Salmon
RRID:SCR_017036
Type: Tool

Proper Citation
Salmon (RRID:SCR_017036)

Resource Information

URL: https://combine-lab.github.io/salmon/

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Description: Software tool for quantifying expression of transcripts using RNA-seq data. Provides fast and bias-aware quantification of transcript expression. Transcriptome-wide quantifier to correct for fragment GC-content bias.

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

Defining Citation: PMID:28263959

Keywords: quantifying, expression, transcript, RNAseq, data, correct, fragment, GC, content, bias

Funding Agency: Gordon and Betty Moore Foundation Data-Driven Discovery Initiative, NHGRI, NHGRI, Alfred P. Sloan Research, NCI, NHGRI, NSF, NSF, NSF, NSF

Availability: Free, Available for download, Freely available

Resource Name: Salmon

Resource ID: SCR_017036

Alternate IDs: OMICS_09075

Ratings and Alerts

No rating or validation information has been found for Salmon.

No alerts have been found for Salmon.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 236 mentions in open access literature.

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


Morozumi Y, et al. (2024) Rapamycin-sensitive mechanisms confine the growth of fission yeast below the temperatures detrimental to cell physiology. iScience, 27(1), 108777.

Yue H, et al. (2024) Host genotype-specific rhizosphere fungus enhances drought resistance in wheat. Microbiome, 12(1), 44.


Tian S, et al. (2024) Nucleus pulposus cells regulate macrophages in degenerated intervertebral discs via the integrated stress response-mediated CCL2/7-CCR2 signaling pathway. Experimental & molecular medicine, 56(2), 408.


Frese AN, et al. (2024) Quantitative proteome dynamics across embryogenesis in a model chordate. iScience, 27(4), 109355.


Manesia JK, et al. (2023) AA2P-mediated DNA demethylation synergizes with stem cell agonists to promote expansion of hematopoietic stem cells. Cell reports methods, 3(12), 100663.


Peng L, et al. (2023) New insights into transcriptome variation during cattle adipocyte adipogenesis by direct RNA sequencing. iScience, 26(10), 107753.

Li JX, et al. (2023) Genomic virulence features of Beauveria bassiana as a biocontrol agent for the mountain pine beetle population. BMC genomics, 24(1), 390.

Burioli EAV, et al. (2023) Transcriptomics of mussel transmissible cancer MtrBTN2 suggests accumulation of multiple cancer traits and oncogenic pathways shared among bilaterians. Open biology, 13(10), 230259.