Resource Summary Report

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Public Expression Profiling Resource

RRID:SCR_007274
Type: Tool

Proper Citation

Public Expression Profiling Resource (RRID:SCR_007274)

Resource Information

URL: http://pepr.cnmcresearch.org/

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Description: An experiment in web-database access to large multi-dimensional data sets using a standardized experimental platform to determine if the larger scientific community can be given simple, intuitive, and user-friendly web-based access to large microarray data sets. All data in PEPR is also available via NCBI GEO. The structure and goals of PEPR differ from other mRNA expression profiling databases in a number of important ways. * The experimental platform in PEPR is standardized, and is an Affymetrix - only database. All microarrays available in the PEPR web database should ascribe to quality control and standard operating procedures. A recent publication has described the QC/SOP criteria utilized in PEPR profiles (The Tumor Analysis Best Practices Working Group 2004). * PEPR permits gene-based queries of large Affymetrix array data sets without any specialized software. For example, a number of large time series projects are available within PEPR, containing 40-60 microarrays, yet these can be simply queried via a dynamic web interface with no prior knowledge of microarray data analysis. * Projects in PEPR originate from scientists world-wide, but all data has been generated by the Research Center for Genetic Medicine, Children""s National Medical Center, Washington DC. Future developments of PEPR will allow remote entry of Affymetrix data ascribing to the same QC/SOP protocols. They have previously described an initial implementation of PEPR, and a dynamic web-queried time series graphical interface (Chen et al. 2004). A publication showing the utility of PEPR for pharmacodynamic data has recently been published (Almon et al. 2003).

Abbreviations: PEPR

Resource Type: data or information resource, database

Defining Citation: PMID:14681485, PMID:14596642

Keywords: microarray, expression profiling, affymetrix, metadata standard, gene, time series, data sharing, visualization, data mining, platform, blood, cell, cancer, bone, brain,

eye, gut, heart, kidney, liver, lung, muscle, spinal cord, spleen, analysis

Funding: NINDS ;
United States Department of Defense ;
NHGRI ;
NHLBI

Availability: Public, Account required, (to download, For the analysis and visualization tools), The community can contribute to this resource

Resource Name: Public Expression Profiling Resource

Resource ID: SCR_007274

Alternate IDs: nif-0000-00014, OMICS_00776

Record Creation Time: 20220129T080240+0000

Record Last Update: 20260801T190937+0000

Ratings and Alerts

No rating or validation information has been found for Public Expression Profiling Resource.

No alerts have been found for Public Expression Profiling Resource.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 16 mentions in open access literature.

Listed below are recent publications. The full list is available at PRECISE-TBI .

Liu Y, et al. (2025) Lcn2 from neutrophil extracellular traps induces astrogliosis and post-stroke emotional disorders. Neuron, 113(24), 4199.

Ruiz C, et al. (2019) Comparative Genomics Reveals a Well-Conserved Intrinsic Resistome in the Emerging Multidrug-Resistant Pathogen Cupriavidus gilardii. mSphere, 4(5).

Dantur KI, et al. (2018) The Endophytic Strain Klebsiella michiganensis Kd70 Lacks Pathogenic Island-Like Regions in Its Genome and Is Incapable of Infecting the Urinary Tract in Mice. Frontiers in microbiology, 9, 1548.

Bello L, et al. (2016) Association Study of Exon Variants in the NF-?B and TGF? Pathways Identifies CD40 as a Modifier of Duchenne Muscular Dystrophy. American

journal of human genetics, 99(5), 1163.

Singhal N, et al. (2015) A role for Galgt1 in skeletal muscle regeneration. Skeletal muscle, 5, 3.

Leikina E, et al. (2015) Annexin A1 Deficiency does not Affect Myofiber Repair but Delays Regeneration of Injured Muscles. Scientific reports, 5, 18246.

Hazra A, et al. (2008) Pharmacodynamic modeling of acute and chronic effects of methylprednisolone on hepatic urea cycle genes in rats. Gene regulation and systems biology, 2, 1.

Partridge CR, et al. (2008) Genetic networks of cooperative redox regulation of osteopontin. Matrix biology : journal of the International Society for Matrix Biology, 27(5), 462.

Nagaraju K, et al. (2008) Dysferlin deficiency enhances monocyte phagocytosis: a model for the inflammatory onset of limb-girdle muscular dystrophy 2B. The American journal of pathology, 172(3), 774.

Yao Z, et al. (2008) Pharmacodynamic/pharmacogenomic modeling of insulin resistance genes in rat muscle after methylprednisolone treatment: exploring regulatory signaling cascades. Gene regulation and systems biology, 2, 141.

Day A, et al. (2007) Celsius: a community resource for Affymetrix microarray data. Genome biology, 8(6), R112.

Urso ML, et al. (2007) Alterations in mRNA expression and protein products following spinal cord injury in humans. The Journal of physiology, 579(Pt 3), 877.

Arnold L, et al. (2007) Inflammatory monocytes recruited after skeletal muscle injury switch into antiinflammatory macrophages to support myogenesis. The Journal of experimental medicine, 204(5), 1057.

Zhao P, et al. (2006) Musculin isoforms and repression of MyoD in muscle regeneration. Biochemical and biophysical research communications, 342(3), 835.

Molon A, et al. (2006) Functional recovery of glycine receptors in spastic murine model of startle disease. Neurobiology of disease, 21(2), 291.

Caretti G, et al. (2006) The RNA helicases p68/p72 and the noncoding RNA SRA are coregulators of MyoD and skeletal muscle differentiation. Developmental cell, 11(4), 547.