Resource Summary Report

Generated by NIF on Aug 2, 2026

Manta

RRID:SCR_022997
Type: Tool

Proper Citation

Manta (RRID:SCR_022997)

Resource Information

URL: https://github.com/Illumina/manta

Proper Citation: Manta (RRID:SCR_022997)

Description: Software tool for rapid detection of structural variants and indels for germline and cancer sequencing applications. Used to call structural variants and indels from mapped paired end sequencing reads.

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

Defining Citation: PMID:26647377

Keywords: rapid detection, structural variants and indels, mapped paired end sequencing reads, structural variant, indel

Availability: Free, Available for download, Freely available

Resource Name: Manta

Resource ID: SCR_022997

License: GPL v3.0 license

Record Creation Time: 20221124T050201+0000

Record Last Update: 20260801T190803+0000

Ratings and Alerts

No rating or validation information has been found for Manta.

No alerts have been found for Manta.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 183 mentions in open access literature.

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

Showpnil IA, et al. (2026) De Novo Heterozygous ZFX Frameshift Variant in a Female With an X-Linked Neurodevelopmental Disorder. American journal of medical genetics. Part A, 200(2), 521.

Ansari M, et al. (2025) Whole Genome Sequencing of "Mutation-Negative" Individuals With Cornelia de Lange Syndrome. Human mutation, 2025, 4711663.

Wei K, et al. (2025) Copy Number Variation Shapes Structural Genomic Diversity Associated With Ecological Adaptation in the Wild Tomato Solanum chilense. Molecular biology and evolution, 42(8).

Leung YY, et al. (2025) Alzheimer's Disease Sequencing Project release 4 whole genome sequencing dataset. Alzheimer's & dementia : the journal of the Alzheimer's Association, 21(5), e70237.

Gong J, et al. (2025) Long-read sequencing of 945 Han individuals identifies structural variants associated with phenotypic diversity and disease susceptibility. Nature communications, 16(1), 1494.

Topham JT, et al. (2025) Multi-omics whole-genome characterization of the copy number landscape of metastatic pancreatic ductal adenocarcinoma. iScience, 28(8), 113176.

Yamashita T, et al. (2025) Biallelic variants in DNAJC7 cause familial amyotrophic lateral sclerosis with the TDP-43 pathology. Acta neuropathologica, 150(1), 19.

Bendixsen DP, et al. (2025) Reproductive Isolation due to Divergent Ecological Selection Is Accompanied by Vast Genomic Instability in Experimentally Evolved Yeast Populations. Molecular ecology, 34(22), e70110.

Lilljebjörn H, et al. (2025) The AML cellular state space unveils NPM1 immune evasion subtypes with distinct clinical outcomes. Nature communications, 16(1), 10592.

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

Wold JR, et al. (2025) The promise and challenges of characterizing genome-wide structural variants: A case study in a critically endangered parrot. Molecular ecology resources, 25(5), e13783.

Chukwu W, et al. (2025) A sequence context-based approach for classifying tumor structural variants without paired normal samples. Cell reports methods, 5(3), 100991.

Couper LI, et al. (2025) Evolutionary adaptation under climate change: Aedes sp. demonstrates potential to adapt to warming. Proceedings of the National Academy of Sciences of the United States of America, 122(2), e2418199122.

Rekhtman N, et al. (2025) Chromothripsis-Mediated Small Cell Lung Carcinoma. Cancer discovery, 15(1), 83.

Barnabas GD, et al. (2025) Proteomics and personalized PDX models identify treatment for a progressive malignancy within an actionable timeframe. EMBO molecular medicine, 17(4), 625.

Zhao Y, et al. (2025) The origin and evolution of cultivated rice and genomic signatures of heterosis for yield traits in super-hybrid rice. BMC biology, 23(1), 153.

Tsai MM, et al. (2025) Optical genome mapping with whole genome sequencing identifies complex chromosomal structural variations in acute leukemia. Frontiers in genetics, 16, 1496847.

Körber V, et al. (2025) Detecting and quantifying clonal selection in somatic stem cells. Nature genetics, 57(7), 1718.

Ku AT, et al. (2025) Radiogenomic Profiling of Prostate Tumors prior to External Beam Radiotherapy Converges on a Transcriptomic Signature of TGF-? Activity Driving Tumor Recurrence. Clinical cancer research : an official journal of the American Association for Cancer Research, 31(24), 5211.

Kersten O, et al. (2025) Single Nucleotide Polymorphisms, Structural Variants, and Short Tandem Repeats Capture Distinct Signals of Adaptive Divergence in the Atlantic Puffin. Genome biology and evolution, 17(9).