Bio Resource for Array Genes Database

RRID:SCR_000748
Type: Tool

Proper Citation

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Resource Information

URL: http://www.biorag.org/index.php

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Description: Bio Resource for array genes is a free online resource for easy access to collective and integrated information from various public biological resources for human, mouse, rat, fly and c. elegans genes. The resource includes information about the genes that are represented in Unigene clusters. This resource provides interactive tools to selectively view, analyze and interpret gene expression patterns against the background of gene and protein functional information. Different query options are provided to mine the biological relationships represented in the underlying database. Search button will take you to the list of query tools available. This Bio resource is a platform designed as an online resource to assist researchers in analyzing results of microarray experiments and developing a biological interpretation of the results. This site is mainly to interpret the unique gene expression patterns found as biological changes that can lead to new diagnostic procedures and drug targets. This interactive site allows users to selectively view a variety of information about gene functions that is stored in an underlying database. Although there are other online resources that provide a comprehensive annotation and summary of genes, this resource differs from these by further enabling researchers to mine biological relationships amongst the genes captured in the database using new query tools. Thus providing a unique way of interpreting the microarray data results based on the knowledge provided for the cellular roles of genes and proteins. A total of six different query tools are provided and each offer different search features, analysis options and different forms of display and visualization of data. The data is collected in relational database from public resources: Unigene, Locus link, OMIM, NCBI dbEST, protein domains from NCBI CDD, Gene Ontology, Pathways (Kegg, Genmapp and Biocarta) and BIND (Protein interactions). Data is dynamically collected and compiled twice a week from public databases. Search options offer capability to organize and cluster genes based on their Interactions in biological pathways, their association with Gene Ontology terms, Tissue/organ specific expression or any other user-chosen functional grouping of genes. A color coding scheme is used to highlight differential gene expression patterns against a background of gene functional information. Concept hierarchies (Anatomy and Diseases) of MESH (Medical Subject Heading) terms are used to organize and display the data related to Tissue specific expression and Diseases. Sponsors: BioRag database is maintained by the Bioinformatics group at Arizona Cancer Center. The material presented here is compiled from different public databases. BioRag is hosted by the Biotechnology Computing Facility of the University of Arizona. 2002,2003 University of Arizona.

Synonyms: BioRag

Resource Type: data or information resource, database

Keywords: drug, experiment, expression, fly, functional, gene, array, biological, biology, c. elegans, cluster, database, disease, human, microarray, mouse, protein, rat, target, tissue

Funding:

Resource Name: Bio Resource for Array Genes Database

Resource ID: SCR_000748

Alternate IDs: nif-0000-10165

Record Creation Time: 20220129T080203+0000

Record Last Update: 20250429T054622+0000

Ratings and Alerts

No rating or validation information has been found for Bio Resource for Array Genes Database.

No alerts have been found for Bio Resource for Array Genes Database.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We have not found any literature mentions for this resource.