

Resource Summary Report

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Java Treeview

RRID:SCR_016916

Type: Tool

Proper Citation

Java Treeview (RRID:SCR_016916)

Resource Information

URL: <https://sourceforge.net/projects/jtreeview/>

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Description: Software as a cross platform gene expression visualization tool. Extensible viewer for microarray data in the PCL or CDT format. Interactive display of clustered gene expression data. Java application for visualizing large data matrices. It can load a dataset, cluster it, browse it, customize its appearance and export it into a figure.

Abbreviations: TreeView

Synonyms: TreeView3, Treeview, Java TreeView

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

Keywords: gene, expression, data, visualization, microarray, interactive, display, cluster, dataset

Availability: Free, Available for download, Freely available

Resource Name: Java Treeview

Resource ID: SCR_016916

Alternate URLs: <https://bitbucket.org/TreeView3Dev/treeview3/>

License: GNU General Public License version 2.0, MIT licence

Record Creation Time: 20220129T080332+0000

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Ratings and Alerts

No rating or validation information has been found for Java Treeview.

No alerts have been found for Java Treeview.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 52 mentions in open access literature.

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

Mogol AN, et al. (2025) ACSS2-Mediated Metabolic-Epigenetic Crosstalk Drives Fulvestrant Resistance and Represents a Novel Therapeutic Target. bioRxiv : the preprint server for biology.

Choi J, et al. (2024) Molecular targets of glucocorticoids that elucidate their therapeutic efficacy in aggressive lymphomas. Cancer cell, 42(5), 833.

Meng Y, et al. (2024) Interplay between acetylation and ubiquitination of imitation switch chromatin remodeler Isw1 confers multidrug resistance in *Cryptococcus neoformans*. eLife, 13.

Fuller T, et al. (2023) A reference assembly for the legume cover crop hairy vetch (*Vicia villosa*). GigaByte (Hong Kong, China), 2023, gigabyte98.

Xu-Monette ZY, et al. (2023) Tumor-Infiltrating Normal B Cells Revealed by Immunoglobulin Repertoire Clonotype Analysis Are Highly Prognostic and Crucial for Antitumor Immune Responses in DLBCL. Clinical cancer research : an official journal of the American Association for Cancer Research, 29(23), 4808.

Mahony CB, et al. (2023) Lineage skewing and genome instability underlie marrow failure in a zebrafish model of GATA2 deficiency. Cell reports, 42(6), 112571.

Humphreys PEA, et al. (2023) Optogenetic manipulation of BMP signaling to drive chondrogenic differentiation of hPSCs. Cell reports, 42(12), 113502.

Pallerla SR, et al. (2022) Custom gene expression panel for evaluation of potential molecular markers in hepatocellular carcinoma. BMC medical genomics, 15(1), 235.

LeBlanc L, et al. (2022) β -catenin links cell seeding density to global gene expression during mouse embryonic stem cell differentiation. iScience, 25(1), 103541.

Park JS, et al. (2022) Temporally distinct regulatory pathways coordinate thermo-responsive storage organ formation in potato. Cell reports, 38(13), 110579.

Dubois-Pot-Schneider H, et al. (2022) Transcriptional and Epigenetic Consequences of DMSO Treatment on HepaRG Cells. Cells, 11(15).

Zuo Q, et al. (2022) Targeting Metabolic Adaptations in the Breast Cancer-Liver Metastatic Niche Using Dietary Approaches to Improve Endocrine Therapy Efficacy. *Molecular cancer research* : MCR, 20(6), 923.

Choi J, et al. (2021) Histone H1 prevents non-CG methylation-mediated small RNA biogenesis in *Arabidopsis* heterochromatin. *eLife*, 10.

Jeronimo C, et al. (2021) FACT is recruited to the +1 nucleosome of transcribed genes and spreads in a Chd1-dependent manner. *Molecular cell*, 81(17), 3542.

Mukherjee K, et al. (2021) EKLF/KLF1 expression defines a unique macrophage subset during mouse erythropoiesis. *eLife*, 10.

Knoener R, et al. (2021) Identification of host proteins differentially associated with HIV-1 RNA splice variants. *eLife*, 10.

Bevington SL, et al. (2020) Chromatin Priming Renders T Cell Tolerance-Associated Genes Sensitive to Activation below the Signaling Threshold for Immune Response Genes. *Cell reports*, 31(10), 107748.

Hamaidi I, et al. (2020) Sirt2 Inhibition Enhances Metabolic Fitness and Effector Functions of Tumor-Reactive T Cells. *Cell metabolism*, 32(3), 420.

Lu Y, et al. (2020) Identification of stress defensive proteins in common wheat-Thinopyron intermedium translocation line YW642 developing grains via comparative proteome analysis. *Breeding science*, 70(5), 517.

Lee J, et al. (2020) QUAKE Regulates Microexon Alternative Splicing of the Rho GTPase Pathway and Controls Microglia Homeostasis. *Cell reports*, 33(13), 108560.