

Resource Summary Report

Generated by [FDI Lab - SciCrunch.org](#) on May 17, 2025

STRViper

RRID:SCR_001179

Type: Tool

Proper Citation

STRViper (RRID:SCR_001179)

Resource Information

URL: <http://bioinf.scmb.uq.edu.au/STRViper/>

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Description: Software tool for detection of short tandem repeat (STR) variations from paired-end next generation sequencing data. It makes variant calls based on deviations in sequence fragment sizes, allowing the analysis of repeats of size up to fragment length. This strategy also helps avoiding false calls resulting from errors arising from sequencing of repeat DNA.

Abbreviations: STRViper

Synonyms: Short Tandem Repeat Variation Identification from Paired-End Reads, STRViper: Short Tandem Repeat Variation Identification from Paired-End Reads

Resource Type: software resource

Defining Citation: [PMID:24353318](#)

Keywords: next-generation sequencing, short tandem repeat variation, short tandem repeat, java, unix, linux, macos, paired-end read

Funding:

Availability: Acknowledgement requested

Resource Name: STRViper

Resource ID: SCR_001179

Alternate IDs: OMICS_02177

Record Creation Time: 20220129T080206+0000

Record Last Update: 20250420T014022+0000

Ratings and Alerts

No rating or validation information has been found for STRViper.

No alerts have been found for STRViper.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Dashnow H, et al. (2018) STretch: detecting and discovering pathogenic short tandem repeat expansions. Genome biology, 19(1), 121.