

Resource Summary Report

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UnifiedGenotyper

RRID:SCR_004710

Type: Tool

Proper Citation

UnifiedGenotyper (RRID:SCR_004710)

Resource Information

URL:

http://www.broadinstitute.org/gatk/gatkdocs/org_broadinstitute_sting_gatk_walkers_genotyper UnifiedGenotyper

Proper Citation: UnifiedGenotyper (RRID:SCR_004710)

Description: A multiple-sample, technology-aware SNP and indel caller.

Abbreviations: UnifiedGenotyper

Resource Type: software resource

Resource Name: UnifiedGenotyper

Resource ID: SCR_004710

Alternate IDs: OMICS_00080

Record Creation Time: 20220129T080226+0000

Record Last Update: 20260801T190244+0000

Ratings and Alerts

No rating or validation information has been found for UnifiedGenotyper.

No alerts have been found for UnifiedGenotyper.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 561 mentions in open access literature.

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

Fu P, et al. (2025) Population Genetics and Trajectory Simulation Reveals the Invasion Process of the Fall Armyworm (*Spodoptera frugiperda*) in the Eastern Hemisphere. *Evolutionary applications*, 18(2), e70086.

Ren X, et al. (2025) Genomic and Metabolomic Analyses of *Streptomyces albulus* with Enhanced γ -Poly-L-lysine Production Through Adaptive Laboratory Evolution. *Microorganisms*, 13(1).

Liu S, et al. (2024) Utilizing non-invasive prenatal test sequencing data for human genetic investigation. *Cell genomics*, 4(10), 100669.

Ausmees K, et al. (2023) Achieving improved accuracy for imputation of ancient DNA. *Bioinformatics (Oxford, England)*, 39(1).

Rodríguez A, et al. (2022) TGF β pathway is required for viable gestation of Fanconi anemia embryos. *PLoS genetics*, 18(11), e1010459.

Ausmees K, et al. (2022) An empirical evaluation of genotype imputation of ancient DNA. *G3 (Bethesda, Md.)*, 12(6).

Bagagli E, et al. (2021) *Paracoccidioides brasiliensis* Isolated from Nine-Banded Armadillos (*Dasypus novemcinctus*) Reveal Population Structure and Admixture in the Amazon Basin. *Journal of fungi (Basel, Switzerland)*, 7(1).

de Melo Teixeira M, et al. (2021) Mitochondrial genomes of the human pathogens *Coccidioides immitis* and *Coccidioides posadasii*. *G3 (Bethesda, Md.)*, 11(7).

Guo X, et al. (2021) Revisiting the evolutionary history of domestic and wild ducks based on genomic analyses. *Zoological research*, 42(1), 43.

Gowans LJJ, et al. (2021) Co-occurrence of orofacial clefts and clubfoot phenotypes in a sub-Saharan African cohort: Whole-exome sequencing implicates multiple syndromes and genes. *Molecular genetics & genomic medicine*, 9(4), e1655.

Witten A, et al. (2020) ADAMTS12, a new candidate gene for pediatric stroke. *PloS one*, 15(8), e0237928.

de Oliveira TC, et al. (2020) Population genomics reveals the expansion of highly inbred *Plasmodium vivax* lineages in the main malaria hotspot of Brazil. *PLoS neglected tropical diseases*, 14(10), e0008808.

Mumm S, et al. (2020) Bruck syndrome 2 variant lacking congenital contractures and involving a novel compound heterozygous PLOD2 mutation. *Bone*, 130, 115047.

Whyte MP, et al. (2020) Juvenile Paget's Disease From Heterozygous Mutation of SP7 Encoding Osterix (Specificity Protein 7, Transcription Factor SP7). *Bone*, 137, 115364.

Diack O, et al. (2020) GWAS unveils features between early- and late-flowering pearl millets. *BMC genomics*, 21(1), 777.

Li R, et al. (2020) FIS1 encodes a GA2-oxidase that regulates fruit firmness in tomato. *Nature communications*, 11(1), 5844.

Cucco F, et al. (2020) Distinct genetic changes reveal evolutionary history and heterogeneous molecular grade of DLBCL with MYC/BCL2 double-hit. *Leukemia*, 34(5), 1329.

Kulkarni R, et al. (2020) Use of Targeted Amplicon Sequencing in Peanut to Generate Allele Information on Allotetraploid Sub-Genomes. *Genes*, 11(10).

Kim KW, et al. (2019) Genetics and evidence for balancing selection of a sex-linked colour polymorphism in a songbird. *Nature communications*, 10(1), 1852.

Lillie M, et al. (2019) Bidirectional Selection for Body Weight on Standing Genetic Variation in a Chicken Model. *G3 (Bethesda, Md.)*, 9(4), 1165.