

Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

SparseAssembler

RRID:SCR_001100

Type: Tool

Proper Citation

SparseAssembler (RRID:SCR_001100)

Resource Information

URL: <http://sourceforge.net/projects/sparseassembler/>

Proper Citation: SparseAssembler (RRID:SCR_001100)

Description: Software for memory-efficient genome assembly. It utilizes sparse k-mer.

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

Defining Citation: [PMID:22537038](#)

Keywords: genome, genomics, genome assembly, k-mer, sequence analysis software, memory

Availability: Free, Available for download, Freely available

Resource Name: SparseAssembler

Resource ID: SCR_001100

Alternate IDs: OMICS_00032

Record Creation Time: 20220129T080205+0000

Record Last Update: 20260728T043107+0000

Ratings and Alerts

No rating or validation information has been found for SparseAssembler.

No alerts have been found for SparseAssembler.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Abbas MM, et al. (2014) Assessment of de novo assemblers for draft genomes: a case study with fungal genomes. BMC genomics, 15 Suppl 9(Suppl 9), S10.