

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: 20260821T194105+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 [dkNET](#) .

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.

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.

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.

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

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).

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).

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).

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*.

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.

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

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

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).

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

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

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.

Boffa F, et al. (2026) TGF- β 3 promotes trophoblast development in sheep embryos via ACSS2-dependent permissive lipid metabolism†. *Biology of reproduction*, 114(3), 773.