

Resource Summary Report

Generated by [dkNET](#) on Aug 6, 2026

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

Availability: Free, Available for download, Freely available

Resource Name: PacBioToCA

Resource ID: SCR_003044

Alternate IDs: OMICS_05093

Alternate URLs: <https://rhallpb.github.io/Applications/pacBioToCA.html>

Record Creation Time: 20220129T080216+0000

Record Last Update: 20260801T190216+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.

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

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.

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.

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.

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

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