Resource Summary Report

Generated by RRID on Aug 15, 2026

GCAT Workflow

RRID:SCR_027692
Type: Tool

Proper Citation

GCAT Workflow (RRID:SCR_027692)

Resource Information

URL: https://github.com/ncc-gap/GCATWorkflow

Proper Citation: GCAT Workflow (RRID:SCR_027692)

Description: Software cancer genome and RNA sequencing data analysis pipeline that detects genomic variants and transcriptomic changes.

Resource Type: software application, software resource, source code

Keywords: cancer genome, RNA sequencing data analysis, detect genomic variants, detect transcriptomic changes,

Availability: Free, Available for download, Freely available

Resource Name: GCAT Workflow

Resource ID: SCR_027692

License: GNU GPL v3

Record Creation Time: 20251122T055350+0000

Record Last Update: 20260815T183306+0000

Ratings and Alerts

No rating or validation information has been found for GCAT Workflow.

No alerts have been found for GCAT Workflow.

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 .

Ikegami M, et al. (2026) Germline Pathogenic Variant Prediction Model for Tumor-Only Sequencing Based on Japanese Clinicogenomic Database. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(4), 770.