Resource Summary Report

Generated by NIF on May 16, 2025

MOSAIK

RRID:SCR_005486
Type: Tool

Proper Citation

MOSAIK (RRID:SCR_005486)

Resource Information

URL: http://code.google.com/p/mosaik-aligner/

Proper Citation: MOSAIK (RRID:SCR_005486)

Description: A reference-guided assembler comprising of two main modular programs: MosaikBuild and MosaikAligner. MosaikBuild converts various sequence formats into Mosaik?s native read format. MosaikAligner pairwise aligns each read to a specified series of reference sequences and produces BAMs as outputs. At this time, the workflow consists of supplying sequences in FASTA, FASTQ, Illumina Bustard & Gerald, or SRF file formats and producing results in the BAM format. Unlike many current read aligners, MOSAIK produces gapped alignments using the Smith-Waterman algorithm. MOSAIK is written in highly portable C++ and currently targetted for the following platforms: Microsoft Windows, Apple Mac OS X, FreeBSD, and Linux operating systems. Other platforms can easily be supported upon request. MOSAIK is multithreaded. If you have a machine with 8 processors, you can use all 8 processors to align reads faster while using the same memory footprint as when using one processor. MOSAIK supports multiple sequencing technologies. In addition to legacy technologies such as Sanger capillary sequencing, our program supports next generation technologies such as Roche 454, Illumina, AB SOLiD, and experimental support for the Helicos Heliscope.

Abbreviations: MOSAIK

Synonyms: mosaik-aligner

Resource Type: software resource

Keywords: next-generation sequencing, alignment, smith-waterman algorithm, c++, computational biology, reference guided aligner

Funding:

Availability: Free, Freely available

Resource Name: MOSAIK

Resource ID: SCR_005486

Alternate IDs: OMICS_00669

Alternate URLs: https://sources.debian.org/src/mosaik-aligner/

License: GNU General Public License, v2+, MIT License

Record Creation Time: 20220129T080230+0000

Record Last Update: 20250420T014253+0000

Ratings and Alerts

No rating or validation information has been found for MOSAIK.

No alerts have been found for MOSAIK.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 84 mentions in open access literature.

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

Yoon H, et al. (2023) Clinical importance of weight gain and associated factors in patients with moderate to severe ulcerative colitis: results from the MOSAIK cohort in Korea. BMC gastroenterology, 23(1), 405.

Su X, et al. (2023) Delineating the interplay between oncogenic pathways and immunity in anaplastic Wilms tumors. Nature communications, 14(1), 7884.

Hejda M, et al. (2022) Water availability, bedrock, disturbance by herbivores, and climate determine plant diversity in South-African savanna. Scientific reports, 12(1), 338.

Jo IH, et al. (2022) Quality of Life in Newly Diagnosed Moderate-to-Severe Ulcerative Colitis: Changes in the MOSAIK Cohort Over 1 Year. Gut and liver, 16(3), 384.

Martins LF, et al. (2022) Motor neurons use push-pull signals to direct vascular remodeling critical for their connectivity. Neuron, 110(24), 4090.

Khandagale A, et al. (2021) Severe congenital neutropenia-associated JAGN1 mutations unleash a calpain-dependent cell death programme in myeloid cells. British journal of haematology, 192(1), 200.

Sjöqvist C, et al. (2021) Ecologically coherent population structure of uncultivated bacterioplankton. The ISME journal, 15(10), 3034.

Murrieta RA, et al. (2021) Impact of extrinsic incubation temperature on natural selection during Zika virus infection of Aedes aegypti and Aedes albopictus. PLoS pathogens, 17(11), e1009433.

Talavera-Aguilar LG, et al. (2021) Infection, dissemination, and transmission efficiencies of Zika virus in Aedes aegypti after serial passage in mosquito or mammalian cell lines or alternating passage in both cell types. Parasites & vectors, 14(1), 261.

Van den Hoecke S, et al. (2021) In Vivo Therapy with M2e-Specific IgG Selects for an Influenza A Virus Mutant with Delayed Matrix Protein 2 Expression. mBio, 12(4), e0074521.

Liu L, et al. (2021) Genetic consequences of long-term small effective population size in the critically endangered pygmy hog. Evolutionary applications, 14(3), 710.

Norouzi-Beirami MH, et al. (2021) CAMAMED: a pipeline for composition-aware mapping-based analysis of metagenomic data. NAR genomics and bioinformatics, 3(1), lqaa107.

Pascall DJ, et al. (2021) Virus Prevalence and Genetic Diversity Across a Wild Bumblebee Community. Frontiers in microbiology, 12, 650747.

Collins DR, et al. (2021) Functional impairment of HIV-specific CD8+ T cells precedes aborted spontaneous control of viremia. Immunity, 54(10), 2372.

Cappai F, et al. (2020) High-Resolution Linkage Map and QTL Analyses of Fruit Firmness in Autotetraploid Blueberry. Frontiers in plant science, 11, 562171.

Ghanbari Maman L, et al. (2020) Co-abundance analysis reveals hidden players associated with high methane yield phenotype in sheep rumen microbiome. Scientific reports, 10(1), 4995.

Joshi VR, et al. (2020) Gp41-targeted antibodies restore infectivity of a fusion-deficient HIV-1 envelope glycoprotein. PLoS pathogens, 16(5), e1008577.

Estrada-Reyes ZM, et al. (2019) Signatures of selection for resistance to Haemonchus contortus in sheep and goats. BMC genomics, 20(1), 735.

Kosugi S, et al. (2019) Comprehensive evaluation of structural variation detection algorithms for whole genome sequencing. Genome biology, 20(1), 117.

Singer JB, et al. (2019) Interpreting Viral Deep Sequencing Data with GLUE. Viruses, 11(4).