

Resource Summary Report

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ExpressionSuite

RRID:SCR_021095

Type: Tool

Proper Citation

ExpressionSuite (RRID:SCR_021095)

Resource Information

URL: <https://www.thermofisher.com/us/en/home/technical-resources/software-downloads/expressionsuite-software.html>

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Description: Software tool to quantify relative gene expression across large number of genes and samples. Allows to analyze gene expression data on any current Applied Biosystems real time PCR instrument.

Synonyms: ExpressionSuite Software, ExpressionSuite v1.3

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

Keywords: QuantStudio Real-Time PCR analysis, quantify relative gene expression, genes large number, analyze gene expression data, Applied Biosystems RT PCR instrument

Availability: Free, Available for download, Freely available

Resource Name: ExpressionSuite

Resource ID: SCR_021095

Record Creation Time: 20220129T080353+0000

Record Last Update: 20260905T132934+0000

Ratings and Alerts

No rating or validation information has been found for ExpressionSuite.

No alerts have been found for ExpressionSuite.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 11 mentions in open access literature.

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

Sebastiani G, et al. (2024) A set of circulating microRNAs belonging to the 14q32 chromosome locus identifies two subgroups of individuals with recent-onset type 1 diabetes. *Cell reports. Medicine*, 5(6), 101591.

Sandau US, et al. (2022) Differential Effects of APOE Genotype on MicroRNA Cargo of Cerebrospinal Fluid Extracellular Vesicles in Females With Alzheimer's Disease Compared to Males. *Frontiers in cell and developmental biology*, 10, 864022.

Favaloro F, et al. (2022) miR-17-92 exerts stage-specific effects in adult V-SVZ neural stem cell lineages. *Cell reports*, 41(10), 111773.

Grieco GE, et al. (2021) Protocol to analyze circulating small non-coding RNAs by high-throughput RNA sequencing from human plasma samples. *STAR protocols*, 2(3), 100606.

Siavrien? E, et al. (2020) A de novo 13q31.3 microduplication encompassing the miR-17 ~ 92 cluster results in features mirroring those associated with Feingold syndrome 2. *Gene*, 753, 144816.

D'Alessandra Y, et al. (2020) Differential Role of Circulating microRNAs to Track Progression and Pre-Symptomatic Stage of Chronic Heart Failure: A Pilot Study. *Biomedicines*, 8(12).

McGowan K, et al. (2020) Expression Profiles of Exosomal MicroRNAs from HEV- and HCV-Infected Blood Donors and Patients: A Pilot Study. *Viruses*, 12(8).

Patamsyt? V, et al. (2020) Long Noncoding RNAs CARMN, LUCAT1, SMILR, and MALAT1 in Thoracic Aortic Aneurysm: Validation of Biomarkers in Clinical Samples. *Disease markers*, 2020, 8521899.

Larson VA, et al. (2018) Oligodendrocytes control potassium accumulation in white matter and seizure susceptibility. *eLife*, 7.

Funahashi Y, et al. (2014) Eribulin mesylate reduces tumor microenvironment abnormality by vascular remodeling in preclinical human breast cancer models. *Cancer science*, 105(10), 1334.

Bouchard-Mercier A, et al. (2014) SREBF1 gene variations modulate insulin sensitivity in response to a fish oil supplementation. *Lipids in health and disease*, 13, 152.