

# Resource Summary Report

Generated by [kravitz2](#) on Sep 4, 2026

## SGA

RRID:SCR\_001982

Type: Tool

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### Proper Citation

SGA (RRID:SCR\_001982)

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### Resource Information

**URL:** <https://github.com/jts/sga>

**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.

**Synonyms:** String Graph Assembler (SGA), String Graph Assembler

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

**Defining Citation:** [DOI:10.1101/gr.126953.111](https://doi.org/10.1101/gr.126953.111)

**Keywords:** string, graph assembler, de novo assembly, bio.tools

**Availability:** Free, Available for download, Freely available

**Resource Name:** SGA

**Resource ID:** SCR\_001982

**Alternate IDs:** OMICS\_00028, biotools:sga

**Alternate URLs:** <https://bio.tools/sga>, <https://sources.debian.org/src/sga/>

**License:** GPL v3

**Record Creation Time:** 20220129T080210+0000

**Record Last Update:** 20260903T235748+0000

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### Ratings and Alerts

No rating or validation information has been found for SGA.

No alerts have been found for SGA.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 18 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [kravitz2](#) .

Richter A, et al. (2025) The master male sex determinant Gdf6Y of the turquoise killifish arose through allelic neofunctionalization. *Nature communications*, 16(1), 540.

Zampirolo G, et al. (2024) Tracing early pastoralism in Central Europe using sedimentary ancient DNA. *Current biology : CB*, 34(20), 4650.

Qi W, et al. (2022) The haplotype-resolved chromosome pairs of a heterozygous diploid African cassava cultivar reveal novel pan-genome and allele-specific transcriptome features. *GigaScience*, 11.

Roscito JG, et al. (2022) Convergent and lineage-specific genomic differences in limb regulatory elements in limbless reptile lineages. *Cell reports*, 38(3), 110280.

Qiu S, et al. (2022) Genome-enabled discovery of candidate virulence loci in *Striga hermonthica*, a devastating parasite of African cereal crops. *The New phytologist*, 236(2), 622.

Wang W, et al. (2020) The draft nuclear genome assembly of *Eucalyptus pauciflora*: a pipeline for comparing de novo assemblies. *GigaScience*, 9(1).

Anava S, et al. (2020) Illuminating Genetic Mysteries of the Dead Sea Scrolls. *Cell*, 181(6), 1218.

Mitchell K, et al. (2020) Benchmarking of computational error-correction methods for next-generation sequencing data. *Genome biology*, 21(1), 71.

Lilue J, et al. (2018) Sixteen diverse laboratory mouse reference genomes define strain-specific haplotypes and novel functional loci. *Nature genetics*, 50(11), 1574.

Shen XX, et al. (2018) Tempo and Mode of Genome Evolution in the Budding Yeast Subphylum. *Cell*, 175(6), 1533.

Roscito JG, et al. (2018) Phenotype loss is associated with widespread divergence of the gene regulatory landscape in evolution. *Nature communications*, 9(1), 4737.

Seersholm FV, et al. (2016) DNA evidence of bowhead whale exploitation by Greenlandic Paleo-Inuit 4,000 years ago. *Nature communications*, 7, 13389.

Sundararaman SA, et al. (2016) Genomes of cryptic chimpanzee *Plasmodium* species reveal key evolutionary events leading to human malaria. *Nature communications*, 7, 11078.

Laehnemann D, et al. (2016) Denoising DNA deep sequencing data-high-throughput sequencing errors and their correction. *Briefings in bioinformatics*, 17(1), 154.

Simpson JT, et al. (2014) Exploring genome characteristics and sequence quality without a reference. *Bioinformatics (Oxford, England)*, 30(9), 1228.

Kleftogiannis D, et al. (2013) Comparing memory-efficient genome assemblers on stand-alone and cloud infrastructures. *PloS one*, 8(9), e75505.

El-Metwally S, et al. (2013) Next-generation sequence assembly: four stages of data processing and computational challenges. *PLoS computational biology*, 9(12), e1003345.

Kremer FS, et al. () Approaches for in silico finishing of microbial genome sequences. *Genetics and molecular biology*, 40(3), 553.