

Resource Summary Report

Generated by [dkNET](#) on Aug 4, 2026

GATK HaplotypeCaller

RRID:SCR_028440

Type: Tool

Proper Citation

GATK HaplotypeCaller (RRID:SCR_028440)

Resource Information

URL: <https://gatk.broadinstitute.org/hc/en-us/articles/360042913231-HaplotypeCaller>

Proper Citation: GATK HaplotypeCaller (RRID:SCR_028440)

Description: Software tool for identifying single nucleotide polymorphisms (SNPs) and insertion/deletion (indels) variants, offering high accuracy via local de-novo assembly of reads. It works by identifying "active regions" with potential variation, reassembling those reads, and calculating genotype likelihoods, making it superior for complex variant detection.

Resource Type: software resource, software application

Defining Citation: [DOI:10.1101/201178](https://doi.org/10.1101/201178)

Keywords: identifying single nucleotide polymorphisms, insertion, deletion, indels, variants, local de-novo assembly of reads,

Availability: Free, Freely available

Resource Name: GATK HaplotypeCaller

Resource ID: SCR_028440

Alternate URLs: <https://gatk.broadinstitute.org/hc/en-us>,
<https://gatk.broadinstitute.org/hc/en-us/articles/360035531412-HaplotypeCaller-in-a-nutshell>

Record Creation Time: 20260514T062433+0000

Record Last Update: 20260801T191442+0000

Ratings and Alerts

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

No alerts have been found for GATK HaplotypeCaller.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.