Resource Summary Report

Generated by dkNET on Apr 29, 2025

Racon

RRID:SCR_017642
Type: Tool

Proper Citation

Racon (RRID:SCR_017642)

Resource Information

URL: https://github.com/isovic/racon

Proper Citation: Racon (RRID:SCR_017642)

Description: Software tool as de novo genome assembly from long uncorrected reads. Used to correct raw contigs generated by rapid assembly methods which do not include consensus step. Supports data produced by Pacific Biosciences and Oxford Nanopore Technologies.

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

Defining Citation: DOI:10.1101/068122

Keywords: Assembly, de novo, long, uncorrected, read, raw, contig, consensus, step, data, sequence, bio.tools

Funding: Croatian Science Foundation ;
Croatian Academy of Sciences and Arts ;
A*STAR ;
Singapore

Availability: Free, Available for download, Freely available

Resource Name: Racon

Resource ID: SCR_017642

Alternate IDs: OMICS_25714, biotools:Racon, BioTools:Racon

Alternate URLs: https://bio.tools/Racon, https://sources.debian.org/src/racon/

License: MIT License

Record Creation Time: 20220129T080336+0000

Record Last Update: 20250429T055921+0000

Ratings and Alerts

No rating or validation information has been found for Racon.

No alerts have been found for Racon.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 126 mentions in open access literature.

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

Iliev I, et al. (2025) Characterization and Probiotic Potential of Levilactobacillus brevis DPL5: A Novel Strain Isolated from Human Breast Milk with Antimicrobial Properties Against Biofilm-Forming Staphylococcus aureus. Microorganisms, 13(1).

Liu J, et al. (2025) Chromosome-level genome assembly of the seasonally polyphenic scorpionfly (Panorpa liui). Scientific data, 12(1), 22.

Wang MY, et al. (2025) Chromosome-level genome assembly, annotation, and population genomic resource of argali (Ovis ammon). Scientific data, 12(1), 57.

Zhang Y, et al. (2024) A trade-off in evolution: the adaptive landscape of spiders without venom glands. GigaScience, 13.

Liu B, et al. (2024) Chromosome-level genome assembly of Oriental chestnut gall wasp (Dryocosmus kuriphilus). Scientific data, 11(1), 963.

Ghezzi H, et al. (2024) PUPpy: a primer design pipeline for substrain-level microbial detection and absolute quantification. mSphere, 9(7), e0036024.

Wiersma AT, et al. (2024) k-mer genome-wide association study for anthracnose and BCMV resistance in a Phaseolus vulgaris Andean Diversity Panel. The plant genome, 17(4), e20523.

Sun B, et al. (2024) The loach haplotype-resolved genome and the identification of Mex3a involved in fish air breathing. Cell genomics, 4(10), 100670.

Leng L, et al. (2024) Cepharanthine analogs mining and genomes of Stephania accelerate anti-coronavirus drug discovery. Nature communications, 15(1), 1537.

Sauerborn E, et al. (2024) Detection of hidden antibiotic resistance through real-time genomics. Nature communications, 15(1), 5494.

Liu YF, et al. (2024) Genetic architecture of long-distance migration and population genomics of the endangered Japanese eel. iScience, 27(8), 110563.

Wang XP, et al. (2024) Insights into the divergence of the photosynthetic LH1 complex obtained from structural analysis of the unusual photocomplexes of Roseospirillum parvum. Communications biology, 7(1), 1658.

Martin? J, et al. (2024) Highly Resolved Genomes of Two Closely Related Lineages of the Rodent Louse Polyplax serrata with Different Host Specificities. Genome biology and evolution, 16(3).

Lu Y, et al. (2024) Whole-genome sequencing of the invasive golden apple snail Pomacea canaliculata from Asia reveals rapid expansion and adaptive evolution. GigaScience, 13.

Nebenführ M, et al. (2024) High-speed whole-genome sequencing of a Whippet: Rapid chromosome-level assembly and annotation of an extremely fast dog's genome. GigaByte (Hong Kong, China), 2024, gigabyte134.

Zhang W, et al. (2024) Chromosome-level genome assembly of the medicinal insect Blaps rhynchopetera using Nanopore and Hi-C technologies. DNA research : an international journal for rapid publication of reports on genes and genomes, 31(6).

Kuznetsov VG, et al. (2024) Proteotranscriptomic Profiling of the Toxic Mucus of Kulikovia alborostrata (Pilidiophora, Nemertea). Toxins, 17(1).

Purushothaman S, et al. (2024) Evaluation of DNA extraction kits for long-read shotgun metagenomics using Oxford Nanopore sequencing for rapid taxonomic and antimicrobial resistance detection. Scientific reports, 14(1), 29531.

Straub C, et al. (2024) Extended-spectrum beta-lactamase, AmpC, and carbapenemase-producing Gram-negative wastewater isolates from Aotearoa New Zealand. Microbiology resource announcements, 13(5), e0013124.

Chen Y, et al. (2024) Telomere-to-telomere genome assembly of Eleocharis dulcis and expression profiles during corm development. Scientific data, 11(1), 869.