

Resource Summary Report

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TISSUES

RRID:SCR_015665

Type: Tool

Proper Citation

TISSUES (RRID:SCR_015665)

Resource Information

URL: <http://tissues.jensenlab.org>

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Description: Database that integrates evidence on tissue expression from manually curated literature, proteomics and transcriptomics screens, and automatic text mining. It maps all evidence to common protein identifiers and Brenda Tissue Ontology terms, and further unifies it by assigning confidence scores that facilitate comparison of the different types and sources of evidence.

Synonyms: TISSUES: Tissue Expression Database, Tissue Expression Database

Resource Type: data or information resource, software resource, web application, database

Defining Citation: [PMID:26157623](#)

Keywords: tissue expression, proteomic, transcriptomic, text-mining, brenda tissue ontology, protein identifier, bio.tools

Funding: Novo Nordisk Foundation NNF14CC0001;
NCI U54 CA189205-01;
CSIRO's OCE Science Leader program

Availability: Freely available, Free, Available for download

Resource Name: TISSUES

Resource ID: SCR_015665

Alternate IDs: biotools:tissues

Alternate URLs: <https://bio.tools/tissues>

Record Creation Time: 20220129T080326+0000

Record Last Update: 20260731T042940+0000

Ratings and Alerts

No rating or validation information has been found for TISSUES.

No alerts have been found for TISSUES.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 42 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Sonmez H, et al. (2025) Integrative bioinformatic and clinical validation reveals dynamic regulation of circulating microRNAs before and after antiretroviral therapy in HIV-positive patients. Scientific reports, 15(1), 44520.

Ma Y, et al. (2025) Systematic dissection of pleiotropic loci and critical regulons in excitatory neurons and microglia relevant to neuropsychiatric and ocular diseases. Translational psychiatry, 15(1), 24.

Poluektov YM, et al. (2025) Mechanisms mediating effects of cardiotonic steroids in mammalian blood cells. Frontiers in pharmacology, 16, 1520927.

Byrd AI, et al. (2025) ChEA-KG: Human Transcription Factor Regulatory Network with a Knowledge Graph Interactive User Interface. bioRxiv : the preprint server for biology.

Falsaperla R, et al. (2025) PPP5C pathogenic variant identified: a potential key to gaining insight into developmental and epileptic encephalopathy? Molecular and cellular pediatrics, 12(1), 3.

Balkan II, et al. (2025) Longitudinal analysis of hsa-miR-3163, hsa-miR-124-3p, hsa-miR-548c-3p, and hsa-miR-27a-3p as prognostic biomarkers in HIV-infected patients. Frontiers in immunology, 16, 1565068.

Wicik Z, et al. (2025) Integrative gene-metabolite network analysis of GLP-1 receptor agonists and related incretin pathways in cardiometabolic health. NPJ systems biology and applications, 11(1), 144.

Zhang W, et al. (2025) Transcriptome-Optimized Hydrogel Design of a Stem Cell Niche for Enhanced Tendon Regeneration. Advanced materials (Deerfield Beach, Fla.), 37(2), e2313722.

Wang G, et al. (2025) Abnormal glycosylation changes in brain tissue of kainic acid-induced epileptic rats. *Scientific reports*, 15(1), 45596.

Nowak-Szwed A, et al. (2025) Sirtuins and regulatory miRNAs as epigenetic determinants of empagliflozin-mediated recovery after acute myocardial infarction. *Cardiovascular diabetology*, 24(1), 463.

Matveev EV, et al. (2024) Genome-wide bioinformatics analysis of human protease capacity for proteolytic cleavage of the SARS-CoV-2 spike glycoprotein. *Microbiology spectrum*, 12(2), e0353023.

Locard-Paulet M, et al. (2024) Functional Analysis of MS-Based Proteomics Data: From Protein Groups to Networks. *Molecular & cellular proteomics : MCP*, 23(12), 100871.

Zhang Y, et al. (2024) Predicting intercellular communication based on metabolite-related ligand-receptor interactions with MRCLinkdb. *BMC biology*, 22(1), 152.

Laviano HD, et al. (2024) Maternal dietary antioxidant supplementation regulates weaned piglets' adipose tissue transcriptome and morphology. *PloS one*, 19(9), e0310399.

Pan X, et al. (2024) MCSdb, a database of proteins residing in membrane contact sites. *Scientific data*, 11(1), 281.

Yan S, et al. (2023) Nanocomposites based on nanoceria regulate the immune microenvironment for the treatment of polycystic ovary syndrome. *Journal of nanobiotechnology*, 21(1), 412.

Cezar-de-Mello PFT, et al. (2023) The microRNA Cargo of Human Vaginal Extracellular Vesicles Differentiates Parasitic and Pathobiont Infections from Colonization by Homeostatic Bacteria. *Microorganisms*, 11(3).

Eyileten C, et al. (2022) Thrombosis-related circulating miR-16-5p is associated with disease severity in patients hospitalised for COVID-19. *RNA biology*, 19(1), 963.

Marinkovic M, et al. (2022) Matrix-bound Cyr61/CCN1 is required to retain the properties of the bone marrow mesenchymal stem cell niche but is depleted with aging. *Matrix biology : journal of the International Society for Matrix Biology*, 111, 108.

Chai H, et al. (2022) In silico prediction of HIV-1-host molecular interactions and their directionality. *PLoS computational biology*, 18(2), e1009720.