# **Resource Summary Report**

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# **STRViper**

RRID:SCR\_001179

Type: Tool

### **Proper Citation**

STRViper (RRID:SCR\_001179)

#### **Resource Information**

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

**Proper Citation:** STRViper (RRID:SCR\_001179)

**Description:** Software tool for detection of short tandem repeat (STR) variations from pairedend 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 stratergy also helps avoiding false calls resulting from errors arised from sequencing of repeat DNA.

**Abbreviations:** STRViper

**Synonyms:** Short Tandem Repeat Variation Indentification from Paired-End Reads, STRViper: Short Tandem Repeat Variation Indentification 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 dkNET.

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