Resource Summary Report

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L2L Microarray Analysis Tool

RRID:SCR_013440
Type: Tool

Proper Citation

L2L Microarray Analysis Tool (RRID:SCR_013440)

Resource Information

URL: https://omictools.com/l2l-tool

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Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented May 10, 2017. A pilot effort that has developed a centralized, web-based biospecimen locator that presents biospecimens collected and stored at participating Arizona hospitals and biospecimen banks, which are available for acquisition and use by researchers. Researchers may use this site to browse, search and request biospecimens to use in qualified studies. The development of the ABL was guided by the Arizona Biospecimen Consortium (ABC), a consortium of hospitals and medical centers in the Phoenix area, and is now being piloted by this Consortium under the direction of ABRC. You may browse by type (cells, fluid, molecular, tissue) or disease. Common data elements decided by the ABC Standards Committee, based on data elements on the National Cancer Institute''s (NCI''s) Common Biorepository Model (CBM), are displayed. These describe the minimum set of data elements that the NCI determined were most important for a researcher to see about a biospecimen. The ABL currently does not display information on whether or not clinical data is available to accompany the biospecimens. However, a requester has the ability to solicit clinical data in the request. Once a request is approved, the biospecimen provider will contact the requester to discuss the request (and the requester''s questions) before finalizing the invoice and shipment. The ABL is available to the public to browse. In order to request biospecimens from the ABL, the researcher will be required to submit the requested required information. Upon submission of the information, shipment of the requested biospecimen(s) will be dependent on the scientific and institutional review approval. Account required. Registration is open to everyone.. Documented on August 26, 2019.

Database of published microarray gene expression data, and a software tool for comparing that published data to a user''''s own microarray results. It is very simple to use - all you need is a web browser and a list of the probes that went up or down in your experiment. If you find

L2L useful please consider contributing your published data to the L2L Microarray Database in the form of list files. L2L finds true biological patterns in gene expression data by systematically comparing your own list of genes to lists of genes that have been experimentally determined to be co-expressed in response to a particular stimulus - in other words, published lists of microarray results. The patterns it finds can point to the underlying disease process or affected molecular function that actually generated the observed changed in gene expression. Its insights are far more systematic than critical gene analyses, and more biologically relevant than pure Gene Ontology-based analyses. The publications included in the L2L MDB initially reflected topics thought to be related to Cockayne syndrome: aging, cancer, and DNA damage. Since then, the scope of the publications included has expanded considerably, to include chromatin structure, immune and inflammatory mediators, the hypoxic response, adipogenesis, growth factors, hormones, cell cycle regulators, and others. Despite the parochial origins of the database, the wide range of topics covered will make L2L of general interest to any investigator using microarrays to study human biology. In addition to the L2L Microarray Database, L2L contains three sets of lists derived from Gene Ontology categories: Biological Process, Cellular Component, and Molecular Function. As with the L2L MDB, each GO sub-category is represented by a text file that contains annotation information and a list of the HUGO symbols of the genes assigned to that sub-category or any of its descendants. You don""t need to download L2L to use it to analyze your microarray data. There is an easy-to-use web-based analysis tool, and you have the option of downloading your results so you can view them at any time on your own computer, using any web browser. However, if you prefer, the entire L2L project, and all of its components, can be downloaded from the download page. Platform: Online tool, Windows compatible, Mac OS X compatible, Linux compatible, Unix compatible

Abbreviations: L2L

Synonyms: L2L Microarray Database, L2L Microarray Analysis Tool: A simple tool for discovering the hidden biological significance in microarray expression data, L2L MDB

Resource Type: software application, service resource, production service resource, data analysis service, data analysis software, database, data processing software, analysis service resource, data or information resource, software resource, storage service resource, data repository

Defining Citation: PMID:16168088

Keywords: microarray, gene expression, adipogenesis, biological, biological process, cancer, cell cycle regulator, cellular component, chromatin, cockayne syndrome, dna damage, growth factor, hormone, human biology, hypoxic response, immune mediator, inflammatory mediator, molecular function, molecular neuroanatomy resource, adipocyte, development, hypoxia, immune, inflammation, metabolism, mitogen, neuro, rna, vascular, transcription, tissue, splicing, mouse, human, rat, source code, statistical analysis, gene, chromatin structure

Related Condition: Cockayne syndrome, DNA damage, Other, Aging, Cancer

Funding: Cora May Poncin Foundation ;

NIGMS GM41624

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: L2L Microarray Analysis Tool

Resource ID: SCR_013440

Alternate IDs: nif-0000-10463

Old URLs: http://depts.washington.edu/l2l/about.html

Record Creation Time: 20220129T080316+0000

Record Last Update: 20250519T203809+0000

Ratings and Alerts

No rating or validation information has been found for L2L Microarray Analysis Tool.

No alerts have been found for L2L Microarray Analysis Tool.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Matsumoto M, et al. (2011) Longevity in mice is promoted by probiotic-induced suppression of colonic senescence dependent on upregulation of gut bacterial polyamine production. PloS one, 6(8), e23652.