

# Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 19, 2026

## [glfMultiples](#)

RRID:SCR\_010763

Type: Tool

### Proper Citation

glfMultiples (RRID:SCR\_010763)

### Resource Information

**URL:** <http://genome.sph.umich.edu/wiki/GlfMultiples>

**Proper Citation:** glfMultiples (RRID:SCR\_010763)

**Description:** A GLF-based variant caller for next-generation sequencing data.

**Abbreviations:** glfMultiples

**Resource Type:** software resource

**Resource Name:** glfMultiples

**Resource ID:** SCR\_010763

**Alternate IDs:** OMICS\_00061

**Record Creation Time:** 20220129T080300+0000

**Record Last Update:** 20260912T195723+0000

### Ratings and Alerts

No rating or validation information has been found for glfMultiples.

No alerts have been found for glfMultiples.

### Data and Source Information

**Source:** [SciCrunch Registry](#)

### Usage and Citation Metrics

We found 3 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [PRECISE-TBI](#) .

Onda Y, et al. (2018) Multiplex PCR Targeted Amplicon Sequencing (MTA-Seq): Simple, Flexible, and Versatile SNP Genotyping by Highly Multiplexed PCR Amplicon Sequencing. *Frontiers in plant science*, 9, 201.

Jun G, et al. (2015) An efficient and scalable analysis framework for variant extraction and refinement from population-scale DNA sequence data. *Genome research*, 25(6), 918.

Emond MJ, et al. (2015) Exome Sequencing of Phenotypic Extremes Identifies CAV2 and TMC6 as Interacting Modifiers of Chronic *Pseudomonas aeruginosa* Infection in Cystic Fibrosis. *PLoS genetics*, 11(6), e1005273.