

Resource Summary Report

Generated by [PRECISE-TBI](#) on Aug 1, 2026

Fast-SG

RRID:SCR_015934

Type: Tool

Proper Citation

Fast-SG (RRID:SCR_015934)

Resource Information

URL: <https://github.com/adigenova/fast-sg>

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Description: Algorithm for alignment-free scaffolding graph construction from short or long reads. It allows the reuse of efficient algorithms designed for short read data and permits the definition of novel modular hybrid assembly pipelines.

Synonyms: Fast SG

Resource Type: software resource, algorithm resource

Defining Citation: [DOI:10.1101/209122](https://doi.org/10.1101/209122)

Keywords: scaffolding, genome, assembly, illumina, nanopore, pacbio, hybrid, alignment, free, algorithm

Funding: CMM PFB03;
CONICYT BECA DOCTORADO NACIONAL 21140124

Availability: Open source, Free, Available for download, Runs on MAC OS, Runs on Linux

Resource Name: Fast-SG

Resource ID: SCR_015934

License: MIT License

License URLs: <https://github.com/adigenova/fast-sg/blob/master/LICENSE>

Record Creation Time: 20220129T080328+0000

Record Last Update: 20260729T044401+0000

Ratings and Alerts

No rating or validation information has been found for Fast-SG.

No alerts have been found for Fast-SG.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Unneberg P, et al. (2024) Ecological genomics in the Northern krill uncovers loci for local adaptation across ocean basins. Nature communications, 15(1), 6297.

Parisot N, et al. (2021) The transposable element-rich genome of the cereal pest *Sitophilus oryzae*. BMC biology, 19(1), 241.

Nguyen SH, et al. (2021) Real-time resolution of short-read assembly graph using ONT long reads. PLoS computational biology, 17(1), e1008586.

Di Genova A, et al. (2018) Fast-SG: an alignment-free algorithm for hybrid assembly. GigaScience, 7(5).