Resource Summary Report

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EDGE: Environment, Drugs and Gene Expression

RRID:SCR_008187
Type: Tool

Proper Citation

EDGE: Environment, Drugs and Gene Expression (RRID:SCR_008187)

Resource Information

URL: http://edge.oncology.wisc.edu/edge.php

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Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented on July 15, 2013. EDGE is a scientific resource for toxicology-related gene expression information. The site contains databases and analyses of gene expression studies following exposure to a variety of chemicals or physiological changes. The ultimate goal of the EDGE is to map transcriptional changes from chemical exposure that will someday be used as a diagnostic fingerprint to predict toxicity as well as provide valuable insights into the basic molecular changes responsible. EDGE gives you the ability to easily answer the following fundamental questions about your data 1. Can I compare transcriptional profiles across treatments? 2. What genes respond to my treatment? 3. What influences my favorite gene(s)? One of the major objectives of toxicology is to understand the adverse health effects that result from exposure to foreign chemicals. The traditional method for assessing the toxicity of a test chemical is very resource intensive; requiring the commitment of large amounts of money, time, and animals. According to the National Toxicology Program (NTP), each chemical study requires between 2 and 4 million dollars and several years to complete. Due to the cost and labor intensive nature of these studies, the number of chemicals currently tested by the NTP stands at less than 500. Given these statistics and the fact that there are approximately 70,000 chemicals in commerce today, it is increasingly apparent that alternative methods for assessing toxic potential must be explored if a significant portion of the remaining chemicals is to be tested. One potential solution is to develop a comprehensive database that describes alterations in gene expression resulting from chemical exposure. The pattern of transcriptional activity will not only be highly sensitive indicator of chemical exposure, but that this pattern will be diagnostic for mechanistically linked toxicants. In our laboratory, we have chosen to address this problem through a combination of high throughput sequencing of expressed sequence tags (ESTs) and construction of custom toxicology-related cDNA microarrays derived from the unique ESTs identified in the sequencing effort. By using this approach, we can simultaneously develop a quantitative gene expression profile using ESTs and the reagents for further analyzing these changes in a rapid, highly parallel manner. In addition,

the expression profiles are not biased for preselected favorite genes. The resulting gene expression pattern can then be used as diagnostic fingerprint to predict toxicity and/or carcinogenicity as well as provide valuable insight into the basic biochemical and molecular changes responsible for toxicity. Submission of total RNA for Bradfield Lab Microarray Microarray comparisons are made between untreated, control animals and animals treated with ONE treatment. Please make sure the RNA submitted adheres to this experimental design. Necessary information is available on the site.

Abbreviations: EDGE

Synonyms: Drugs and Gene Expression, Environment

Resource Type: analysis service resource, biomaterial analysis service, data or information resource, experimental protocol, material analysis service, narrative resource, production service resource, service resource

Keywords: expressed sequence tags (ests), gene expression, gene expression profile, genes, alterations, cdna microarray, chemical exposure, predictive statistical models, sequencing, toxicogenomics, toxicology, transcriptional changes

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: EDGE: Environment, Drugs and Gene Expression

Resource ID: SCR_008187

Alternate IDs: nif-0000-21140

Record Creation Time: 20220129T080246+0000

Record Last Update: 20260905T132619+0000

Ratings and Alerts

No rating or validation information has been found for EDGE: Environment, Drugs and Gene Expression.

No alerts have been found for EDGE: Environment, Drugs and Gene Expression.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 13 mentions in open access literature.

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

Yahara K, et al. (2021) Long-read metagenomics using PromethION uncovers oral bacteriophages and their interaction with host bacteria. Nature communications, 12(1), 27.

Maganga GD, et al. (2020) Genetic diversity and ecology of coronaviruses hosted by cave-dwelling bats in Gabon. Scientific reports, 10(1), 7314.

Gupta S, et al. (2016) Meiotic Interactors of a Mitotic Gene TAO3 Revealed by Functional Analysis of its Rare Variant. G3 (Bethesda, Md.), 6(8), 2255.

Prescott J, et al. (2015) Body Mass Index Genetic Risk Score and Endometrial Cancer Risk. PloS one, 10(11), e0143256.

Cao Y, et al. (2013) Congenic mice provide evidence for a genetic locus that modulates spontaneous arthritis caused by deficiency of IL-1RA. PloS one, 8(6), e68158.

Housden BE, et al. (2013) Transcriptional dynamics elicited by a short pulse of notch activation involves feed-forward regulation by E(spl)/Hes genes. PLoS genetics, 9(1), e1003162.

Jiao Y, et al. (2013) Genome-wide gene expression profiles in antioxidant pathways and their potential sex differences and connections to vitamin C in mice. International journal of molecular sciences, 14(5), 10042.

Sakellariou A, et al. (2012) Combining multiple hypothesis testing and affinity propagation clustering leads to accurate, robust and sample size independent classification on gene expression data. BMC bioinformatics, 13, 270.

Jiao Y, et al. (2011) Differential gene expression between wild-type and Gulo-deficient mice supplied with vitamin C. Genetics and molecular biology, 34(3), 386.

Caesar R, et al. (2010) A combined transcriptomics and lipidomics analysis of subcutaneous, epididymal and mesenteric adipose tissue reveals marked functional differences. PloS one, 5(7), e11525.

Gomez SK, et al. (2009) Medicago truncatula and Glomus intraradices gene expression in cortical cells harboring arbuscules in the arbuscular mycorrhizal symbiosis. BMC plant biology, 9, 10.

Perelman E, et al. (2007) Detecting differential expression in microarray data: comparison of optimal procedures. BMC bioinformatics, 8, 28.

Cheng KC, et al. (2007) Ganoderma lucidum polysaccharides in human monocytic leukemia cells: from gene expression to network construction. BMC genomics, 8, 411.