

Resource Summary Report

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Falcon

RRID:SCR_016089

Type: Tool

Proper Citation

Falcon (RRID:SCR_016089)

Resource Information

URL: <https://github.com/PacificBiosciences/FALCON>

Proper Citation: Falcon (RRID:SCR_016089)

Description: Software package for aligning long sequencing reads as a diploid-aware genome assembler. Used for assembling non-inbred or rearranged heterozygous genomes.

Resource Type: alignment software, data processing software, image analysis software, software application, software resource

Defining Citation: [PMID:27749838](#)

Keywords: fast, aligner, sequencing, diploid, genome, assembly, non-inbred, rearranged, heterozygous, single-molecule

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National Science Foundation DBI-1350041;
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Availability: Free, Available for download, Freely available

Resource Name: Falcon

Resource ID: SCR_016089

Alternate IDs: OMICS_13514

Alternate URLs: <https://sources.debian.org/src/falcon/>

License URLs: <https://github.com/PacificBiosciences/FALCON/blob/master/LICENSE>

Record Creation Time: 20220129T080328+0000

Record Last Update: 20260829T182530+0000

Ratings and Alerts

No rating or validation information has been found for Falcon.

No alerts have been found for Falcon.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 293 mentions in open access literature.

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

Yao W, et al. (2026) Chromosome-level genome assemblies of two maize inbred lines with contrasting plant architectures. *Scientific data*, 13(1), 276.

Martin FM, et al. (2026) Draft Genomes of Geographically Distinct Strains and Progeny of the Ectomycorrhizal Basidiomycete *Laccaria bicolor*. *Journal of genomics*, 14, 10.

Wang Q, et al. (2026) *Candolleomyces candolleanus* P9 from *Altay Glycyrrhiza*: ??-glucosidase-mediated biotransformation. *Microbial cell factories*, 25(1).

Liang X, et al. (2025) Whole-Genome Sequencing of *Flammulina filiformis* and Multi-Omics Analysis in Response to Low Temperature. *Journal of fungi (Basel, Switzerland)*, 11(3).

Gu C, et al. (2025) Long-read genome sequencing reveals the sequence characteristics of pear self-incompatibility locus. *Molecular horticulture*, 5(1), 13.

Tu XD, et al. (2025) Genomic insights into *Castanopsis carlesii* and *Castanea henryi*: flower and fruit development and evolution of NLR genes in the beech-oak family. *Molecular horticulture*, 5(1), 33.

Yuan S, et al. (2025) Multiomic Analyses Reveal the Molecular Mechanisms of Arid Adaptation in a Desert Rodent Species. *Molecular biology and evolution*, 42(10).

Roberts WR, et al. (2025) Reference genome for the benthic marine diatom *Psammoneis japonica*: Bacterial associations and repeat-driven genome size evolution in diatoms. *Journal of phycology*, 61(6), 1556.

Ma P, et al. (2025) First fine mapping of a strain of *Rhizoctonia Solani* AG-3, causing tobacco target spot. *BMC genomic data*, 26(1), 24.

Xihui Z, et al. (2025) Infection and resistance mechanisms of phage vB_VpM-PP270 in *Vibrio parahaemolyticus* via capsular polysaccharide. *iScience*, 28(11), 113811.

Baroncelli R, et al. (2024) Genome evolution and transcriptome plasticity is associated with adaptation to monocot and dicot plants in *Colletotrichum* fungi. *GigaScience*, 13.

Yuan F, et al. (2024) Mechanism of Action of *Fusarium oxysporum* CCS043 Utilizing Allelochemicals for Rhizosphere Colonization and Enhanced Infection Activity in *Rehmannia glutinosa*. *Plants (Basel, Switzerland)*, 14(1).

Alami MM, et al. (2024) Chromosome-scale genome assembly of medicinal plant *Tinospora sagittata* (Oliv.) Gagnep. from the Menispermaceae family. *Scientific data*, 11(1), 610.

Lax C, et al. (2024) Symmetric and asymmetric DNA N6-adenine methylation regulates different biological responses in *Mucorales*. *Nature communications*, 15(1), 6066.

Wang Y, et al. (2023) Time-ordering japonica/geng genomes analysis indicates the importance of large structural variants in rice breeding. *Plant biotechnology journal*, 21(1), 202.

Herrera S, et al. (2023) Genome assembly of the deep-sea coral *Lophelia pertusa*. *GigaByte (Hong Kong, China)*, 2023, gigabyte78.

Signor S, et al. (2023) Rapid evolutionary diversification of the flamenco locus across simulans clade *Drosophila* species. *PLoS genetics*, 19(8), e1010914.

Li J, et al. (2023) Decoupling subgenomes within hybrid lavandin provide new insights into speciation and monoterpenoid diversification of *Lavandula*. *Plant biotechnology journal*, 21(10), 2084.

Song H, et al. (2023) Scaphopoda is the sister taxon to Bivalvia: Evidence of ancient incomplete lineage sorting. *Proceedings of the National Academy of Sciences of the United States of America*, 120(40), e2302361120.

Hixson KK, et al. (2023) Annotated genome sequence of a fast-growing diploid clone of red alder (*Alnus rubra* Bong.). *G3 (Bethesda, Md.)*, 13(6).