Resource Summary Report

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PBJelly

RRID:SCR_012091
Type: Tool

Proper Citation

PBJelly (RRID:SCR_012091)

Resource Information

URL: http://sourceforge.net/projects/pb-jelly/

Proper Citation: PBJelly (RRID:SCR_012091)

Description: Software that automates the finishing process using long sequence reads in a reference-guided assembly process.

Resource Type: software resource

Defining Citation: PMID:23185243

Keywords: standalone software, roche, pacific biosciences

Resource Name: PBJelly

Resource ID: SCR_012091

Alternate IDs: OMICS_05098

Ratings and Alerts

No rating or validation information has been found for PBJelly.

No alerts have been found for PBJelly.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 153 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Hu Z, et al. (2024) Genomics insights into flowering and floral pattern formation: regional duplication and seasonal pattern of gene expression in Camellia. BMC biology, 22(1), 50.

Silliman K, et al. (2023) Epigenetic and Genetic Population Structure is Coupled in a Marine Invertebrate. Genome biology and evolution, 15(2).

Xu Z, et al. (2023) The chromosome-scale reference genome of mirid bugs (Adelphocoris suturalis) genome provides insights into omnivory, insecticide resistance, and survival adaptation. BMC biology, 21(1), 195.

Yang XZ, et al. (2023) A-to-I RNA Editing in Klebsiella pneumoniae Regulates Quorum Sensing and Affects Cell Growth and Virulence. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 10(17), e2206056.

Wang YW, et al. (2023) Invasive Californian death caps develop mushrooms unisexually and bisexually. Nature communications, 14(1), 6560.

Bista I, et al. (2023) Genomics of cold adaptations in the Antarctic notothenioid fish radiation. Nature communications, 14(1), 3412.

Hsiao TH, et al. (2023) Circulating androgen regulation by androgen-catabolizing gut bacteria in male mouse gut. Gut microbes, 15(1), 2183685.

Hu L, et al. (2023) The complex genome and adaptive evolution of polyploid Chinese pepper (Zanthoxylum armatum and Zanthoxylum bungeanum). Plant biotechnology journal, 21(1), 78.

Yu S, et al. (2023) Resequencing of a Pekin duck breeding population provides insights into the genomic response to short-term artificial selection. GigaScience, 12.

Ballard JWO, et al. (2023) The Australasian dingo archetype: De novo chromosome-length genome assembly, DNA methylome, and cranial morphology. bioRxiv : the preprint server for biology.

Marlétaz F, et al. (2023) The hagfish genome and the evolution of vertebrates. bioRxiv : the preprint server for biology.

Hart SFM, et al. (2023) Centuries of genome instability and evolution in soft-shell clam, Mya? arenaria, bivalve transmissible neoplasia. Nature cancer, 4(11), 1561.

Ballard JWO, et al. (2023) The Australasian dingo archetype: de novo chromosome-length genome assembly, DNA methylome, and cranial morphology. GigaScience, 12.

Ling ZL, et al. (2023) Insights into the genomic evolution and the alkali tolerance mechanisms of Agaricus sinodeliciosus by comparative genomic and transcriptomic analyses. Microbial genomics, 9(3).

Ludwig A, et al. (2022) DENTIST-using long reads for closing assembly gaps at high accuracy. GigaScience, 11.

Field MA, et al. (2022) The Australian dingo is an early offshoot of modern breed dogs. Science advances, 8(16), eabm5944.

Baptista RP, et al. (2022) Long-read assembly and comparative evidence-based reanalysis of Cryptosporidium genome sequences reveal expanded transporter repertoire and duplication of entire chromosome ends including subtelomeric regions. Genome research, 32(1), 203.

Park M, et al. (2022) Chromosome-level genome sequence assembly and genome-wide association study of Muscadinia rotundifolia reveal the genetics of 12 berry-related traits. Horticulture research, 9.

Kwon YM, et al. (2022) Genomic consequences of domestication of the Siamese fighting fish. Science advances, 8(10), eabm4950.

Smolander OP, et al. (2022) Improved chromosome-level genome assembly of the Glanville fritillary butterfly (Melitaea cinxia) integrating Pacific Biosciences long reads and a high-density linkage map. GigaScience, 11(1).