Resource Summary Report

Generated by RRID on Aug 12, 2026

Clair3

RRID:SCR_026063
Type: Tool

Proper Citation

Clair3 (RRID:SCR_026063)

Resource Information

URL: https://github.com/HKU-BAL/Clair3

Proper Citation: Clair3 (RRID:SCR_026063)

Description: Software tool as germline small variant caller for long-reads. Symphonizing pileup and full-alignment for high-performance long-read variant calling.

Resource Type: source code, software resource

Defining Citation: PMID:38177392

Keywords: full-alignment, long-read variant calling, germline small variant caller, long-reads, variant caller,

Availability: Free, Available for download, Freely available

Resource Name: Clair3

Resource ID: SCR_026063

License: BSD 3-Clause license

Record Creation Time: 20241121T053249+0000

Record Last Update: 20260810T040856+0000

Ratings and Alerts

No rating or validation information has been found for Clair3.

No alerts have been found for Clair3.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 28 mentions in open access literature.

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

Chamchoy K, et al. (2026) Resolving haplotypes of the glucose-6-phosphate dehydrogenase gene using long-range polymerase chain reaction and Oxford Nanopore sequencing. Biology methods & protocols, 11(1), bpag008.

Bimbocci A, et al. (2026) SnakeBITE: A SNAKEmake-Based Interface for Third-Generation Sequencing Data Analysis. Biomolecules, 16(2).

Nicholas LL, et al. (2026) Identification and characterization of Schizosaccharomyces pombe splicing mutants. microPublication biology, 2026.

Gil MF, et al. (2026) Biopesticidal Properties of the Probiotic Brevibacillus laterosporus Strain B.O.D. Toxins, 18(6).

Cottingham H, et al. (2026) Nanopore sequencing enables highly accurate genotyping and identification of resistance determinants in key nosocomial pathogens. Microbial genomics, 12(3).

Sigalova OM, et al. (2026) Modeling cis-regulatory variation in human brain enhancers across a large Parkinson's Disease cohort. bioRxiv : the preprint server for biology.

Fakoya AO, et al. (2026) HapAsmbl: A reference-aided pipeline for assembling haplotypes in Nanopore amplicon sequence data of polymorphic populations. Applications in plant sciences, 14(3), e70062.

White RT, et al. (2026) Decentralized nanopore genomics reveals diverse Klebsiella pneumoniae and no evidence of patient-patient transmission in a New Zealand hospital. Microbial genomics, 12(4).

Izydorczyk MB, et al. (2025) Single cell long read whole genome sequencing reveals somatic transposon activity in human brain. Communications biology, 8(1), 1627.

Khare K, et al. (2025) Inter-host diversity associated with age, sex, and menstrual cycle modulates clinical manifestations in DENV-2 patients. iScience, 28(5), 112478.

Li R, et al. (2025) SUMMER: an integrated nanopore sequencing pipeline for variants detection and clinical annotation on the human genome. Functional & integrative genomics, 25(1), 21.

Claps A, et al. (2025) High precision characterization of RCCX rearrangements in a 21-hydroxylase deficiency Latin American cohort using oxford nanopore long read sequencing. Scientific reports, 15(1), 24983.

Ye F, et al. (2025) Characteristics and filtering of low-frequency artificial short deletion variations based on nanopore sequencing. GigaScience, 14.

Akçimen F, et al. (2025) A CGG Repeat Expansion in CSNK1E Associated with Progressive Myoclonic Epilepsy with Incomplete Penetrance. Movement disorders : official journal of the Movement Disorder Society, 40(11), 2469.

Vrbacká A, et al. (2025) Long-Read Sequencing of the MUC1 VNTR: Genomic Variation, Mutational Landscape, and Its Impact on ADTKD Diagnosis and Progression. bioRxiv : the preprint server for biology.

Hämmerli AF, et al. (2025) Case Report: Loss-of-function TRPM4 mutation p.L91? implicated in progressive cardiac conduction defect. Frontiers in physiology, 16, 1681438.

Jamshidi J, et al. (2025) Long-range PCR and Nanopore sequencing for localisation and phasing variants: an end-to-end clinical application workflow. BMC medical genomics, 18(1), 186.

Gan PHP, et al. (2025) Targeted adaptive sampling enables clinical pharmacogenomics testing and genome-wide genotyping. Scientific reports, 15(1), 39346.

Opassathian K, et al. (2025) A study of genomic complexity underlying multidrug resistance in Candida auris strains in Thailand. Scientific reports, 15(1), 41478.

Ahting S, et al. (2025) Incorporating Nanopore Sequencing Into a Diverse Diagnostic Toolkit for Incontinentia Pigmenti. Human mutation, 2025, 6657400.