

Resource Summary Report

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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, software application, sequence analysis software, 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: the Cancer Prevention and Research Institute of Texas ;
NHGRI R01 HG006677;
NIGMS R01 GM105705;
NHGRI R01 HG006102;
NCI R01 CA120185;
NCI R01 CA134292

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: 20260810T040640+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 [NIF](#) .

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.

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.

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.

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

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

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.

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

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).