Resource Summary Report

Generated by RRID on Aug 5, 2026

longshot

RRID:SCR_025318
Type: Tool

Proper Citation

longshot (RRID:SCR_025318)

Resource Information

URL: https://github.com/pjedge/longshot

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Description: Software variant calling tool for diploid genomes using long error prone reads such as Pacific Biosciences (PacBio) SMRT and Oxford Nanopore Technologies (ONT). Enables accurate variant calling in diploid genomes from single-molecule long read sequencing. Takes as input aligned BAM/CRAM file and outputs phased VCF file with variants and haplotype information.

Resource Type: software resource, source code

Defining Citation: DOI:10.1038/s41467-019-12493-y

Keywords: variant calling, diploid genomes, long error prone reads, single molecule long read sequencing,

Funding: NHGRI R01 HG010149

Availability: Free, Available for download, Freely available

Resource Name: longshot

Resource ID: SCR_025318

License: MIT license

Record Creation Time: 20240511T053259+0000

Record Last Update: 20260804T043908+0000

Ratings and Alerts

No rating or validation information has been found for longshot.

No alerts have been found for longshot.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Bertholim-Nasciben L, et al. (2025) Exploring potential mechanisms of an African protective locus for Alzheimer's disease in APOE??4 carriers. Alzheimer's & dementia : the journal of the Alzheimer's Association, 21(7), e70500.

Kaplan SJ, et al. (2024) CRISPR screening uncovers a long-range enhancer for ONECUT1 in pancreatic differentiation and links a diabetes risk variant. Cell reports, 43(8), 114640.

Schwarz JM, et al. (2021) Novel sequencing technologies and bioinformatic tools for deciphering the non-coding genome. Medizinische Genetik : Mitteilungsblatt des Berufsverbandes Medizinische Genetik e.V, 33(2), 133.