

Resource Summary Report

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GATK

RRID:SCR_001876

Type: Tool

Proper Citation

GATK (RRID:SCR_001876)

Resource Information

URL: <https://software.broadinstitute.org/gatk/>

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Description: A software package to analyze next-generation resequencing data. The toolkit offers a wide variety of tools, with a primary focus on variant discovery and genotyping as well as strong emphasis on data quality assurance. Its robust architecture, powerful processing engine and high-performance computing features make it capable of taking on projects of any size. This software library makes writing efficient analysis tools using next-generation sequencing data very easy, and second it's a suite of tools for working with human medical resequencing projects such as 1000 Genomes and The Cancer Genome Atlas. These tools include things like a depth of coverage analyzers, a quality score recalibrator, a SNP/indel caller and a local realigner. (entry from Genetic Analysis Software)

Abbreviations: GATK

Synonyms: Genome Analysis ToolKit

Resource Type: data analysis software, software resource, software application, software library, data processing software, software toolkit

Defining Citation: [PMID:21478889](#)

Keywords: gene, genetic, genomic, next-generation resequencing, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: GATK

Resource ID: SCR_001876

Alternate IDs: nlx_154324, OMICS_00286, biotools:gatk

Alternate URLs:

http://www.broadinstitute.org/gsa/wiki/index.php/The_Genome_Analysis_Toolkit,
<https://bio.tools/gatk>

Record Creation Time: 20220129T080210+0000

Record Last Update: 20260728T043119+0000

Ratings and Alerts

No rating or validation information has been found for GATK.

No alerts have been found for GATK.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 16663 mentions in open access literature.

Listed below are recent publications. The full list is available at [nidm-terms](#).

Cappadona C, et al. (2026) Multi-omics identifies oxidative stress, prothrombotic pathways, and lactoperoxidase variants as key factors in COVID-19 severity. EBioMedicine, 123, 106111.

Morrissey RL, et al. (2026) Elucidating cooperative genetic events in DCIS progression in mutant p53-driven breast cancer. Proceedings of the National Academy of Sciences of the United States of America, 123(2), e2526544123.

Yang Q, et al. (2026) Molecular mechanism of resistance to lonafarnib conferred by mutations in the cysteine-rich region of respiratory syncytial virus fusion glycoprotein and discovery of a lonafarnib-derived antiviral PROTAC. Journal of virology, 100(1), e0148725.

Yang W, et al. (2026) Multi-omics reveals co-regulation of hepatic bile acid metabolism in laying hens by host genetics and the cecal Anaerostipes. Poultry science, 105(3), 106388.

Kerstens M, et al. (2026) PLETHORAs shape Arabidopsis phyllotaxis through modulation of patterning robustness and accelerated inflorescence development. The New phytologist, 249(1), 495.

Taylor RS, et al. (2026) Accurate Runs of Homozygosity Estimation From Low Coverage Genome Sequences in Non-Model Species. Molecular ecology resources, 26(1), e70083.

Burns R, et al. (2026) Diploid origins and early genome stabilization in the allotetraploid Arabidopsis suecica. The New phytologist, 249(1), 524.

Huang X, et al. (2026) PMEL governs autosomal dominant inheritance of white-tail independent of yellow body plumage in chickens (*Gallus gallus domesticus*). *Poultry science*, 105(1), 106127.

Upadhyayula BS, et al. (2026) Mutational Spectrum of T-Cell Large Granular Lymphocytic Leukemia: Insights From the AACR Project GENIE Consortium. *Cancer genomics & proteomics*, 23(1), 135.

Rajtmajerova M, et al. (2026) Genetic differences between primary colorectal cancer and its paired synchronous and metachronous metastases. *International journal of cancer*, 158(1), 120.

Showpnil IA, et al. (2026) De Novo Heterozygous ZFX Frameshift Variant in a Female With an X-Linked Neurodevelopmental Disorder. *American journal of medical genetics. Part A*, 200(2), 521.

Teng CS, et al. (2026) Actomyosin contractility and a threshold of cadherin cell adhesion are required during tissue fusion. *The Journal of cell biology*, 225(1).

Yang R, et al. (2026) Population structure and genome-wide association study of body conformation traits of two native goat breeds in China. *Animal bioscience*, 39(1), 250334.

Navarro D, et al. (2026) Development of High-Throughput Genomic Resources to Inform White-Tailed Deer Population and Disease Management. *Molecular ecology resources*, 26(1), e70085.

Tu Y, et al. (2026) Identification of molecular markers associated with comb traits through genome-wide association study on a specialized strain of yellow feathered broilers. *Poultry science*, 105(1), 106125.

Lim KHJ, et al. (2026) Cross-presentation of dead cell-associated antigens shapes the neoantigenic landscape of tumor immunity. *Nature immunology*, 27(1), 72.

Ma WH, et al. (2026) Targeting PTPN13 with 11-amino-acid peptides of C-terminal APC prevents immune evasion of colorectal cancer. *Cell research*, 36(1), 72.

Zhang X, et al. (2026) Genetic and Functional Evidence Links Germline Biallelic Inactivating Variants in *WWOX* to Histological Mixed-Type Thyroid Cancer. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(1), e07602.

Kim CY, et al. (2026) Integrative multi-omics of matched primary and liver metastatic colorectal cancer organoids identifies putative molecular targets. *Translational oncology*, 63, 102592.

Miya F, et al. (2026) Augmenting cost-effectiveness in clinical diagnosis using extended whole-exome sequencing: SNVs, SVs, and beyond. *Journal of human genetics*, 71(1), 13.