

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 processing software, software toolkit, data analysis software, software resource, software library, software application

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: 20260731T042621+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 [kravitz2](#) .

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.