

Resource Summary Report

Generated by [NIF](#) on Aug 10, 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 [NIF](#) .

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.