Resource Summary Report

Generated by dkNET on Apr 29, 2025

PacBioToCA

RRID:SCR_003044
Type: Tool

Proper Citation

PacBioToCA (RRID:SCR_003044)

Resource Information

URL: https://github.com/PacificBiosciences/Bioinformatics-Training/wiki/pacBioToCA

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Description: A module in the Celera Assembler software package that performs error correction on PacBio long reads by mapping shorter, high accuracy reads onto the long reads.

Synonyms: pacBioToCA (error correction via Celera Assembler)

Resource Type: software resource

Defining Citation: PMID:22750884

Keywords: standalone software

Funding:

Resource Name: PacBioToCA

Resource ID: SCR_003044

Alternate IDs: OMICS_05093

Record Creation Time: 20220129T080216+0000

Record Last Update: 20250420T014134+0000

Ratings and Alerts

No rating or validation information has been found for PacBioToCA.

No alerts have been found for PacBioToCA.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 13 mentions in open access literature.

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

Mishra A, et al. (2021) Decoding the genome of superior chapatti quality Indian wheat variety 'C 306' unravelled novel genomic variants for chapatti and nutrition quality related genes. Genomics, 113(4), 1919.

Deng C, et al. (2019) Metabolic engineering of Corynebacterium glutamicum S9114 based on whole-genome sequencing for efficient N-acetylglucosamine synthesis. Synthetic and systems biotechnology, 4(3), 120.

Cai H, et al. (2019) A draft genome assembly of the solar-powered sea slug Elysia chlorotica. Scientific data, 6, 190022.

Schmid-Hempel P, et al. (2018) The genomes of Crithidia bombi and C. expoeki, common parasites of bumblebees. PloS one, 13(1), e0189738.

Miller WG, et al. (2017) Comparative Genomics of All Three Campylobacter sputorum Biovars and a Novel Cattle-Associated C. sputorum Clade. Genome biology and evolution, 9(6), 1513.

Zhao L, et al. (2017) Genomics of parallel adaptation at two timescales in Drosophila. PLoS genetics, 13(10), e1007016.

Massilamany C, et al. (2016) Whole genomic sequence analysis of Bacillus infantis: defining the genetic blueprint of strain NRRL B-14911, an emerging cardiopathogenic microbe. BMC genomics, 17 Suppl 7(Suppl 7), 511.

Ross DE, et al. (2016) Comparative Genomic Analysis of Sulfurospirillum cavolei MES Reconstructed from the Metagenome of an Electrosynthetic Microbiome. PloS one, 11(3), e0151214.

Okura VK, et al. (2016) BAC-Pool Sequencing and Assembly of 19 Mb of the Complex Sugarcane Genome. Frontiers in plant science, 7, 342.

Yan X, et al. (2015) Genome sequencing and comparative genomics provides insights on the evolutionary dynamics and pathogenic potential of different H-serotypes of Shiga toxin-producing Escherichia coli O104. BMC microbiology, 15, 83.

Miller WG, et al. (2014) Comparative genomics of the Campylobacter lari group. Genome biology and evolution, 6(12), 3252.

Dmytrenko O, et al. (2014) The genome of the intracellular bacterium of the coastal bivalve, Solemya velum: a blueprint for thriving in and out of symbiosis. BMC genomics, 15, 924.

Biller SJ, et al. (2014) Genomes of diverse isolates of the marine cyanobacterium Prochlorococcus. Scientific data, 1, 140034.