Resource Summary Report

Generated by NIF on Apr 8, 2025

IndelGenotyper

RRID:SCR_016663
Type: Tool

Proper Citation

IndelGenotyper (RRID:SCR_016663)

Resource Information

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

Proper Citation: IndelGenotyper (RRID:SCR_016663)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on July 18th,2023. Software package for genome analysis. Used for analysis of next generation genomic data in cancer.

Abbreviations: GATK

Synonyms: GATK Indel Genotyper, Genome Analysis Toolkit (GATK) Indel Genotyper, Indel Genotyper, GATK IndelGenotyper

Resource Type: software application, sequence analysis software, data analysis software, data processing software, software resource

Keywords: next, generation, analysis, genomic, data, cancer, genome

Funding:

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: IndelGenotyper

Resource ID: SCR_016663

Alternate URLs: https://github.com/broadinstitute/gatk/, https://sources.debian.org/src/gatk/

License: BSD 3-clause licence

Record Creation Time: 20220129T080331+0000

Record Last Update: 20250407T220339+0000

Ratings and Alerts

No rating or validation information has been found for IndelGenotyper.

No alerts have been found for IndelGenotyper.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 39 mentions in open access literature.

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

Martins Rodrigues F, et al. (2025) Germline predisposition in multiple myeloma. iScience, 28(1), 111620.

Cui J, et al. (2025) Telomere-to-telomere Phragmites australis reference genome assembly with a B chromosome provides insights into its evolution and polysaccharide biosynthesis. Communications biology, 8(1), 73.

Silveira AB, et al. (2024) Base-excision repair pathway shapes 5-methylcytosine deamination signatures in pan-cancer genomes. Nature communications, 15(1), 9864.

Liu P, et al. (2024) Investigation of Imidazolinone Herbicide Resistance Gene with KASP Markers for Japonica/Geng Rice Varieties in the Huanghuaihai Region of China. Plants (Basel, Switzerland), 13(8).

Huang X, et al. (2024) The genome of African manatee Trichechus senegalensis reveals secondary adaptation to the aquatic environment. iScience, 27(7), 110394.

Foley NM, et al. (2024) Karyotypic stasis and swarming influenced the evolution of viral tolerance in a species-rich bat radiation. Cell genomics, 4(2), 100482.

Xu W, et al. (2024) Multiple-Wave Admixture and Adaptive Evolution of the Pamirian Wakhi People. Molecular biology and evolution, 41(12).

Antunes LN, et al. (2024) Genetic heterogeneity in autosomal recessive hearing loss: a survey of Brazilian families. Frontiers in genetics, 15, 1409306.

Zheng H, et al. (2024) Grain Protein Content Phenotyping in Rice via Hyperspectral Imaging Technology and a Genome-Wide Association Study. Plant phenomics (Washington, D.C.), 6, 0200.

Qin T, et al. (2024) Genomic profiling of a multi-lineage and multi-passage patient-derived xenograft biobank reflects heterogeneity of ovarian cancer. Cell reports. Medicine, 5(7), 101631.

Tian P, et al. (2024) Genomic Single Nucleotide Polymorphism (SNP) markers and mitochondrial haplotypes illuminate the origins of Crown-of-Thorns Starfish (Acanthaster solaris) outbreaks in the South China Sea. BMC genomics, 25(1), 1094.

Du Y, et al. (2024) Clinical Analysis of Pediatric Acute Megakaryocytic Leukemia With CBFA2T3-GLIS2 Fusion Gene. Journal of pediatric hematology/oncology, 46(2), 96.

Karunakaran C, et al. (2024) Exploring the Role of Non-synonymous and Deleterious Variants Identified in Colorectal Cancer: A Multi-dimensional Computational Scrutiny of Exomes. Current genomics, 25(1), 41.

Zhang B, et al. (2024) Drought response revealed by chromatin organization variation and transcriptional regulation in cotton. BMC biology, 22(1), 114.

Liu HK, et al. (2024) A Cysteinyl-tRNA Synthetase Mutation Causes Novel Autosomal-Dominant Inheritance of a Parkinsonism/Spinocerebellar-Ataxia Complex. Neuroscience bulletin, 40(10), 1489.

Anurag M, et al. (2024) Multiomics profiling of urothelial carcinoma in situ reveals CIS-specific gene signature and immune characteristics. iScience, 27(3), 109179.

Xu S, et al. (2024) Whole-exome sequencing reveals novel genomic signatures and potential therapeutic targets during the progression of rectal neuroendocrine neoplasm. Cell death & disease, 15(11), 833.

He Q, et al. (2024) A genome-wide association study of neonatal metabolites. Cell genomics, 4(10), 100668.

Xiao R, et al. (2024) Disruption of mitochondrial energy metabolism is a putative pathogenesis of Diamond-Blackfan anemia. iScience, 27(3), 109172.

Liu Z, et al. (2024) Nuclear environmental DNA resolves fine-scale population genetic structure in an aquatic habitat. iScience, 27(1), 108669.