

Resource Summary Report

Generated by [kravitz2](#) on Aug 2, 2026

RelocaTE

RRID:SCR_002308

Type: Tool

Proper Citation

RelocaTE (RRID:SCR_002308)

Resource Information

URL: <https://github.com/srobb1/RelocaTE>

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Description: Software toolkit of a collection of scripts in which short reads (paired or unpaired), a fasta containing the sequences of transposable elements and a reference genome sequence, are the input and the output is a series of files containing the locations of TE insertions in the reference and short reads.

Resource Type: software resource, software toolkit

Defining Citation: [PMID:23576519](#)

Keywords: short read, TE insertion, genomic sequencing script, transposable element

Availability: Open source, Free

Resource Name: RelocaTE

Resource ID: SCR_002308

Alternate IDs: OMICS_03506

License: BSD License

License URLs: <https://github.com/srobb1/RelocaTE/blob/master/LICENSE>

Record Creation Time: 20220129T080212+0000

Record Last Update: 20260801T191044+0000

Ratings and Alerts

No rating or validation information has been found for RelocaTE.

No alerts have been found for RelocaTE.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 8 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Daigle AT, et al. (2022) Bergerac strains of *Caenorhabditis elegans* revisited: expansion of Tc1 elements imposes a significant genomic and fitness cost. *G3* (Bethesda, Md.), 12(11).

Macko-Podgorni A, et al. (2019) Stowaway miniature inverted repeat transposable elements are important agents driving recent genomic diversity in wild and cultivated carrot. *Mobile DNA*, 10, 47.

Lu L, et al. (2017) Tracking the genome-wide outcomes of a transposable element burst over decades of amplification. *Proceedings of the National Academy of Sciences of the United States of America*, 114(49), E10550.

Kang H, et al. (2016) A novel method for identifying polymorphic transposable elements via scanning of high-throughput short reads. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 23(3), 241.

Ewing AD, et al. (2015) Transposable element detection from whole genome sequence data. *Mobile DNA*, 6, 24.

Makarevitch I, et al. (2015) Transposable elements contribute to activation of maize genes in response to abiotic stress. *PLoS genetics*, 11(1), e1004915.

Nakagome M, et al. (2014) Transposon Insertion Finder (TIF): a novel program for detection of de novo transpositions of transposable elements. *BMC bioinformatics*, 15, 71.

Robb SM, et al. (2013) The use of RelocaTE and unassembled short reads to produce high-resolution snapshots of transposable element generated diversity in rice. *G3* (Bethesda, Md.), 3(6), 949.