

Resource Summary Report

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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: Alfred P. Sloan Research ;
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NCI T32 CA009337;
NHGRI R01 HG005220;
NHGRI R01 HG007104;
NHGRI R21 HG006913;
NSF BIO-1564917;
NSF CCF-1053918;
NSF CCF-1256087;
NSF EF-0849899

Availability: Free, Available for download, Freely available

Resource Name: Salmon

Resource ID: SCR_017036

Alternate IDs: OMICS_09075

Alternate URLs: <https://github.com/COMBINE-lab/salmon>,
<https://sources.debian.org/src/salmon/>

License: GNU GPL 3

Record Creation Time: 20220129T080333+0000

Record Last Update: 20260912T195847+0000

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 439 mentions in open access literature.

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

Gong Y, et al. (2026) Prophylactic impact of cecal fermentation broth against gut microbiota dysbiosis of broiler chickens challenged with Escherichia coli. Animal microbiome, 8(1), 11.

Tishina S, et al. (2026) Oncogenic KRAS-driven type I interferon signalling primes pancreatic cancer for necroptosis. Nature communications, 17(1).

Li C, et al. (2026) Altered rumen bacterial flora is associated with increased lipogenesis of adipose tissue in obese dairy cows before calving. Microbiome, 14(1), 66.

Liu L, et al. (2026) The function of Toll-like receptor 2 in control of transcriptome responses to the microbiome and microbiome composition. Animal microbiome, 8(1), 5.

Ahmad AA, et al. (2026) Integrative multi-omics analysis of dietary fibre-induced modulations in the composition and function of chicken caecal microbiota. NPJ biofilms and microbiomes, 12(1).

Sakthikumar S, et al. (2026) Genomic Landscape Analysis of Canine Pulmonary Adenocarcinoma Reveals Candidate Targetable Gene Fusions. Veterinary and comparative oncology, 24(2), 393.

Maeda M, et al. (2026) CRISPR screen of human pancreatic cancer xenografts identifies a KLF5 proliferation vulnerability through epigenetic modifiers NCAPD2 and MTHFD1.

Molecular cancer, 25(1).

Park Y, et al. (2026) Physiological Changes and Transposition of Insertion Sequences in the dps-Double-Knockout Mutant of *Deinococcus geothermalis*. International journal of molecular sciences, 27(3).

Kioko M, et al. (2026) Variation in antiviral immunity and inflammation pathways precedes HIV-1 infection in a high-risk African cohort. The Journal of clinical investigation, 136(7).

Ciccone V, et al. (2026) A Beetle In Vitro: Establishment of a Short-Term Cell Culture from the Pest *Popillia japonica*. Insects, 17(2).

Grossi-Soyster EN, et al. (2026) Distinct virus-derived circular RNA molecule influences host response during SARS-CoV-2 infection. bioRxiv : the preprint server for biology.

Domingo J, et al. (2026) Nonlinear transcriptional responses to gradual modulation of transcription factor dosage. eLife, 13.

Li FQ, et al. (2026) Transcriptomic Resource of *Trissolcus cultratus*: A Key Biological Control Agent for *Halyomorpha halys*. Scientific data, 13(1).

Corral Nieto Y, et al. (2026) Identification of ACBP as a potential target in ciliopathic obesity through multi-omics network analysis. Nature communications, 17(1), 362.

Sun M, et al. (2026) Identification of the ZmDUF966 Gene Family in Maize, Analysis of Its Expression Under Cold Stress, and Preliminary Investigation of the ZmDUF966-10 Regulatory Network. Biology, 15(6).

Sahin IH, et al. (2026) Clinical and molecular characteristics of Class II and III BRAF mutations in colorectal cancer. NPJ precision oncology, 10(1).

Ren T, et al. (2026) scSurvival: Single-Cell Survival Analysis of Clinical Cancer Cohort Data at Cellular Resolution. Cancer discovery, 16(5), 931.

Colanero S, et al. (2026) Editing of SIMYB60 Reveals a Role in Cuticle Formation in Tomato. Physiologia plantarum, 178(3), e70922.

Tang C, et al. (2026) Investigating the determinants of immunotherapy response in the primary tumour of clear cell renal cell carcinoma (RCC). BMJ oncology, 5(2), e001031.

Katagirya E, et al. (2026) Conserved neutrophil degranulation transcripts in HIV-TB coinfecting children across East and Southern Africa. Communications medicine, 6(1).