

Resource Summary Report

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Racon

RRID:SCR_017642

Type: Tool

Proper Citation

Racon (RRID:SCR_017642)

Resource Information

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

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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 application, software resource

Defining Citation: [DOI:10.1101/068122](https://doi.org/10.1101/068122)

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

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

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

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 177 mentions in open access literature.

Listed below are recent publications. The full list is available at [SPARC SAWG](#) .

Meyer D, et al. (2026) Unlocking the full potential of nanopore sequencing: tips, tricks, and advanced data analysis techniques. *Nucleic acids research*, 54(3).

Buthasane W, et al. (2026) Endangered Steppe Eagle (*Aquila nipalensis*) (Aves, Accipitriformes, Accipitridae) genome and mitogenome assembly: A resource for molecular evolution and comparative genomics. *ZooKeys*, 1281, 105.

Yang Y, et al. (2026) Complete genome sequencing of *Bacillus velezensis* Jin12 revealed its great ability for starch degradation in flue-cured tobacco leaves. *BMC microbiology*, 26(1).

Fiesinger A, et al. (2026) The genome of the reef-building coral *Porites harrisoni* from the southern Persian/Arabian Gulf. *GigaByte (Hong Kong, China)*, 2026, gigabyte174.

Zheng C, et al. (2026) Biological characteristics and genetics differentiation of smut fungi in *Coix L*. *Frontiers in microbiology*, 17, 1746178.

Gao C, et al. (2026) High-Quality Genome Assembly of *Diplocarpon coronariae* Unveils LTR Retrotransposon-Driven Structural Dynamics in Fungi Evolution. *Molecular ecology resources*, 26(1), e70070.

Li F, et al. (2026) An ancient genome duplication event drives the development and evolution of spinnerets in spiders. *Science advances*, 12(3), eadw2173.

Ilieva L, et al. (2026) Potential of Fermented Food-Derived *Lactiplantibacillus* Cell-Free Supernatants to Control *Staphylococcus aureus* Growth and Biofilm Development. *International journal of molecular sciences*, 27(2).

Hung JY, et al. (2026) Microbial Metabolism and Disease Virulence Changes Across Day and Night in Coral Black Band Disease Lesions. *Environmental microbiology*, 28(2), e70219.

Sandholm RM, et al. (2026) Paired genomic and proteomic analysis of *Acinetobacter towneri* from waste sludge reveals an extensive repertoire of enzymes for breakdown of hydrocarbons. *Microbiology spectrum*, 14(4), e0005426.

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

Ritter EJ, et al. (2025) The assembly and annotation of two teinturier grapevine varieties, Dakapo and Rubired. *GigaByte* (Hong Kong, China), 2025, gigabyte149.

Schell T, et al. (2025) Establishing genome sequencing and assembly for non-model and emerging model organisms: a brief guide. *Frontiers in zoology*, 22(1), 7.

Dai H, et al. (2025) Mining expansin-like proteins from rumen microbiota and functional characterization of two anaerobic fungal expansin-like proteins. *Journal of animal science and biotechnology*, 16(1), 155.

Moore ML, et al. (2025) Hybridization and low-light adaptability in California eelgrass (*Zostera* spp.). *Nature plants*, 11(11), 2409.

Liu H, et al. (2025) A telomere-to-telomere gapless genome reveals *SIPRR1* control of circadian rhythm and photoperiodic flowering in tomato. *GigaScience*, 14.

Qin H, et al. (2025) The complete genome assembly of *Astragalus membranaceus*: enabling more accurate genetic research. *GigaScience*, 14.

Liu J, et al. (2025) Comparative genomics provides insights into the biogeographic and biochemical diversity of meliaceous species. *Nature communications*, 16(1), 2603.

T??th AG, et al. (2025) First Animal Source Metagenome Assembly of *Lawsonella clevelandensis* from Canine External Otitis. *Pathogens* (Basel, Switzerland), 14(5).

Franco Ortega S, et al. (2025) Assembly and annotation of *Solanum dulcamara* and *Solanum nigrum* plant genomes, two nightshades with contrasting susceptibilities to *Ralstonia solanacearum*. *G3* (Bethesda, Md.), 15(7).