

Resource Summary Report

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[fermi](#)

RRID:SCR_016652

Type: Tool

Proper Citation

fermi (RRID:SCR_016652)

Resource Information

URL: <https://github.com/lh3/fermi>

Proper Citation: fermi (RRID:SCR_016652)

Description: Software assembler and analysis tool for whole-genome short-gun sequencing for Illumina reads. Provides tools for error correction, sequence-to-read alignment and comparison between read sets. Used for large genomes.

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

Defining Citation: [PMID:22569178](#)

Keywords: assembler, analysis, whole, genome, short, gun, sequencing, error, correction

Funding: NHGRI U01 HG005208

Availability: Free, Available for download, Freely available

Resource Name: fermi

Resource ID: SCR_016652

Record Creation Time: 20220129T080331+0000

Record Last Update: 20260912T195842+0000

Ratings and Alerts

No rating or validation information has been found for fermi.

No alerts have been found for fermi.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.