

Resource Summary Report

Generated by [kravitz2](#) on Sep 18, 2026

StringTie

RRID:SCR_016323

Type: Tool

Proper Citation

StringTie (RRID:SCR_016323)

Resource Information

URL: <https://ccb.jhu.edu/software/stringtie/>

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Description: Software application for assembling of RNA-Seq alignments into potential transcripts. It enables improved reconstruction of a transcriptome from RNA-seq reads. This transcript assembling and quantification program is implemented in C++ .

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

Defining Citation: [PMID:25690850](#), [DOI:10.1038/nbt.3122](#)

Keywords: assembling, RNA, sequence, transcript, gene, alignment, reconstruction, read, analysis, process, bio.tools

Funding: NCI R01 CA120185;
NCI R01 CA134292;
NHGRI R01 HG006102;
NHGRI R01 HG006677;
NIGMS R01 GM105705;
the Cancer Prevention and Research Institute of Texas

Availability: Open source, Free, Freely available, Available for download

Resource Name: StringTie

Resource ID: SCR_016323

Alternate IDs: biotools:stringtie, OMICS_07226

Alternate URLs: <https://github.com/gperte/stringtie>, <https://bio.tools/stringtie>, <https://sources.debian.org/src/stringtie/>

License: Artistic License

Record Creation Time: 20220129T080330+0000

Record Last Update: 20260912T200018+0000

Ratings and Alerts

No rating or validation information has been found for StringTie .

No alerts have been found for StringTie .

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4976 mentions in open access literature.

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

Gauthier J, et al. (2026) B cell-intrinsic IL-2 signaling regulates inflammation by promoting IL-10 expression in CD25+ age-associated B cells. *Immunity*, 59(2), 354.

Zhao Y, et al. (2026) IDH1 Reprograms Nucleotide Metabolism by Inducing Chromatin Remodeling and DHODH Transcription to Drive Chemoresistance in Nasopharyngeal Carcinoma. *Cancer research*, 86(8), 2004.

Lyu P, et al. (2026) Genetic variation reveals a homeotic long noncoding RNA that modulates human hematopoietic stem cells. *Cell*, 189(13), 4022.

Tao H, et al. (2026) NSD1-Mediated PPAR γ Methylation Enhances PTEN Activity to Suppress Glycolysis and Tumor Progression in Endometrial Cancer. *Cancer research*, 86(10), 2464.

Mao C, et al. (2026) Chromosome-level genome assembly and transcriptomes of the leaf insect *Cryptophyllum westwoodii* provide insights into the evolution of leaf-like masquerade. *GigaScience*, 15.

Lee D, et al. (2026) Microglial VRK2 Regulates Astrocytic GABA Synthesis and Tonic Inhibition in the Thalamus. *Glia*, 74(1), e70101.

Li P, et al. (2026) Global mapping of circRNA-target RNA interactions reveal P-body-mediated translational repression. *Molecular cell*, 86(5), 868.

Zhang Y, et al. (2026) A sequential dual-drug delivery system for multi-target inhibition of subretinal fibrosis. *Journal of nanobiotechnology*, 24(1).

Shi M, et al. (2026) Transcriptomic landscape of transposable elements reveals LTR7-PLAAT4 as a potential oncogene and therapeutic target in pancreatic adenocarcinoma. *Genome research*, 36(2), 275.

Kim H, et al. (2026) Thyroid cancer-associated EZH1 Q571R mutation drives chromatin compaction and H3K27me3 invasion into active chromatin. *Molecular cell*, 86(14), 2739.

Liu H, et al. (2026) The genomes of 5 mantises provide insights into sex chromosome evolution and Mantodea phylogeny clarification. *GigaScience*, 15.

Lee JB, et al. (2026) Lazertinib with stereotactic body radiotherapy in oligometastatic EGFR-mutant non-small-cell lung cancer. *ESMO open*, 11(2), 106057.

Kumar H, et al. (2026) FusionTarget: Computational framework for drug repurposing against modeled fusion protein structures from genomic breakpoints. *iScience*, 29(6), 116076.

Schlebusch SA, et al. (2026) Sex chromosome turnover and structural genome divergence shape meiotic outcomes in hybridizing *Cobitis*. *GigaScience*, 15.

Pastrana CC, et al. (2026) Nonsense-Mediated RNA Decay Is a Targetable Vulnerability in Splicing Factor Mutant Myeloid Neoplasms by Enhancing R-Loop Accumulation and DNA Damage. *Cancer research*, 86(14), 3537.

Zhang L, et al. (2026) Bcl11a orchestrates multilineage integrity in aging hematopoiesis by regulating multipotent progenitor fate decisions. *Cell reports*, 45(7), 117716.

Wang D, et al. (2026) IGF2BP3 recognizes m6A to regulate histone-to-protamine replacement during mouse sperm development. *The EMBO journal*, 45(2), 504.

Liu R, et al. (2026) iFish: a comprehensive multi-omics database for fish genetics, transcriptional regulation, and epigenetic research. *Nucleic acids research*, 54(D1), D1108.

Yang W, et al. (2026) Genome-wide identification of GAPDH gene family and functional analysis of CaGAPC2-mediated autophagy during BWYV infection in pepper. *BMC genomics*, 27(1), 123.

Baráth BR, et al. (2026) Distinct transcriptional and epigenomic programs define Hofbauer cells in term placenta. *JCI insight*, 11(3).