

Resource Summary Report

Generated by [RRID](#) on Aug 15, 2026

Ccube

RRID:SCR_027721

Type: Tool

Proper Citation

Ccube (RRID:SCR_027721)

Resource Information

URL: <https://github.com/keyuan/ccube>

Proper Citation: Ccube (RRID:SCR_027721)

Description: Software R package for clustering and estimating cancer cell fractions (CCF) of somatic variants (SNVs/SVs) from bulk whole genome/exome data. Used for estimating cancer cell fractions .

Resource Type: software toolkit, source code, software resource

Defining Citation: [DOI:10.1101/484402v1](https://doi.org/10.1101/484402v1)

Keywords: Single nucleotide variant, cancer, estimating cancer cell fractions,

Availability: Free, Available for download, Freely available

Resource Name: Ccube

Resource ID: SCR_027721

License: GNU GPL v3

Record Creation Time: 20251209T055452+0000

Record Last Update: 20260815T183309+0000

Ratings and Alerts

No rating or validation information has been found for Ccube.

No alerts have been found for Ccube.

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 [RRID](#) .

Hong J, et al. (2026) Convergence for Inactivation of TGF β Signaling Is a Common Feature of Advanced Pancreatic Cancer. Cancer discovery, 16(6), 1087.