataxia. eLife, 6.

Vairamani K, et al. (2017) RNA SEQ Analysis Indicates that the AE3 Cl-/HCO3- Exchanger Contributes to Active Transport-Mediated CO2 Disposal in Heart. Scientific reports, 7(1), 7264.

Kleinstreuer NC, et al. (2016) A Curated Database of Rodent Uterotrophic Bioactivity. Environmental health perspectives, 124(5), 556.

Xiong M, et al. (2016) Identification of lung-specific genes by meta-analysis of multiple tissue RNA-seq data. FEBS open bio, 6(7), 774.

Schissler AG, et al. (2016) Analysis of aggregated cell-cell statistical distances within pathways unveils therapeutic-resistance mechanisms in circulating tumor cells. Bioinformatics (Oxford, England), 32(12), i80.

Arner P, et al. (2016) The epigenetic signature of systemic insulin resistance in obese women. Diabetologia, 59(11), 2393.

Grigoryev DN, et al. (2015) Identification of new biomarkers for Acute Respiratory Distress Syndrome by expression-based genome-wide association study. BMC pulmonary medicine, 15, 95.

Ma J, et al. (2015) Lysosome and Cytoskeleton Pathways Are Robustly Enriched in the Blood of Septic Patients: A Meta-Analysis of Transcriptomic Data. Mediators of inflammation,

2015, 984825.