Resource Summary Report

Generated by FDI Lab - SciCrunch.org on May 25, 2025

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_UnifiedG

Proper Citation: UnifiedGenotyper (RRID:SCR_004710)

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

Abbreviations: UnifiedGenotyper

Resource Type: software resource

Funding:

Resource Name: UnifiedGenotyper

Resource ID: SCR_004710

Alternate IDs: OMICS_00080

Record Creation Time: 20220129T080226+0000

Record Last Update: 20250525T030833+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 560 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Ren X, et al. (2025) Genomic and Metabolomic Analyses of Streptomyces albulus with Enhanced ?-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).

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

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

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.

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.

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

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.

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

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

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

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).

Song B, et al. (2019) Draft genome sequence of Solanum aethiopicum provides insights into disease resistance, drought tolerance, and the evolution of the genome. GigaScience, 8(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.

Baniecki ML, et al. (2019) Development of a SNP barcode to genotype Babesia microti infections. PLoS neglected tropical diseases, 13(3), e0007194.