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

Defining Citation: PMID:21478889

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

Funding:

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

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Record Last Update: 20250505T053402+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 14330 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Rostamzadeh Mahdabi E, et al. (2025) Comparative Analysis of Runs of Homozygosity Islands in Indigenous and Commercial Chickens Revealed Candidate Loci for Disease Resistance and Production Traits. Veterinary medicine and science, 11(1), e70074.

Tejedor JR, et al. (2025) Integration of multi-omics layers empowers precision diagnosis through unveiling pathogenic mechanisms on maple syrup urine disease. Journal of inherited metabolic disease, 48(1), e12829.

Aizpurua-Iraola J, et al. (2025) A reduction in effective population size has not relaxed purifying selection in the human population of Eivissa (Balearic Islands). Scientific reports, 15(1), 660.

Sasa N, et al. (2025) Blood DNA virome associates with autoimmune diseases and COVID-19. Nature genetics, 57(1), 65.

Mapendano CK, et al. (2025) Longer survival with precision medicine in late-stage cancer patients. ESMO open, 10(1), 104089.

Peillard-Fiorente F, et al. (2025) Point mutations in functionally diverse genes are associated with increased natural DNA transformation in multidrug resistant Streptococcus pneumoniae. Nucleic acids research, 53(1).

Liu JN, et al. (2025) Pan-genome analyses of 11 Fraxinus species provide insights into salt adaptation in ash trees. Plant communications, 6(1), 101137.

Alfayyadh MM, et al. (2025) PathVar: A Customisable NGS Variant Calling Algorithm Implicates Novel Candidate Genes and Pathways in Hemiplegic Migraine. Clinical genetics, 107(2), 157.

Heimer G, et al. (2025) Biallelic PIGM Coding Variant Causes Intractable Epilepsy and Intellectual Disability Without Thrombotic Events. Clinical genetics, 107(2), 179.

Shi W, et al. (2025) VDGE: a data repository of variation database for gene-edited animals across multiple species. Nucleic acids research, 53(D1), D1250.

Xu X, et al. (2025) Redefining the accumulated temperature index for accurate prediction of rice flowering time in diverse environments. Plant biotechnology journal, 23(1), 302.

McGuire E, et al. (2025) A case of penicillin-resistant group B Streptococcus isolated from a patient in the UK. The Journal of antimicrobial chemotherapy, 80(2), 399.

Van Haute L, et al. (2025) Pathogenic PDE12 variants impair mitochondrial RNA processing causing neonatal mitochondrial disease. EMBO molecular medicine, 17(1), 193.

Wang J, et al. (2025) Research note: A low-density SNP genotyping panel for Chinese native chickens. Poultry science, 104(1), 104609.

Bayam E, et al. (2025) Bi-allelic variants in WDR47 cause a complex neurodevelopmental syndrome. EMBO molecular medicine, 17(1), 129.

Lei JT, et al. (2025) Patient-Derived Xenografts of Triple-Negative Breast Cancer Enable Deconvolution and Prediction of Chemotherapy Responses. bioRxiv : the preprint server for biology.

Peng J, et al. (2025) Integration of machine learning and genome-wide association study to explore the genomic prediction accuracy of agronomic trait in oats (Avena sativa L.). The plant genome, 18(1), e20549.

Lee H, et al. (2025) A Korean Patient With Leber Congenital Amaurosis and a Homozygous RPE65 Variant Originating From a Paternal Uniparental Isodisomy. Molecular genetics & genomic medicine, 13(1), e70060.

Wang M, et al. (2025) YHSeqY3000 panel captures all founding lineages in the Chinese paternal genomic diversity database. BMC biology, 23(1), 18.

Su Q, et al. (2025) Allelic variation in an expansin, MdEXP-A1, contributes to flesh firmness at harvest in apples. Molecular horticulture, 5(1), 3.