Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 9, 2025

eXpress

RRID:SCR_006873
Type: Tool

Proper Citation

eXpress (RRID:SCR_006873)

Resource Information

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

Proper Citation: eXpress (RRID:SCR_006873)

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

Defining Citation: DOI:10.1038/nmeth.2251

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

Funding: NSF ;
NHGRI R01HG006129

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: 20250409T060559+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.

Warden CD, et al. (2024) Critical Differential Expression Assessment for Individual Bulk RNA-Seq Projects. bioRxiv : the preprint server for biology.

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).

Hao W, et al. (2024) Identification of lncRNA-miRNA-mRNA Networks in the Lenticular Nucleus Region of the Brain Contributes to Hepatolenticular Degeneration Pathogenesis and Therapy. Molecular neurobiology, 61(3), 1673.

Chen B, et al. (2024) ATG7/GAPLINC/IRF3 axis plays a critical role in regulating pathogenesis of influenza A virus. PLoS pathogens, 20(1), e1011958.

Salgado H, et al. (2024) RegulonDB v12.0: a comprehensive resource of transcriptional regulation in E. coli K-12. Nucleic acids research, 52(D1), D255.

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).

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

Alm S, et al. (2023) Prevalence and Risk Factors for Post-Discharge Feeding Problems in Children Born Extremely Preterm. Journal of pediatric gastroenterology and nutrition, 76(4), 498.

Wan YC, et al. (2023) Selection on Visual Opsin Genes in Diurnal Neotropical Frogs and Loss of the SWS2 Opsin in Poison Frogs. Molecular biology and evolution, 40(10).

Wang X, et al. (2023) LncRNA-XR_002792574.1-mediated ceRNA network reveals potential biomarkers in myopia-induced retinal ganglion cell damage. Journal of translational medicine, 21(1), 785.

Gnanagobal H, et al. (2023) Role of riboflavin biosynthesis gene duplication and transporter in Aeromonas salmonicida virulence in marine teleost fish. Virulence, 14(1), 2187025.

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).

Gulinuer A, et al. (2023) Host Transcriptome Analysis of Spodoptera frugiperda Larvae Parasitized by Microplitis manilae. Insects, 14(2).

Bakhshani A, et al. (2023) Prevalence of Human Papillomavirus (HPV) Genotypes among Women During 2015-2020 in Mashhad, Iran. Archives of Iranian medicine, 26(8), 419.

Katayama N, et al. (2023) Subgenome evolutionary dynamics in allotetraploid ferns: insights from the gene expression patterns in the allotetraploid species Phegopteris decursivepinnata (Thelypteridacea, Polypodiales). Frontiers in plant science, 14, 1286320.

Bodelón A, et al. (2023) Impact of Heat Stress on Transposable Element Expression and Derived Small RNAs in Drosophila subobscura. Genome biology and evolution, 15(11).

Pascual-Morales E, et al. (2023) Role of a LORELEI- like gene from Phaseolus vulgaris during a mutualistic interaction with Rhizobium tropici. PloS one, 18(12), e0294334.

Jo Y, et al. (2023) Exploring Tomato Fruit Viromes through Transcriptome Data Analysis. Viruses, 15(11).

Chen M, et al. (2023) Integrative Metabolic and Transcriptomic Profiling in Camellia oleifera and Camellia meiocarpa Uncover Potential Mechanisms That Govern Triacylglycerol Degradation during Seed Desiccation. Plants (Basel, Switzerland), 12(14).

Fablet M, et al. (2023) A Quantitative, Genome-Wide Analysis in Drosophila Reveals Transposable Elements' Influence on Gene Expression Is Species-Specific. Genome biology and evolution, 15(9).