Resource Summary Report

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TissueNet - The Database of Human Tissue Protein-Protein Interactions

RRID:SCR_002052
Type: Tool

Proper Citation

TissueNet - The Database of Human Tissue Protein-Protein Interactions (RRID:SCR_002052)

Resource Information

URL: http://netbio.bgu.ac.il/tissuenet/

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Description: Database of human tissue protein-protein interactions (PPIs) that associates each interaction with human tissues that express both pair mates. This was achieved by integrating current data of experimentally detected PPIs with extensive data of gene and protein expression across 16 main human tissues. Users can query TissueNet using a protein and retrieve its PPI partners per tissue, or using a PPI and retrieve the tissues expressing both pair mates. The graphical representation of the output highlights tissue-specific and tissue-wide PPIs. Thus, TissueNet provides a unique platform for assessing the roles of human proteins and their interactions across tissues.

Abbreviations: TissueNet

Resource Type: data or information resource, database

Defining Citation: PMID:23193266

Keywords: protein-protein interaction, protein, tissue, adipose, adrenal, brain, breast, colon, heart, kidney, liver, lung, lymph node, ovary, prostate, skeletal muscle, testis, thyroid, white blood cell, protein expression, dna-microarray

Funding:

Availability: Free, Public

Resource Name: TissueNet - The Database of Human Tissue Protein-Protein Interactions

Resource ID: SCR_002052

Alternate IDs: OMICS_01913

Record Creation Time: 20220129T080211+0000

Record Last Update: 20250422T055015+0000

Ratings and Alerts

No rating or validation information has been found for TissueNet - The Database of Human Tissue Protein-Protein Interactions.

No alerts have been found for TissueNet - The Database of Human Tissue Protein-Protein Interactions.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 19 mentions in open access literature.

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

Gaber M, et al. (2025) Obesity increases DNA damage in the breast epithelium. Breast cancer research : BCR, 27(1), 11.

Wang Y, et al. (2024) A systematic evaluation of computation methods for cell segmentation. bioRxiv : the preprint server for biology.

Munquad S, et al. (2024) Uncovering the subtype-specific disease module and the development of drug response prediction models for glioma. Heliyon, 10(5), e27190.

Lingegowda H, et al. (2024) Endocannabinoids and their receptors modulate endometriosis pathogenesis and immune response. eLife, 13.

Alaoui L, et al. (2023) Functional specialization of short-lived and long-lived macrophage subsets in human tonsils. The Journal of experimental medicine, 220(7).

Shrestha P, et al. (2023) Efficient end-to-end learning for cell segmentation with machine

generated weak annotations. Communications biology, 6(1), 232.

Han S, et al. (2023) Optimizing Deep Learning-Based Segmentation of Densely Packed Cells using Cell Surface Markers. Research square.

Greenwald NF, et al. (2022) Whole-cell segmentation of tissue images with human-level performance using large-scale data annotation and deep learning. Nature biotechnology, 40(4), 555.

Chignon A, et al. (2022) Genome-wide chromatin contacts of super-enhancer-associated lncRNA identify LINC01013 as a regulator of fibrosis in the aortic valve. PLoS genetics, 18(1), e1010010.

Pachitariu M, et al. (2022) Cellpose 2.0: how to train your own model. Nature methods, 19(12), 1634.

Prasad K, et al. (2021) Brain Disease Network Analysis to Elucidate the Neurological Manifestations of COVID-19. Molecular neurobiology, 58(5), 1875.

Ma F, et al. (2021) Applications and analytical tools of cell communication based on ligand-receptor interactions at single cell level. Cell & bioscience, 11(1), 121.

Das AB, et al. (2021) Lung disease network reveals impact of comorbidity on SARS-CoV-2 infection and opportunities of drug repurposing. BMC medical genomics, 14(1), 226.

Erola P, et al. (2020) Model-based clustering of multi-tissue gene expression data. Bioinformatics (Oxford, England), 36(6), 1807.

Sardina DS, et al. (2018) INBIA: a boosting methodology for proteomic network inference. BMC bioinformatics, 19(Suppl 7), 188.

Basha O, et al. (2017) The TissueNet v.2 database: A quantitative view of protein-protein interactions across human tissues. Nucleic acids research, 45(D1), D427.

Ostrow SL, et al. (2016) The Somatic Nature of Cancer Allows It to Affect Highly Constrained Genes. Genome biology and evolution, 8(5), 1614.

Basha O, et al. (2015) MyProteinNet: build up-to-date protein interaction networks for organisms, tissues and user-defined contexts. Nucleic acids research, 43(W1), W258.

Zhang X, et al. (2015) Forward Individualized Medicine from Personal Genomes to Interactomes. Frontiers in physiology, 6, 364.