Resource Summary Report

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Mouse Gene Expression at the BC Cancer Agency

RRID:SCR_008091
Type: Tool

Proper Citation

Mouse Gene Expression at the BC Cancer Agency (RRID:SCR_008091)

Resource Information

URL: http://www.mouseatlas.org/

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Description: A portal to the Mouse Atlas of Gene Expression Project and Dissecting Gene Expression Networks in Mammalian Organogenesis Project. This Atlas will define the normal state for many tissues by determining, in a comprehensive and quantitative fashion, the number and identity of genes expressed throughout development. The resource will be comprehensive, quantitative, and publicly accessible, containing data on essentially all genes expressed throughout select stages of mouse development. Serial Analysis of Gene Expression (SAGE) is the gene expression methodology of choice for this work. Unlike expressed sequence tags (ESTs) and gene chip data, SAGE data are independent of prior gene discovery and are quantitative. Furthermore, SAGE data are digital, easily exchanged between laboratories for comparison and can be added to by scientists for years to come. Thus, this Atlas will include a data structure and data curation strategy that will facilitate the ongoing collection of gene expression data, even after the completion of this project. The Mouse Atlas project compromises 202 SAGE Libraries from 198 tissues. The list of libraries is available in a number of different groupings, including groups of libraries taken from specific tissue locations and libraries taken from specific developmental stages. Furthermore, this atlas will assemble gene expression profiles for a few focused experiments that will test hypotheses related to the techniques employed, tumor models and models of abnormal development. This will test the resource and provide quality control, validation and demonstrate applicability. Additionally, The Mammalian Organogenesis - Regulation by Gene Expression Networks (MORGEN) project will provide a complete, permanent, and accurate picture of mouse gene expression in the heart (atrioventricular canal and outflow tract), pancreas, and liver; new techniques to understand the interplay of proteins governing the expression of genes key to the development of these organ systems; and the identification of the master regulatory switches that control development of the tissues.

Abbreviations: Mouse Gene Expression at the BC Cancer Agency

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

Keywords: gene, gene expression, abnormal development, development, heart, liver, mouse, organ system, pancreas, protein, tissue, tumor

Funding: Genome Canada ;
BC Cancer Agency ;
BC Cancer Foundation ;
NCI

Resource Name: Mouse Gene Expression at the BC Cancer Agency

Resource ID: SCR_008091

Alternate IDs: nif-0000-11029

Record Creation Time: 20220129T080245+0000

Record Last Update: 20260912T195700+0000

Ratings and Alerts

No rating or validation information has been found for Mouse Gene Expression at the BC Cancer Agency.

No alerts have been found for Mouse Gene Expression at the BC Cancer Agency.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 15 mentions in open access literature.

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

Mouton AJ, et al. (2019) Fibroblast polarization over the myocardial infarction time continuum shifts roles from inflammation to angiogenesis. Basic research in cardiology, 114(2), 6.

Priest JR, et al. (2016) De Novo and Rare Variants at Multiple Loci Support the Oligogenic Origins of Atrioventricular Septal Heart Defects. PLoS genetics, 12(4), e1005963.

Zhang D, et al. (2016) Phenylpropanoids from the stems of Ephedra sinica. Journal of Asian natural products research, 18(3), 260.

Schmouth JF, et al. (2015) Combined serial analysis of gene expression and transcription factor binding site prediction identifies novel-candidate-target genes of Nr2e1 in neocortex development. BMC genomics, 16(1), 545.

Tennant BR, et al. (2012) The transcription factor Myt3 acts as a pro-survival factor in ??-cells. PloS one, 7(12), e51501.

MacIsaac JL, et al. (2012) Tissue-specific alternative polyadenylation at the imprinted gene Mest regulates allelic usage at Copg2. Nucleic acids research, 40(4), 1523.

Chang AC, et al. (2011) Notch initiates the endothelial-to-mesenchymal transition in the atrioventricular canal through autocrine activation of soluble guanylyl cyclase. Developmental cell, 21(2), 288.

Hassan AS, et al. (2010) Expression of two novel transcripts in the mouse definitive endoderm. Gene expression patterns : GEP, 10(2-3), 127.

Aftab S, et al. (2008) Identification and characterization of novel human tissue-specific RFX transcription factors. BMC evolutionary biology, 8, 226.

McLeod K, et al. (2008) Towards the use of argumentation in bioinformatics: a gene expression case study. Bioinformatics (Oxford, England), 24(13), i304.

Lee CK, et al. (2008) Quantitative methods for genome-scale analysis of in situ hybridization and correlation with microarray data. Genome biology, 9(1), R23.

Hoffman BG, et al. (2008) Identification of transcripts with enriched expression in the developing and adult pancreas. Genome biology, 9(6), R99.

Wederell ED, et al. (2008) Global analysis of in vivo Foxa2-binding sites in mouse adult liver using massively parallel sequencing. Nucleic acids research, 36(14), 4549.

Kuo BY, et al. (2006) SAGE2Splice: unmapped SAGE tags reveal novel splice junctions. PLoS computational biology, 2(4), e34.

Zhang TJ, et al. (2006) SAGE reveals expression of Wnt signalling pathway members during mouse prostate development. Gene expression patterns : GEP, 6(3), 310.