## **Resource Summary Report**

Generated by NIF on Apr 25, 2025

# **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, data processing software, 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: 20250425T060252+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 <u>NIF</u>.

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.

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

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.

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.

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.

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.

Kelsang GA, et al. (2024) Insights from the first chromosome-level genome assembly of the alpine gentian Gentiana straminea Maxim. DNA research : an international journal for rapid publication of reports on genes and genomes, 31(5).

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

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).

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

Roothans N, et al. (2024) Aerobic denitrification as an N2O source from microbial communities. The ISME journal, 18(1).

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).

Chen Y, et al. (2024) Haplotype-resolved assembly of diploid and polyploid genomes using quantum computing. Cell reports methods, 4(5), 100754.

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