

# Resource Summary Report

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## [Winnowmap](#)

RRID:SCR\_025349

Type: Tool

### Proper Citation

Winnowmap (RRID:SCR\_025349)

### Resource Information

**URL:** <https://github.com/marbl/Winnowmap>

**Proper Citation:** Winnowmap (RRID:SCR\_025349)

**Description:** Software tool as long-read mapping algorithm optimized for mapping ONT and PacBio reads to repetitive reference sequences. Winnowmap2 computes each read mapping through collection of confident subalignments. This approach is more tolerant of structural variation and more sensitive to paralog-specific variants within repeats.

**Synonyms:** Winnowmap2

**Resource Type:** source code, software resource

**Defining Citation:** [PMID:35365778](#)

**Keywords:** long-read mapping, ONT and PacBio reads, repetitive reference sequences, paralog specific variants within repeats,

**Funding:** NHGRI ;  
Indian Institute of Science

**Availability:** Free, Available for download, Freely available

**Resource Name:** Winnowmap

**Resource ID:** SCR\_025349

**License URLs:** <https://github.com/marbl/Winnowmap/blob/master/LICENSE>

**Record Creation Time:** 20240521T053244+0000

**Record Last Update:** 20260810T040842+0000

### Ratings and Alerts

No rating or validation information has been found for Winnowmap.

No alerts have been found for Winnowmap.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 26 mentions in open access literature.

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

Kou Y, et al. (2026) Haplotype-resolved T2T genome and population resequencing provide insights into the domestication and mogroside biosynthesis of *Siraitia grosvenorii* (Cucurbitaceae). *Horticulture research*, 13(7), uhag103.

Zhuang Z, et al. (2026) A new integrated genetic and transcriptomic approach for investigating DUX4 and DUX4C. *Journal of human genetics*, 71(6), 373.

Guo Z, et al. (2026) Deciphering the Evolution Pattern of Structural Variations Overlapped With Repetitive Sequence During Cattle Evolution. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(28), e23333.

Delaive S, et al. (2026) The genomic architecture of local adaptation in two connected populations of three-spined stickleback. *G3* (Bethesda, Md.), 16(6).

Liu P, et al. (2026) Telomere-to-telomere genome of *Stylosanthes guianensis* uncovers symbiotic adaptation to phosphorus-deficient soils. *Genome biology*, 27(1).

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

Xu Y, et al. (2026) Haplotype-resolved centromeric chromatin organization from a complete diploid human genome. *bioRxiv : the preprint server for biology*.

Son DR, et al. (2026) Germline hypomethylation shapes dynamic CpG reservoirs in ape genomes. *bioRxiv : the preprint server for biology*.

Liang YY, et al. (2025) Pan-Genome Analysis Reveals Local Adaptation to Climate Driven by Introgression in Oak Species. *Molecular biology and evolution*, 42(5).

Huang L, et al. (2025) Telomere-to-telomere gapless genome assembly of *Acorus tatarinowii*. *Scientific data*, 12(1), 1640.

Liu D, et al. (2025) Use of the CHM13-T2T genome improves metagenomic analysis by minimizing host DNA contamination. *mSystems*, 10(10), e0084025.

Jiang D, et al. (2025) The telomere-to-telomere genome of flowering cherry (*Prunus campanulata*) reveals genomic evolution of the subgenus *Cerasus*. *GigaScience*, 14.

Cao C, et al. (2025) A near telomere-to-telomere genome assembly of the Jinhua pig: enabling more accurate genetic research. *GigaScience*, 14.

Liu F, et al. (2025) The telomere-to-telomere gapless genome of grass carp provides insights for genetic improvement. *GigaScience*, 14.

Movilli A, et al. (2025) Long-read detection of transposable element mobilization in the soma of hypomethylated *Arabidopsis thaliana* individuals. *Genome biology*, 26(1), 231.

Volpe E, et al. (2025) The reference genome of the human diploid cell line RPE-1. *Nature communications*, 16(1), 7751.

Yuan J, et al. (2025) A telomere-to-telomere genome assembly of koi carp (*Cyprinus carpio*) using long reads and Hi-C technology. *GigaScience*, 14.

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.

Pang J, et al. (2025) Telomere-to-Telomere genome assembly of an endangered tree *Berchemiella wilsonii* (Rhamnaceae). *Scientific data*, 13(1), 118.