

Resource Summary Report

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FGED

RRID:SCR_001897

Type: Tool

Proper Citation

FGED (RRID:SCR_001897)

Resource Information

URL: <http://www.fged.org/>

Proper Citation: FGED (RRID:SCR_001897)

Description: Society that develop standards for biological research data quality, annotation and exchange. They facilitate the creation and use of software tools that build on these standards and allow researchers to annotate and share their data easily. They promote scientific discovery that is driven by genome wide and other biological research data integration and meta-analysis. Historically, FGED began with a focus on microarrays and gene expression data. However, the scope of FGED now includes data generated using any technology when applied to genome-scale studies of gene expression, binding, modification and other related applications.

Abbreviations: FGED

Synonyms: Functional Genomics Data Society, MGED Society, The Microarray Gene Expression Data Society, The Functional Genomics Data Society, MGED

Resource Type: data or information resource, knowledge environment, portal

Keywords: gene expression, gene modification, biological, biologist, biomedical, computer scientist, data analyst, genomic, integration, life science, microarray, technology, functional genomics, annotate, data sharing, genome, data integration, software

Resource Name: FGED

Resource ID: SCR_001897

Alternate IDs: OMICS_01778, nif-0000-10466

Alternate URLs: <http://www.mged.org/>

Record Creation Time: 20220129T080210+0000

Record Last Update: 20260829T182829+0000

Ratings and Alerts

No rating or validation information has been found for FGED.

No alerts have been found for FGED.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 24 mentions in open access literature.

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

Tatsumi D, et al. (2018) DNMTs and SETDB1 function as co-repressors in MAX-mediated repression of germ cell-related genes in mouse embryonic stem cells. PloS one, 13(11), e0205969.

Prasad N, et al. (2016) A comparative genomic analysis of targets of Hox protein Ultrabithorax amongst distant insect species. Scientific reports, 6, 27885.

Durmu? S, et al. (2015) A review on computational systems biology of pathogen-host interactions. Frontiers in microbiology, 6, 235.

Lapatas V, et al. (2015) Data integration in biological research: an overview. Journal of biological research (Thessalonike, Greece), 22(1), 9.

Wiesner M, et al. (2014) Functional identification of genes responsible for the biosynthesis of 1-methoxy-indol-3-ylmethyl-glucosinolate in Brassica rapa ssp. chinensis. BMC plant biology, 14, 124.

Lamot L, et al. (2014) Aberrant expression of shared master-key genes contributes to the immunopathogenesis in patients with juvenile spondyloarthritis. PloS one, 9(12), e115416.

Nieto-Diaz M, et al. (2014) MicroRNA dysregulation in spinal cord injury: causes, consequences and therapeutics. Frontiers in cellular neuroscience, 8, 53.

Mewis I, et al. (2012) UV-B irradiation changes specifically the secondary metabolite profile in broccoli sprouts: induced signaling overlaps with defense response to biotic stressors. Plant & cell physiology, 53(9), 1546.

Martens L, et al. (2011) mzML--a community standard for mass spectrometry data. Molecular & cellular proteomics : MCP, 10(1), R110.000133.

Suen JY, et al. (2010) Profiling gene expression induced by protease-activated receptor 2 (PAR2) activation in human kidney cells. PloS one, 5(11), e13809.

Tra YV, et al. (2010) Enhancing interdisciplinary mathematics and biology education: a microarray data analysis course bridging these disciplines. CBE life sciences education,

9(3), 217.

Janji B, et al. (2010) The actin filament cross-linker L-plastin confers resistance to TNF- α in MCF-7 breast cancer cells in a phosphorylation-dependent manner. *Journal of cellular and molecular medicine*, 14(6A), 1264.

Bilsland AE, et al. (2009) Dynamic telomerase gene suppression via network effects of GSK3 inhibition. *PloS one*, 4(7), e6459.

Liu Z, et al. (2009) Prediction of disease severity in patients with early rheumatoid arthritis by gene expression profiling. *Human genomics and proteomics : HGP*, 2009.

Quackenbush J, et al. (2006) Standardizing the standards. *Molecular systems biology*, 2, 2006.0010.

Weis-Müller BT, et al. (2006) Gene expression in acute Stanford type A dissection: a comparative microarray study. *Journal of translational medicine*, 4, 29.

Gkoutos GV, et al. (2005) Using ontologies to describe mouse phenotypes. *Genome biology*, 6(1), R8.

Newman JC, et al. (2005) L2L: a simple tool for discovering the hidden significance in microarray expression data. *Genome biology*, 6(9), R81.

Hancock D, et al. (2005) maxdLoad2 and maxdBrowse: standards-compliant tools for microarray experimental annotation, data management and dissemination. *BMC bioinformatics*, 6, 264.

Frueh FW, et al. (2004) Regulatory acceptance of toxicogenomics data. *Environmental health perspectives*, 112(12), A663.