Resource Summary Report

Generated by RRID on Apr 28, 2025

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

Defining Citation: DOI: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: 20250428T054147+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 RRID.

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