SGA
RRID:SCR_001982
Type: Tool

Proper Citation

SGA (RRID:SCR_001982)

Description: Software package that functions as a de novo genome assembler based on the concept of string graphs. It is designed as a modular set of programs used to assemble large genomes from high coverage short read data.

Resource Information

URL: https://github.com/jts/sga

Description: Software package that functions as a de novo genome assembler based on the concept of string graphs. It is designed as a modular set of programs used to assemble large genomes from high coverage short read data.

Resource Name: SGA

Proper Citation: SGA (RRID:SCR_001982)

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

Keywords: string, graph assembler, de novo assembly

Resource ID: SCR_001982

References: DOI:10.1101/gr.126953.111

Availability: Open source

Website Status: Last checked up

Alternate IDs: OMICS_00028

Mentions Count: 11

Ratings and Alerts
No rating or validation information has been found for SGA.

No alerts have been found for SGA.

Data and Source Information
Source: SciCrunch Registry

Usage and Citation Metrics

We found 11 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [FDI Lab - SciCrunch Infrastructure](#).


