

Resource Summary Report

Generated by [nidm-terms](#) on Jul 29, 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: 20260725T190704+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 [nidm-terms](#) .

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.