

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>

Proper Citation: Flye (RRID:SCR_017016)

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

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: 20260801T190549+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 267 mentions in open access literature.

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

Detcharoen M, et al. (2025) Phylogenomic Analysis Reveals Evolutionary Relationships of Tropical Drosophilidae: From Drosophila to Scaptodrosophila. Ecology and evolution, 15(3), e71100.

Lax C, et al. (2025) Symmetric adenine methylation is an essential DNA modification in the early-diverging fungus Rhizopus microsporus. Nature communications, 16(1), 3843.

Amr RM, et al. (2025) A novel thermostable lytic phage vB_EF_Enf3_CCASU-2024-3 against clinical Enterococcus faecium and Enterococcus faecalis. AMB Express, 15(1), 65.

Yen EC, et al. (2025) Chromosome-level genome assembly and methylome profile yield insights for the conservation of endangered loggerhead sea turtles. GigaScience, 14.

Das J, et al. (2025) Genomic insights into novel predatory myxobacteria isolated from human feces. Microbiology spectrum, 13(7), e0214724.

Lanclos VC, et al. (2025) New isolates refine the ecophysiology of the Roseobacter CHAB-I-5 lineage. ISME communications, 5(1), ycaf068.

Vela AI, et al. (2025) Antibiotic Resistance to Critically Important Antimicrobials and Virulence Genes in Enterococcus faecalis Strains Isolated from Eurasian Griffon Vultures (Gyps fulvus) and Their Association with Mobile Genetic Elements. Veterinary sciences, 12(11).

Nasr E, et al. (2025) PathoGFAIR: a collection of FAIR and adaptable (meta)genomics workflows for (foodborne) pathogens detection and tracking. GigaScience, 14.

White RT, et al. (2025) The rapid detection of a neonatal unit outbreak of a wild-type Klebsiella variicola using decentralized Oxford Nanopore sequencing. Antimicrobial resistance and infection control, 14(1), 6.

Han Y, et al. (2025) Antibiotic-associated changes in Akkermansia muciniphila alter its effects on host metabolic health. Microbiome, 13(1), 48.

Clark MS, et al. (2025) Assessing the impact of sewage and wastewater on antimicrobial resistance in nearshore Antarctic biofilms and sediments. Environmental microbiome,

20(1), 9.

Mehta I, et al. (2025) Control of pili synthesis and putrescine homeostasis in *Escherichia coli*. *eLife*, 13.

Saavedra-Tralma D, et al. (2025) Functional and Genomic Evidence of L-Arginine-Dependent Bacterial Nitric Oxide Synthase Activity in *Paenibacillus nitricinens* sp. nov. *Biology*, 14(6).

Ramon-Mateu J, et al. (2025) Aboral cell types of *Clytia* and coral larvae have shared features and link taurine to the regulation of settlement. *Science advances*, 11(20), eadv1159.

Gasser MT, et al. (2025) Complete genome sequences of two shipworm endosymbiont strains, *Teredinibacter turnerae* SR01903 and SR02026. *Microbiology resource announcements*, 14(6), e0026525.

Tonon E, et al. (2025) Chromosomal-level assembly of *Magnusiomyces clavatus*: novel genetic insights on an emerging fungal pathogen. *G3 (Bethesda, Md.)*, 15(11).

Hou T, et al. (2025) The cytonuclear interactions during grapevine domestication. *Journal of integrative plant biology*, 67(10), 2686.

Kirigo J, et al. (2025) Adsorption of phage T2 is inhibited due to inversion of cryptic prophage DNA by the serine recombinase PinQ. *Nucleic acids research*, 53(19).

Lau NS, et al. (2025) Comparative genomics and multiomics analyses reveal the evolution and physiological basis of rubber biosynthesis in *Hevea* species. *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.