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

Proper Citation: StringTie (RRID:SCR_016323)

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.


