Resource Summary Report

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BMDExpress

RRID:SCR_006823
Type: Tool

Proper Citation

BMDExpress (RRID:SCR_006823)

Resource Information

URL: http://sourceforge.net/projects/bmdexpress/

Proper Citation: BMDExpress (RRID:SCR_006823)

Description: Bioinformatics tool used to analyze microarray dose-response data. The analysis provides benchmark dose estimates at which different cellular processes are altered in toxicogenomic experiments.

Abbreviations: BMDExpress

Resource Type: data analysis software, data processing software, software application, software resource

Keywords: bioinformatics, microarray, software, toxicogenomics

Availability: MIT License

Resource Name: BMDExpress

Resource ID: SCR_006823

Alternate IDs: nlx_152743

Record Creation Time: 20220129T080238+0000

Record Last Update: 20260905T132602+0000

Ratings and Alerts

No rating or validation information has been found for BMDExpress.

No alerts have been found for BMDExpress.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 38 mentions in open access literature.

Listed below are recent publications. The full list is available at PRECISE-TBI .

Yang W, et al. (2026) Perfluorooctane sulfonic acid impairs spermatogenesis via the liver-gut microbiota-testis axis: a central role of chenodeoxycholic acid metabolism. Journal of advanced research, 81, 897.

Zhao N, et al. (2026) Exploring the Influence of Chemical Exposures in Breast Cancer Disparities: High-Throughput Transcriptomic Analysis in Normal Breast Cells from Diverse Donors. bioRxiv : the preprint server for biology.

Matteo G, et al. (2026) Cross-study analysis identifies estrogen depletion and exposure duration as key determinants of bisphenol A transcriptomic potency in MCF-7 cells. Toxicology reports, 17, 102305.

Heintz MM, et al. (2026) Hepatic transcriptomic responses in gravid and non-gravid rats exposed to HFPO-DA: Analyses to inform the role of maternal effects in neonatal toxicity. PloS one, 21(4), e0345643.

Shin S, et al. (2025) Comprehensive analysis of high-throughput transcriptomics to distinguish drug-induced liver injury (DILI) phenotypes. Archives of toxicology, 99(9), 3721.

Addicks GC, et al. (2025) Identification of four mechanisms of toxicity for per- and polyfluoroalkyl substances through transcriptomic profiling in human liver spheroids exposed to 24 PFAS. Toxicological sciences : an official journal of the Society of Toxicology, 207(1), 161.

Heintz MM, et al. (2025) Comparison of phenotypic and transcriptomic profiles between HFPO-DA and prototypical PPAR?, PPAR?, and cytotoxic agents in wild-type and Ppara-null mouse livers. Toxicological sciences : an official journal of the Society of Toxicology, 206(1), 183.

Li Z, et al. (2025) The effects of house dust-derived mixtures of organophosphate esters on Leydig cell phenotype, function, and lipidome†. Biology of reproduction, 113(6), 1587.

Rowan-Carroll A, et al. (2025) Deciphering per- and polyfluoroalkyl substances mode of action: comparative gene expression analysis in human liver spheroids. Toxicological sciences : an official journal of the Society of Toxicology, 205(1), 124.

Mauge-Lewis KA, et al. (2025) Unraveling Human Hepatocellular Responses to PFAS and Aqueous Film-Forming Foams (AFFFs) for Molecular Hazard Prioritization and In Vivo Translation. Environmental science & technology, 59(5), 2423.

Barutcu AR, et al. (2024) Integrating gene expression and splicing dynamics across dose-response oxidative modulators. Frontiers in genetics, 15, 1389095.

Lee H, et al. (2024) Empirical Characterization of False Discovery Rates of Differentially Expressed Genes and Transcriptomic Benchmark Concentrations in Zebrafish Embryos. Environmental science & technology, 58(14), 6128.

Heintz MM, et al. (2024) Comparison of transcriptomic profiles between HFPO-DA and prototypical PPAR?, PPAR?, and cytotoxic agents in mouse, rat, and pooled human hepatocytes. Toxicological sciences : an official journal of the Society of Toxicology, 200(1), 165.

Heintz MM, et al. (2024) Comparison of transcriptomic profiles between HFPO-DA and prototypical PPAR?, PPAR?, and cytotoxic agents in wild-type and PPAR? knockout mouse hepatocytes. Toxicological sciences : an official journal of the Society of Toxicology, 200(1), 183.

Thienpont A, et al. (2024) Unlocking the Power of Transcriptomic Biomarkers in Qualitative and Quantitative Genotoxicity Assessment of Chemicals. Chemical research in toxicology, 37(3), 465.

Martin R, et al. (2023) Short-Term Transcriptomic Points of Departure Are Consistent with Chronic Points of Departure for Three Organophosphate Pesticides across Mouse and Fathead Minnow. Toxics, 11(10).

Jennings P, et al. (2023) Capturing time-dependent activation of genes and stress-response pathways using transcriptomics in iPSC-derived renal proximal tubule cells. Cell biology and toxicology, 39(4), 1773.

Solorio-Rodriguez SA, et al. (2023) Single-Walled vs. Multi-Walled Carbon Nanotubes: Influence of Physico-Chemical Properties on Toxicogenomics Responses in Mouse Lungs. Nanomaterials (Basel, Switzerland), 13(6).

Addicks GC, et al. (2023) Per- and polyfluoroalkyl substances (PFAS) in mixtures show additive effects on transcriptomic points of departure in human liver spheroids. Toxicological sciences : an official journal of the Society of Toxicology, 194(1), 38.

Malinowska JM, et al. (2023) Derivation of metabolic point of departure using high-throughput in vitro metabolomics: investigating the importance of sampling time points on benchmark concentration values in the HepaRG cell line. Archives of toxicology, 97(3), 721.