

Resource Summary Report

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Functional Genomics Data Society

RRID:SCR_004358

Type: Tool

Proper Citation

Functional Genomics Data Society (RRID:SCR_004358)

Resource Information

URL: <http://www.mged.org/index.html>

Proper Citation: Functional Genomics Data Society (RRID:SCR_004358)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on July 7, 2022. Functional Genomics Data Society - FGED Society, founded in 1999 as the MGED Society, advocates for open access to genomic data sets and works towards providing concrete solutions to achieve this. Our goal is to assure that investment in functional genomics data generates the maximum public benefit. Our work on defining minimum information specifications for reporting data in functional genomics papers have already enabled large data sets to be used and reused to their greater potential in biological and medical research. We work with other organizations to develop standards for biological research data quality, annotation and exchange. We facilitate the creation and use of software tools that build on these standards and allow researchers to annotate and share their data easily. We promote scientific discovery that is driven by genome wide and other biological research data integration and meta-analysis.

Abbreviations: FGED, MGED

Synonyms: MGED Society, FGED Society

Resource Type: data or information resource, topical portal, portal

Keywords: functional genomics

Funding: Illumina

Availability: THIS RESOURCE IS NO LONGER IN SERVICE.

Resource Name: Functional Genomics Data Society

Resource ID: SCR_004358

Alternate IDs: nlx_37824

Record Creation Time: 20220129T080224+0000

Record Last Update: 20260806T054401+0000

Ratings and Alerts

No rating or validation information has been found for Functional Genomics Data Society.

No alerts have been found for Functional Genomics Data Society.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 30 mentions in open access literature.

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

Jiménez-Gutiérrez E, et al. (2022) Neomycin Interferes with Phosphatidylinositol-4,5-Bisphosphate at the Yeast Plasma Membrane and Activates the Cell Wall Integrity Pathway. *International journal of molecular sciences*, 23(19).

Moshitzky G, et al. (2020) Cholinergic Stress Signals Accompany MicroRNA-Associated Stereotypic Behavior and Glutamatergic Neuromodulation in the Prefrontal Cortex. *Biomolecules*, 10(6).

Boldt ABW, et al. (2019) The blood transcriptome of childhood malaria. *EBioMedicine*, 40, 614.

Neugart S, et al. (2016) Influence of Light and Temperature on Gene Expression Leading to Accumulation of Specific Flavonol Glycosides and Hydroxycinnamic Acid Derivatives in Kale (*Brassica oleracea* var. *sabellica*). *Frontiers in plant science*, 7, 326.

Jantsch J, et al. (2015) Cutaneous Na⁺ storage strengthens the antimicrobial barrier function of the skin and boosts macrophage-driven host defense. *Cell metabolism*, 21(3), 493.

Sitras V, et al. (2015) Gene expression profile in cardiovascular disease and preeclampsia: a meta-analysis of the transcriptome based on raw data from human studies deposited in Gene Expression Omnibus. *Placenta*, 36(2), 170.

Sirard MA, et al. (2014) Toward building the cow folliculome. *Animal reproduction science*, 149(1-2), 90.

Montañana F, et al. (2014) ICeE an interface for *C. elegans* experiments. *Worm*, 3(3), e959420.

Carlson MA, et al. (2013) Attachment-regulated signaling networks in the fibroblast-populated 3D collagen matrix. *Scientific reports*, 3, 1880.

Diala I, et al. (2013) Telomere protection and TRF2 expression are enhanced by the canonical Wnt signalling pathway. *EMBO reports*, 14(4), 356.

Wend P, et al. (2013) Wnt/ β -catenin signalling induces MLL to create epigenetic changes in salivary gland tumours. *The EMBO journal*, 32(14), 1977.

Koul S, et al. (2012) Genome wide analysis of differentially expressed genes in HK-2 cells, a line of human kidney epithelial cells in response to oxalate. *PloS one*, 7(9), e43886.

Mamo S, et al. (2011) Sequential analysis of global gene expression profiles in immature and in vitro matured bovine oocytes: potential molecular markers of oocyte maturation. *BMC genomics*, 12, 151.

Quinn TA, et al. (2011) Minimum Information about a Cardiac Electrophysiology Experiment (MICEE): standardised reporting for model reproducibility, interoperability, and data sharing. *Progress in biophysics and molecular biology*, 107(1), 4.

Barrette B, et al. (2010) Transcriptional profiling of the injured sciatic nerve of mice carrying the Wld(S) mutant gene: identification of genes involved in neuroprotection, neuroinflammation, and nerve regeneration. *Brain, behavior, and immunity*, 24(8), 1254.

Hardy B, et al. (2010) Collaborative development of predictive toxicology applications. *Journal of cheminformatics*, 2(1), 7.

Guillen N, et al. (2009) Apolipoprotein E determines the hepatic transcriptional profile of dietary maslinic acid in mice. *The Journal of nutritional biochemistry*, 20(11), 882.

Praz V, et al. (2009) CleanEx: new data extraction and merging tools based on MeSH term annotation. *Nucleic acids research*, 37(Database issue), D880.

Haferlach T, et al. (2007) Gene expression profiling for the diagnosis of acute leukaemia. *British journal of cancer*, 96(4), 535.

Salahshor S, et al. (2005) Differential gene expression profile reveals deregulation of pregnancy specific beta1 glycoprotein 9 early during colorectal carcinogenesis. *BMC cancer*, 5, 66.