

Resource Summary Report

Generated by SPARC SAWG on Sep 17, 2026

FusionHunter

RRID:SCR_011895

Type: Tool

Proper Citation

FusionHunter (RRID:SCR_011895)

Resource Information

URL: <http://bioen-compbio.bioen.illinois.edu/FusionHunter/>

Proper Citation: FusionHunter (RRID:SCR_011895)

Description: Software for identifying fusion transcripts using paired-end RNA-seq.

Abbreviations: FusionHunter

Synonyms: FusionHunter: identifying fusion transcripts using paired-end RNA-seq

Resource Type: software resource, source code

Keywords: perl, annotation, bio.tools

Resource Name: FusionHunter

Resource ID: SCR_011895

Alternate IDs: OMICS_01350, biotools:fusionhunter

Alternate URLs: <https://bio.tools/fusionhunter>

Record Creation Time: 20220129T080307+0000

Record Last Update: 20260912T200337+0000

Ratings and Alerts

No rating or validation information has been found for FusionHunter.

No alerts have been found for FusionHunter.

Data and Source Information

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Matsumoto Y, et al. (2021) Detection of novel and recurrent conjoined genes in non-Hodgkin B-cell lymphoma. Journal of clinical and experimental hematopathology : JCEH, 61(2), 71.

Haas BJ, et al. (2019) Accuracy assessment of fusion transcript detection via read-mapping and de novo fusion transcript assembly-based methods. Genome biology, 20(1), 213.

Yu Y, et al. (2018) SeqOthello: querying RNA-seq experiments at scale. Genome biology, 19(1), 167.

Lee M, et al. (2017) ChimerDB 3.0: an enhanced database for fusion genes from cancer transcriptome and literature data mining. Nucleic acids research, 45(D1), D784.

Kumar S, et al. (2016) Comparative assessment of methods for the fusion transcripts detection from RNA-Seq data. Scientific reports, 6, 21597.

Liu S, et al. (2016) Comprehensive evaluation of fusion transcript detection algorithms and a meta-caller to combine top performing methods in paired-end RNA-seq data. Nucleic acids research, 44(5), e47.

Latysheva NS, et al. (2016) Discovering and understanding oncogenic gene fusions through data intensive computational approaches. Nucleic acids research, 44(10), 4487.

Thangam M, et al. (2015) CRCDA--Comprehensive resources for cancer NGS data analysis. Database : the journal of biological databases and curation, 2015.