

# Resource Summary Report

Generated by [FDI Lab - SciCrunch.org](#) on Apr 24, 2025

## ScanITD

RRID:SCR\_018886

Type: Tool

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### Proper Citation

ScanITD (RRID:SCR\_018886)

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### 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:** data analysis software, sequence 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

**Funding:**

**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:** 20250424T065607+0000

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## Ratings and Alerts

No rating or validation information has been found for ScanITD.

No alerts have been found for ScanITD.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 1 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [FDI Lab - SciCrunch.org](#).

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