# Resource Summary Report

Generated by PRECISE-TBI on Aug 2, 2026

## 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 processing software, data analysis 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:** 20260801T190318+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 32 mentions in open access literature.

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


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.

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.

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.

Chappell GA, et al. (2022) Crypt and Villus Transcriptomic Responses in Mouse Small Intestine Following Oral Exposure to Hexavalent Chromium. Toxicological sciences : an official journal of the Society of Toxicology, 186(1), 43.

Buick JK, et al. (2021) A Modern Genotoxicity Testing Paradigm: Integration of the High-Throughput CometChip® and the TGx-DDI Transcriptomic Biomarker in Human HepaRG™ Cell Cultures. Frontiers in public health, 9, 694834.

Chappell GA, et al. (2020) Assessment of the Mode of Action Underlying the Effects of GenX in Mouse Liver and Implications for Assessing Human Health Risks. Toxicologic pathology, 48(3), 494.

Shockley KR, et al. (2020) Comparative toxicity and liver transcriptomics of legacy and emerging brominated flame retardants following 5-day exposure in the rat. Toxicology letters, 332, 222.

Soufan O, et al. (2019) T1000: a reduced gene set prioritized for toxicogenomic studies. PeerJ, 7, e7975.

Qutob SS, et al. (2018) The application of transcriptional benchmark dose modeling for deriving thresholds of effects associated with solar-simulated ultraviolet radiation exposure. Environmental and molecular mutagenesis, 59(6), 502.