

Resource Summary Report

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Onto-Express

RRID:SCR_005670

Type: Tool

Proper Citation

Onto-Express (RRID:SCR_005670)

Resource Information

URL: <http://vortex.cs.wayne.edu/projects.htm#Onto-Express>

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Description: The typical result of a microarray experiment is a list of tens or hundreds of genes found to be differentially regulated in the condition under study. Independently of the methods used to select these genes, the common task faced by any researcher is to translate these lists of genes into a better understanding of the biological phenomena involved. Currently, this is done through a tedious combination of searches through the literature and a number of public databases. We developed Onto-Express (OE) as a novel tool able to automatically translate such lists of differentially regulated genes into functional profiles characterizing the impact of the condition studied. OE constructs functional profiles (using Gene Ontology terms) for the following categories: biochemical function, biological process, cellular role, cellular component, molecular function and chromosome location. Statistical significance values are calculated for each category. We demonstrated the validity and the utility of this comprehensive global analysis of gene function by analyzing two breast cancer data sets from two separate laboratories. OE was able to identify correctly all biological processes postulated by the original authors, as well as discover novel relevant mechanisms (Draghici et.al, Genomics, 81(2), 2003). Other results obtained with Onto-Express can be found in Khatri et.al., Genomics. 79(2), 2002. Custom level of abstraction of the Gene Ontology. User account required. Platform: Online tool

Abbreviations: OE

Synonyms: Onto-Express (OE)

Resource Type: analysis service resource, data analysis service, data or information resource, database, production service resource, service resource

Defining Citation: [PMID:12620386](#), [PMID:11829497](#), [PMID:15215428](#)

Keywords: microarray, gene, ontology, gene expression, biochemical function, biological process, cellular role, cellular component, molecular function, chromosome location, java, data-mining, browser, visualization, analysis, statistical analysis, term enrichment, search engine, other analysis, ontology or annotation browser, ontology or annotation search engine, ontology or annotation visualization, database or data warehouse, custom level of abstraction of the gene ontology, FASEB list

Funding: Wayne State University School of Medicine; Michigan; USA ;
NICHD HD36512

Availability: Free for academic use

Resource Name: Onto-Express

Resource ID: SCR_005670

Alternate IDs: nlx_149110

Old URLs: <http://vortex.cs.wayne.edu:8080>

Record Creation Time: 20220129T080231+0000

Record Last Update: 20260905T132539+0000

Ratings and Alerts

No rating or validation information has been found for Onto-Express.

No alerts have been found for Onto-Express.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 85 mentions in open access literature.

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

Yang C, et al. (2023) Mechanical Ventilation-Related High Stretch Mainly Induces Endoplasmic Reticulum Stress and Thus Mediates Inflammation Response in Cultured Human Primary Airway Smooth Muscle Cells. International journal of molecular sciences, 24(4).

Dong L, et al. (2018) Identification of genes related to consecutive trauma-induced sepsis via gene expression profiling analysis. Medicine, 97(15), e0362.

Kim SH, et al. (2016) Upregulated expression of BCL2, MCM7, and CCNE1 indicate cisplatin-resistance in the set of two human bladder cancer cell lines: T24 cisplatin

sensitive and T24R2 cisplatin resistant bladder cancer cell lines. Investigative and clinical urology, 57(1), 63.

Cohen PY, et al. (2015) Bleomycin-Treated Chimeric Thy1-Deficient Mice with Thy1-Deficient Myofibroblasts and Thy-Positive Lymphocytes Resolve Inflammation without Affecting the Fibrotic Response. Mediators of inflammation, 2015, 942179.

Bayerlov?? M, et al. (2015) Comparative study on gene set and pathway topology-based enrichment methods. BMC bioinformatics, 16, 334.

Mariotti V, et al. (2014) Modulation of gene expression by 3-iodothyronamine: genetic evidence for a lipolytic pattern. PloS one, 9(11), e106923.

Eftang LL, et al. (2013) Up-regulation of CLDN1 in gastric cancer is correlated with reduced survival. BMC cancer, 13, 586.

Guerrero-Bosagna C, et al. (2013) Environmentally induced epigenetic transgenerational inheritance of altered Sertoli cell transcriptome and epigenome: molecular etiology of male infertility. PloS one, 8(3), e59922.

Lubovac-Pilav Z, et al. (2013) Using expression profiling to understand the effects of chronic cadmium exposure on MCF-7 breast cancer cells. PloS one, 8(12), e84646.

Pociask DA, et al. (2013) IL-22 is essential for lung epithelial repair following influenza infection. The American journal of pathology, 182(4), 1286.

Bracchi-Ricard V, et al. (2013) Inhibition of astroglial NF-??B enhances oligodendrogenesis following spinal cord injury. Journal of neuroinflammation, 10, 92.

Chen J, et al. (2013) Molecular signature of cancer at gene level or pathway level? Case studies of colorectal cancer and prostate cancer microarray data. Computational and mathematical methods in medicine, 2013, 909525.

Skinner MK, et al. (2013) Environmentally induced transgenerational epigenetic reprogramming of primordial germ cells and the subsequent germ line. PloS one, 8(7), e66318.

Wrzesinski SH, et al. (2013) Genetic profiles of plasmacytoid (BDCA-4 expressing) DC subtypes-clues to DC subtype function in vivo. Experimental hematology & oncology, 2(1), 8.

Peng Q, et al. (2013) Biological characteristics and genetic heterogeneity between carcinoma-associated fibroblasts and their paired normal fibroblasts in human breast cancer. PloS one, 8(4), e60321.

Nilsson E, et al. (2012) Environmentally induced epigenetic transgenerational inheritance of ovarian disease. PloS one, 7(5), e36129.

Bhandari RK, et al. (2012) Global genome analysis of the downstream binding targets of testis determining factor SRY and SOX9. PloS one, 7(9), e43380.

Li C, et al. (2012) Genome-wide expression analysis in Down syndrome: insight into immunodeficiency. PloS one, 7(11), e49130.

Eftang LL, et al. (2012) Interleukin-8 is the single most up-regulated gene in whole genome profiling of H. pylori exposed gastric epithelial cells. BMC microbiology, 12, 9.

Post J, et al. (2012) Systemic virus distribution and host responses in brain and intestine of chickens infected with low pathogenic or high pathogenic avian influenza virus. Virology journal, 9, 61.