eXpress
RRID:SCR_006873
Type: Tool

Proper Citation

eXpress (RRID:SCR_006873)

Resource Information

URL: http://bio.math.berkeley.edu/eXpress/index.html

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Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented January 29, 2018.
From website: "Note that the eXpress software is also no longer being developed. We recommend you use kallisto instead." Kallisto can be found at http://pachterlab.github.io/kallisto/.

Software for streaming quantification for high-throughput DNA/RNA sequencing. Can be used in any application where abundances of target sequences need to be estimated from short reads sequenced from them.

Abbreviations: eXpress

Synonyms: eXpress - Streaming quantification for high-throughput sequencing, Berkeley-eXpress

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

Defining Citation: DOI:10.1038/nmeth.2251

Keywords: quantification, high-throughput, DNA, RNA, sequencing, target, fragment, analysis

Funding Agency: NSF, NHGRI
Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: eXpress

Resource ID: SCR_006873

Alternate IDs: SCR_015990, OMICS_01275

Alternate URLs: https://sources.debian.org/src/berkeley-express/

Record Creation Time: 20220129T080238+0000

Record Last Update: 20240702T053509+0000

Ratings and Alerts

No rating or validation information has been found for eXpress.

No alerts have been found for eXpress.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 493 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Liu Q, et al. (2024) Transcriptome Analysis of Brain and Skin Reveals Immune Responses to Acute Hypoxia and Reoxygenation in Pseudobagrus ussuriensis. Animals : an open access journal from MDPI, 14(2).


Jiang WR, et al. (2024) A circRNA ceRNA network involved in cognitive dysfunction after chronic cerebral hypoperfusion. Aging, 16(2), 1161.

Zhang S, et al. (2024) Whole-Transcriptome Sequencing Reveals the Global Molecular Responses and NAC Transcription Factors Involved in Drought Stress in Dendrobium catenatum. Antioxidants (Basel, Switzerland), 13(1).

Wang Q, et al. (2023) Integrated Transcriptomic and Metabolomic Analyses Reveal the Effects of Grafting on Special Metabolites of Acanthopanax senticosus Leaves. Molecules (Basel, Switzerland), 28(12).


Kashkooli AB, et al. (2023) Individual lipid transfer proteins from Tanacetum parthenium
show different specificity for extracellular accumulation of sesquiterpenes. Plant molecular biology, 111(1-2), 153.