Resource Summary Report

Generated by NIF on May 20, 2025

TISSUES

RRID:SCR_015665
Type: Tool

Proper Citation

TISSUES (RRID:SCR_015665)

Resource Information

URL: http://tissues.jensenlab.org

Proper Citation: TISSUES (RRID:SCR_015665)

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: software resource, data or information 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: 20250519T203900+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 34 mentions in open access literature.

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

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.

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.

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.

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

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.

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

Laviano HD, et al. (2024) Maternal dietary antioxidant supplementation regulates weaned

piglets' adipose tissue transcriptome and morphology. PloS one, 19(9), e0310399.

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).

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.

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.

Johnson KA, et al. (2022) Robust normalization and transformation techniques for constructing gene coexpression networks from RNA-seq data. Genome biology, 23(1), 1.

Qiu A, et al. (2021) Spatio-temporal correlates of gene expression and cortical morphology across lifespan and aging. NeuroImage, 224, 117426.

Lin S, et al. (2021) Circular RNA circFLNA inhibits the development of bladder carcinoma through microRNA miR-216a-3p/BTG2 axis. Bioengineered, 12(2), 11376.

Kirmizi DA, et al. (2021) The effect of a natural molecule in ovary ischemia reperfusion damage: does lycopene protect ovary? Experimental animals, 70(1), 37.

Lange S, et al. (2021) MicroRNAs for Virus Pathogenicity and Host Responses, Identified in SARS-CoV-2 Genomes, May Play Roles in Viral-Host Co-Evolution in Putative Zoonotic Host Species. Viruses, 13(1).

Zhang Y, et al. (2021) Cellinker: a platform of ligand-receptor interactions for intercellular communication analysis. Bioinformatics (Oxford, England).

Dachet F, et al. (2021) Selective time-dependent changes in activity and cell-specific gene expression in human postmortem brain. Scientific reports, 11(1), 6078.

Hu K, et al. (2021) The novel roles of virus infection-associated gene CDKN1A in chemoresistance and immune infiltration of glioblastoma. Aging, 13(5), 6662.