

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: software resource, software application, data processing software

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: 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

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 149 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

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.

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).

Landis JB, et al. (2025) Reference genome of *Calochortus tolmiei* Hook. & Arn. (Liliaceae), a cat's ear mariposa lily. *G3* (Bethesda, Md.), 15(3).

Bian C, et al. (2025) Chromosome-level genome assemblies of five *Sinocyclocheilus* species. *GigaByte* (Hong Kong, China), 2025, gigabyte155.

Wang ZF, et al. (2025) Chromosome-scale assemblies of three *Ormosia* species: repetitive sequences distribution and structural rearrangement. *GigaScience*, 14.

Zhang Y, et al. (2025) An annotated chromosome-level genome of a troglophilic spider (*Pimoa clavata*). *Scientific data*, 12(1), 1398.

DeWeese K, et al. (2025) Scaffolded and annotated nuclear and organelle genomes of the North American brown alga *Saccharina latissima*. *Frontiers in genetics*, 16, 1494480.

Wang Y, et al. (2025) Telomere-to-telomere genome of common bean (*Phaseolus vulgaris* L., YP4). *GigaScience*, 14.

Rao X, et al. (2025) Genomic and transcriptomic insights into the molecular responses of a biocrust-derived oleaginous microalga *Vischeria* sp. WL1 to nitrogen depletion and recovery. *Synthetic and systems biotechnology*, 10(4), 1160.

Lovell JT, et al. (2025) Comparative Analyses of Four Reference Genomes Reveal Exceptional Diversity and Weak Linked Selection in the Yellow Monkeyflower (*Mimulus*

guttatus) Complex. Molecular ecology resources, 25(8), e70012.

Qi J, et al. (2025) Genomic Sequencing and Characterization of Two Auricularia Species from the Qinling Region: Insights into Evolutionary Dynamics and Secondary Metabolite Potential. Journal of fungi (Basel, Switzerland), 11(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).

Jiang D, et al. (2025) The telomere-to-telomere genome of flowering cherry (Prunus campanulata) reveals genomic evolution of the subgenus Cerasus. 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.

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.

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

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

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.

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