**StringTie**

RRID:SCR_016323  
Type: Tool

**Proper Citation**

StringTie (RRID:SCR_016323)

**Resource Information**

**URL:** https://ccb.jhu.edu/software/stringtie/

**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 Name:** StringTie

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

**Keywords:** assembling, RNA, sequence, transcript, gene, alignment, reconstruction, read, analysis, process

**Resource ID:** SCR_016323

**Funding Agency:** NCI, NHGRI, NIGMS, the Cancer Prevention and Research Institute of Texas

**References:** PMID:25690850

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

**Website Status:** Last checked down

**Alternate URLs:** https://github.com/gpertea/stringtie

**Mentions Count:** 121
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 121 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch Infrastructure.

Ng‘oma E, et al. (2020) Diverse biological processes coordinate the transcriptional response to nutritional changes in a Drosophila melanogaster multiparent population. BMC genomics, 21(1), 84.


