

Resource Summary Report

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Flye

RRID:SCR_017016

Type: Tool

Proper Citation

Flye (RRID:SCR_017016)

Resource Information

URL: <https://github.com/fenderglass/Flye>

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Description: Software package as de novo assembler for single molecule sequencing reads. Used for assembling long, error prone reads such as those produced by PacBio and Oxford Nanopore Technologies, for fast and accurate genome reconstructions. Available for Linux and MacOS platforms.

Resource Type: data analysis software, data processing software, sequence analysis software, software application, software resource, software toolkit

Defining Citation: [PMID:27956617](#)

Keywords: assembler, single, molecule, sequencing, long, error, read, fast, accurate, genome, reconstruction, nucleotide, quality, data, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: Flye

Resource ID: SCR_017016

Alternate IDs: biotools:Flye

Alternate URLs: <https://bio.tools/Flye>, <https://sources.debian.org/src/flye/>

License: BSD 3-Clause "New" or "Revised" License

Record Creation Time: 20220129T080333+0000

Record Last Update: 20260912T195847+0000

Ratings and Alerts

No rating or validation information has been found for Flye.

No alerts have been found for Flye.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 324 mentions in open access literature.

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

Sauerborn E, et al. (2026) Resolving plasmid-encoded carbapenem resistance dynamics and reservoirs in a hospital setting through nanopore sequencing. *Microbial genomics*, 12(2).

Zhang R, et al. (2026) HiFi-Assembled Mitogenomes of Four Pygmy Grasshoppers Reveal Mito-Nuclear Discordance in *Zhengitettix transpicula* and Lineage-Specific Mitochondrial Intergenic Length Variation. *Life (Basel, Switzerland)*, 16(6).

Joel GS, et al. (2026) Genome sequencing reveals variation of African swine fever virus in Nigerian outbreaks and identification of two major West African viral lineages. *Microbial genomics*, 12(2).

Breman FC, et al. (2026) Comparison of whole genome sequencing approaches for Capripox viruses. *BMC genomics*, 27(1), 174.

Xia P, et al. (2026) Genomic analysis of *Enterococcus faecium* co-carrying *optrA* and *poxtA* from a swine farm: dissemination across the human-animal-environment interface. *BMC microbiology*, 26(1), 125.

Huaman JL, et al. (2026) Novel features of *Mycoplasma genitalium* genomes identified through Oxford Nanopore sequence analysis of isolates from Australia. *Microbial genomics*, 12(1).

Zhan J, et al. (2026) Iron plaques as terminal electron acceptors optimize clostridial fermentation and nitrogen fixation in rice rhizospheres. *The ISME journal*, 20(1).

Cowell TC, et al. (2026) Lifestyle-associated variation in type IV secretion systems between phytopathogenic and environmental *Ralstonia*. *Microbial genomics*, 12(4).

Doré G, et al. (2026) First draft genome of the decaploid species, *Ludwigia grandiflora* subsp. *hexapetala*, validated through gene expression. *GigaByte (Hong Kong, China)*, 2026, gigabyte176.

Salazar-Sánchez A, et al. (2026) Construction and characterization of the first *Arcobacter butzleri* - *Escherichia coli* shuttle vector. *Archives of microbiology*, 208(6).

Li J, et al. (2026) Evolutionary dynamics and phylogenetic analysis of the mitochondrial genome of the medicinal plant *Peucedanum praeruptorum*. *BMC plant biology*, 26(1).

Flatau R, et al. (2026) Metabolic potential structures gill symbiont communities in two common shipworm species. *The ISME journal*, 20(1).

Maehana S, et al. (2026) Emergence of Tigecycline-Resistant *Pseudomonas aeruginosa* Harboring *tmexC6D6-toprJ1b* From Hospital Sewage in Japan. *Environmental microbiology reports*, 18(2), e70275.

Schmitt MS, et al. (2026) Learning functional groups in complex microbiomes. *ArXiv*.

Popelá?ová B, et al. (2026) Mind the Porins: Differential Effects of Porin Knockouts and Overexpression on Glucose and Xylose Uptake and Utilization in *Pseudomonas putida*. *Microbial biotechnology*, 19(7), e70406.

Ding J, et al. (2026) Highly Resolved Community Sewage Metagenomics Unveiling Landscape and Transmission Patterns of Antibiotic Resistome in Hong Kong Populations. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(20), e08389.

Moreira G, et al. (2026) Antimicrobial Resistance, Virulence Factors and Plasmid Replicon Patterns of *Klebsiella pneumoniae* and *Klebsiella grimontii* Isolates from Bovine Mastitic Milk in the Northwest of Portugal: Pilot Genomic Characterization. *Antibiotics (Basel, Switzerland)*, 15(2).

Schlebusch SA, et al. (2026) Sex chromosome turnover and structural genome divergence shape meiotic outcomes in hybridizing *Cobitis*. *GigaScience*, 15.

Deng F, et al. (2026) Microoxic conditions promote *Escherichia*-associated cellulase expression in the giant panda gut. *The ISME journal*, 20(1).

Michniewski S, et al. (2026) Rolling out Plaque-2-seq: a single plaque sequencing approach enabling rapid, low-cost sequencing of phages directly from plaques. *Microbial genomics*, 12(4).