

# Resource Summary Report

Generated by T1D on Sep 5, 2026

## PoPoolation TE

RRID:SCR\_005131

Type: Tool

### Proper Citation

PoPoolation TE (RRID:SCR\_005131)

### Resource Information

**URL:** <https://code.google.com/p/popoolationte/>

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**Description:** A quick and simple pipeline for the analysis of transposable element (TE) insertions in (natural) populations using next generation sequencing. It calculates TE insertion frequencies for TEs that are present in the reference genome as well as for novel TE insertions. PoPoolation TE requires paired-end reads from a pooled population, a reference sequence and transposable element sequences (fasta-file).

**Abbreviations:** PoPoolation TE

**Resource Type:** software resource

**Defining Citation:** [PMID:22291611](#)

**Keywords:** next generation sequencing, transposable element, insertion frequency, genomics, population genetics, illumina

**Availability:** Acknowledgement requested, New BSD License

**Resource Name:** PoPoolation TE

**Resource ID:** SCR\_005131

**Alternate IDs:** OMICS\_00119

**Record Creation Time:** 20220129T080228+0000

**Record Last Update:** 20260903T234748+0000

### Ratings and Alerts

No rating or validation information has been found for PoPoolation TE.

No alerts have been found for PoPoolation TE.

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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 [T1D](#) .

Zhuang J, et al. (2014) TEMP: a computational method for analyzing transposable element polymorphism in populations. Nucleic acids research, 42(11), 6826.