

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 7, 2026

GATK VariantFiltration

RRID:SCR_028441

Type: Tool

Proper Citation

GATK VariantFiltration (RRID:SCR_028441)

Resource Information

URL: <https://gatk.broadinstitute.org/hc/en-us/articles/360036350452-VariantFiltration>

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Description: Software command-line tool designed for hard-filtering variant callsets (VCF files) by applying user-defined criteria to annotate, rather than remove, low-quality variants. It marks fails in the FILTER field (e.g., using JEXL expressions to filter by DP, QD, or FS), making it essential for filtering small datasets, non-model organisms, or whenever Variant Quality Score Recalibration (VQSR) is not feasible

Resource Type: software application, software resource

Keywords: hard-filtering variant callsets, annotate low-quality variants,

Availability: Free, Freely available

Resource Name: GATK VariantFiltration

Resource ID: SCR_028441

Alternate URLs: <https://gatk.broadinstitute.org/hc/en-us>

Record Creation Time: 20260514T062433+0000

Record Last Update: 20260905T133612+0000

Ratings and Alerts

No rating or validation information has been found for GATK VariantFiltration.

No alerts have been found for GATK VariantFiltration.

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 [PRECISE-TBI](#) .

Dong YP, et al. (2026) Early replication fragile sites are associated with cancer-related CNVs and SNVs in human embryonic stem cells. Stem cell reports, 21(7), 102968.