

# Resource Summary Report

Generated by [PRECISE-TBI](#) on Aug 9, 2026

## VCAKE

RRID:SCR\_013060

Type: Tool

### Proper Citation

VCAKE (RRID:SCR\_013060)

### Resource Information

**URL:** <http://sourceforge.net/projects/vcake/>

**Proper Citation:** VCAKE (RRID:SCR\_013060)

**Description:** A genetic sequence assembler capable of assembling millions of small nucleotide reads even in the presence of sequencing error.

**Abbreviations:** VCAKE

**Resource Type:** software resource

**Resource Name:** VCAKE

**Resource ID:** SCR\_013060

**Alternate IDs:** OMICS\_00037

**Record Creation Time:** 20220129T080314+0000

**Record Last Update:** 20260808T190007+0000

### Ratings and Alerts

No rating or validation information has been found for VCAKE.

No alerts have been found for VCAKE.

### Data and Source Information

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

### Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Yao W, et al. (2020) Features of sRNA biogenesis in rice revealed by genetic dissection of sRNA expression level. Computational and structural biotechnology journal, 18, 3207.

Kong J, et al. (2019) GAAP: A Genome Assembly + Annotation Pipeline. BioMed research international, 2019, 4767354.

Dierckxsens N, et al. (2017) NOVOPlasty: de novo assembly of organelle genomes from whole genome data. Nucleic acids research, 45(4), e18.

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