Resource Summary Report

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Affymetrix Transcriptome Analysis Console Software

RRID:SCR_018718
Type: Tool

Proper Citation

Affymetrix Transcriptome Analysis Console Software (RRID:SCR_018718)

Resource Information

URL: http://tools.thermofisher.com/content/sfs/brochures/geneatlas_system_brochure.pdf

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Description: Software to generate differential expression analysis and visualization for easy interpretation. Takes normalized and summarized data from Affymetrix Expression Console software to next level, providing differential expression analysis and visualization for easy interpretation.

Abbreviations: Affymetrix TAC

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

Keywords: Affymetrix, transcriptome analysis, analysis console, differential expression analysis, data visualization

Availability: Restricted

Resource Name: Affymetrix Transcriptome Analysis Console Software

Resource ID: SCR_018718

Record Creation Time: 20220129T080341+0000

Record Last Update: 20260803T040759+0000

Ratings and Alerts

No rating or validation information has been found for Affymetrix Transcriptome Analysis Console Software.

No alerts have been found for Affymetrix Transcriptome Analysis Console Software.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 15 mentions in open access literature.

Listed below are recent publications. The full list is available at T1D .

Rodemann MM, et al. (2025) Identification of a Growth-Promoting Gene Cluster in the Region 2q24 as a Driver of Tumorigenesis in Childhood Hepatoblastoma. The American journal of pathology, 195(8), 1553.

Marques-da-Silva C, et al. (2025) Type I interferons induce guanylate-binding proteins and lysosomal defense in hepatocytes to control malaria. Cell host & microbe, 33(4), 529.

Lin HP, et al. (2024) DELE1 maintains muscle proteostasis to promote growth and survival in mitochondrial myopathy. The EMBO journal, 43(22), 5548.

Sulsenti R, et al. (2024) Intracellular Osteopontin Promotes the Release of TNF? by Mast Cells to Restrain Neuroendocrine Prostate Cancer. Cancer immunology research, 12(9), 1147.

Miyahara K, et al. (2023) Investigating the impact of paternal aging on murine sperm miRNA profiles and their potential link to autism spectrum disorder. Scientific reports, 13(1), 20608.

Larionova I, et al. (2023) Tumor-associated macrophages respond to chemotherapy by detrimental transcriptional reprogramming and suppressing stabilin-1 mediated clearance of EGF. Frontiers in immunology, 14, 1000497.

Spella M, et al. (2023) Non-Oncogene Addiction of KRAS-Mutant Cancers to IL-1? via Versican and Mononuclear IKK?. Cancers, 15(6).

Leduc-Gaudet JP, et al. (2023) Autophagy ablation in skeletal muscles worsens sepsis-induced muscle wasting, impairs whole-body metabolism, and decreases survival. iScience, 26(8), 107475.

Matsuo K, et al. (2022) Transcriptome Analysis in Hippocampus of Rats Prenatally Exposed to Valproic Acid and Effects of Intranasal Treatment of Oxytocin. Frontiers in psychiatry, 13, 859198.

Kuriyama S, et al. (2022) Pigment Epithelium Derived Factor Is Involved in the Late Phase of Osteosarcoma Metastasis by Increasing Extravasation and Cell-Cell Adhesion.

Frontiers in oncology, 12, 818182.

Tham SM, et al. (2021) Intravesical High Dose BCG Tokyo and Low Dose BCG Tokyo with GMCSF+IFN ? Induce Systemic Immunity in a Murine Orthotopic Bladder Cancer Model. Biomedicines, 9(12).

Hurst CD, et al. (2021) Stage-stratified molecular profiling of non-muscle-invasive bladder cancer enhances biological, clinical, and therapeutic insight. Cell reports. Medicine, 2(12), 100472.

Raimundo L, et al. (2021) BBIT20 inhibits homologous DNA repair with disruption of the BRCA1-BARD1 interaction in breast and ovarian cancer. British journal of pharmacology, 178(18), 3627.

Nandadasa S, et al. (2020) Vascular dimorphism ensured by regulated proteoglycan dynamics favors rapid umbilical artery closure at birth. eLife, 9.

Scicluna BP, et al. (2020) The leukocyte non-coding RNA landscape in critically ill patients with sepsis. eLife, 9.