

# 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 ;  
Gordon and Betty Moore Foundation Data-Driven Discovery Initiative ;  
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:** 20260919T195333+0000

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## Ratings and Alerts

No rating or validation information has been found for Salmon.

No alerts have been found for Salmon.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## 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).

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.

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- $\beta$ 3 promotes trophoblast development in sheep embryos via ACSS2-dependent permissive lipid metabolism†. Biology of reproduction, 114(3), 773.