

Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

ScanITD

RRID:SCR_018886

Type: Tool

Proper Citation

ScanITD (RRID:SCR_018886)

Resource Information

URL: <https://github.com/ylab-hi/ScanITD>

Proper Citation: ScanITD (RRID:SCR_018886)

Description: Open source software Python tool for detecting internal tandem duplication with variant allele frequency estimation.

Synonyms: Scan Internal Tandem Duplications

Resource Type: sequence analysis software, data analysis software, software resource, software application, data processing software

Defining Citation: [DOI:10.5524/100775](https://doi.org/10.5524/100775)

Keywords: Internal tandem duplication, FLT3, acute myeloid leukemia, TCGA, chimeric alignment, variant allele frequency, variant allele, frequency estimation, , bio.tools

Related Condition: Acute Myeloid Leukemia

Availability: Free, Available for download, Freely available

Resource Name: ScanITD

Resource ID: SCR_018886

Alternate IDs: biotools:ScanItD

Alternate URLs: <https://bio.tools/ScanITD>, <http://gigadb.org/dataset/100775>

License: MIT

Record Creation Time: 20220129T080342+0000

Record Last Update: 20260728T043548+0000

Ratings and Alerts

No rating or validation information has been found for ScanITD.

No alerts have been found for ScanITD.

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 [nidm-terms](#) .

Wang TY, et al. (2020) ScanITD: Detecting internal tandem duplication with robust variant allele frequency estimation. GigaScience, 9(8).