

# Resource Summary Report

Generated by T1D on Sep 5, 2026

## fermi-lite

RRID:SCR\_016112

Type: Tool

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### Proper Citation

fermi-lite (RRID:SCR\_016112)

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### Resource Information

**URL:** <https://github.com/lh3/fermi-lite>

**Proper Citation:** fermi-lite (RRID:SCR\_016112)

**Description:** Standalone C library as well as a command-line tool for assembling Illumina short reads in small regions. It is an overlap-based assembler used in sequencing to retain heterozygous events and to assemble diploid regions for the purpose of variant calling.

**Synonyms:** FermiKit, Fml-asm

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

**Defining Citation:** [PMID:26220959](#)

**Keywords:** assembling, short, read, small, region, sequencing, retain, heterozygous, event, diploid, variant, calling

**Funding:** NHGRI U54 HG003037;  
NIGMS GM100233

**Availability:** Free, Available for download

**Resource Name:** fermi-lite

**Resource ID:** SCR\_016112

**License:** MIT License

**Record Creation Time:** 20220129T080328+0000

**Record Last Update:** 20260903T235334+0000

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### Ratings and Alerts

No rating or validation information has been found for fermi-lite.

No alerts have been found for fermi-lite.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 4 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [T1D](#) .

Xu Y, et al. (2023) Prevalence and clinico-genomic characteristics of patients with TRK fusion cancer in China. NPJ precision oncology, 7(1), 75.

Tong Z, et al. (2021) Clonal Evolution Dynamics in Primary and Metastatic Lesions of Pancreatic Neuroendocrine Neoplasms. Frontiers in medicine, 8, 620988.

Evans T, et al. (2018) Virtual Genome Walking across the 32 Gb Ambystoma mexicanum genome; assembling gene models and intronic sequence. Scientific reports, 8(1), 618.

Hunt M, et al. (2017) ARIBA: rapid antimicrobial resistance genotyping directly from sequencing reads. Microbial genomics, 3(10), e000131.