Resource Summary Report

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

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

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: 20260905T132812+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 88 mentions in open access literature.

Listed below are recent publications. The full list is available at PRECISE-TBI .

Al-Yazeedi T, et al. (2026) Genetic Mapping of Resistance: ddRADseq-Based QTL and Associated Polymorphism Conferring Resistance to Alpha-Cypermethrin in Anopheles funestus. Molecular ecology, 35(1), e70207.

Dominguez-Alonso S, et al. (2026) Non-coding Regulatory Variants in ASD (Autism Spectrum Disorders) Disrupt CTCF Domains and Shape Cell-Type-Specific Neurodevelopmental Landscapes Revealed by Single-Cell Analyses and Cortical Organoids. Research square.

Dea A, et al. (2026) Physiological architecture and evolutionary origins of cellular adaptability. bioRxiv : the preprint server for biology.

Yang SH, et al. (2026) ML-ExonCNV: a robust XGBoost multi-expert ensemble framework for rare exon CNV detection in whole-exome sequencing data. Briefings in bioinformatics, 27(2).

Litman A, et al. (2026) Variant-resolved prediction of context-specific isoform variation with a graph-based attention model. Cell genomics, 6(4), 101126.

Thambiraja M, et al. (2026) Genetic basis of immunity in Indian cattle as revealed by comparative analysis of Bos genome. Scientific reports, 16(1).

Becquart P, et al. (2026) Wnt-presenting materials sustain H3K14-acetylation in human skeletal stem cells for tissue engineering and bone repair. NPJ Regenerative medicine, 11(1).

Andersen S, et al. (2026) Oncostatin M receptor deficiency as a novel candidate genetic cause of autosomal recessive hyper-IgE syndrome. Journal of human immunity, 2(3), e20250119.

Blazyte A, et al. (2026) Fifteen Years of the Genome Analysis Toolkit as the De Facto Standard in Short-Read Variant Calling. International journal of molecular sciences, 27(9).

Zhao H, et al. (2026) Integrated analyses of host genetics and gut microbiota provide mechanistic insights into feed efficiency in ducks. Journal of animal science and biotechnology, 17(1).

Bi D, et al. (2026) Integrating ANI and phylogenies for re-evaluation of Fusobacterium taxonomy and disease associations. Nature communications, 17(1).

Wang M, et al. (2026) Revision of Amana yunjuensis (Liliaceae) based on morphological and molecular evidence: synonym of Amana anhuiensis. PhytoKeys, 269, 275.

Hackl L, et al. (2025) Homozygous DHCR7 p.Val330Met Variant Associated with Mild Non-Syndromic Intellectual Disability and Elevated Serum 7-Dehydrocholesterol Levels in Two Siblings. Genes, 16(7).

Batlle-Mas?? L, et al. (2025) Somatic reversion in CD137 deficiency correlating with Epstein-Barr virus control and clinical improvement. NPJ genomic medicine, 10(1), 78.

Cheng T, et al. (2025) Genome-wide identification, expression profile and selection analysis of the CPK gene family in Nelumbo nucifera. BMC genomics, 26(1), 461.

Yang T, et al. (2025) Chromosome-level genome assembly provides insights into flavonoid biosynthesis in stems and leaves and fatty acid biosynthesis in kernels of Erythropalum scandens. BMC plant biology, 25(1), 1000.

Sacchi S, et al. (2025) A phosphoserine phosphatase variant present in the brain of Alzheimer's disease patients favors nuclear mistargeting. The FEBS journal, 292(18), 4955.

Rebello RJ, et al. (2025) Whole genome sequencing improves tissue-of-origin diagnosis and treatment options for cancer of unknown primary. Nature communications, 16(1), 4422.

Perez-Riverol Y, et al. (2025) Open-Source and FAIR Research Software for Proteomics. Journal of proteome research, 24(5), 2222.

Messingschlager M, et al. (2025) DNA methylation changes during acute COVID-19 are associated with long-term transcriptional dysregulation in patients' airway epithelial cells. EMBO molecular medicine, 17(5), 923.