Resource Summary Report

Generated by RRID on Apr 29, 2025

SGA

RRID:SCR_001982 Type: Tool

Proper Citation

SGA (RRID:SCR_001982)

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 processing software, sequence analysis software, data analysis software, software resource, software application

Defining Citation: DOI:10.1101/gr.126953.111

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

Funding:

Availability: Open source

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: 20250429T054706+0000

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 18 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>RRID</u>.

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 nextgeneration sequencing data. Genome biology, 21(1), 71. Lilue J, et al. (2018) Sixteen diverse laboratory mouse reference genomes define strainspecific 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 standalone 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.