

Resource Summary Report

Generated by [kravitz2](#) on Sep 4, 2026

Berkeley-express

RRID:SCR_015990

Type: Tool

Proper Citation

Berkeley-express (RRID:SCR_015990)

Resource Information

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

Proper Citation: Berkeley-express (RRID:SCR_015990)

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.

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

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

Funding: National Science Foundation Graduate Research Fellowship ; NHGRI R01 HG006129

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Berkeley-express

Resource ID: SCR_015990

Old URLs: bio.math.berkeley.edu

License: Artistic License 2.0., GPL

Record Creation Time: 20220129T080328+0000

Ratings and Alerts

No rating or validation information has been found for Berkeley-express.

No alerts have been found for Berkeley-express.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 5 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Alleman A, et al. (2018) Comparative analyses of co-evolving host-parasite associations reveal unique gene expression patterns underlying slavemaker raiding and host defensive phenotypes. Scientific reports, 8(1), 1951.

Cervantes-Perez SA, et al. (2018) Transcriptional profiling of the CAM plant Agave salmiana reveals conservation of a genetic program for regeneration. Developmental biology, 442(1), 28.

Boswell WT, et al. (2018) Exposure to 4100K fluorescent light elicits sex specific transcriptional responses in Xiphophorus maculatus skin. Comparative biochemistry and physiology. Toxicology & pharmacology : CBP, 208, 96.

Akkouche A, et al. (2017) Piwi Is Required during Drosophila Embryogenesis to License Dual-Strand piRNA Clusters for Transposon Repression in Adult Ovaries. Molecular cell, 66(3), 411.

Jeon J, et al. (2017) De novo transcriptome analysis and glucosinolate profiling in watercress (Nasturtium officinale R. Br.). BMC genomics, 18(1), 401.