# Resource Summary Report

Generated by NIF on Apr 16, 2025

# 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:** software resource, sequence analysis software, data analysis software, software application, data processing software

**Defining Citation:** PMID:22537038

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

**Funding:**

**Availability:** Available for download

**Resource Name:** SparseAssembler

**Resource ID:** SCR_001100

**Alternate IDs:** OMICS_00032

**Record Creation Time:** 20220129T080205+0000

**Record Last Update:** 20250416T063231+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 NIF.

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.