

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

PASTEClassifier

RRID:SCR_017645

Type: Tool

Proper Citation

PASTEClassifier (RRID:SCR_017645)

Resource Information

URL: <https://urgi.versailles.inra.fr/Tools/PASTEClassifier>

Proper Citation: PASTEClassifier (RRID:SCR_017645)

Description: Software tool for automatic transposable element classification. Used for searching for structural features and similarity to classify transposable elements.

Abbreviations: PASTEC

Synonyms: Pseudo Agent System for Transposable Elements Classification, PASTEC

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

Defining Citation: [PMID:24786468](https://pubmed.ncbi.nlm.nih.gov/24786468/)

Keywords: Automatic, transposable, element, classification, bio.tools, bio.tools

Funding: French National Research Agency

Availability: Free, Available for download, Freely available

Resource Name: PASTEClassifier

Resource ID: SCR_017645

Alternate IDs: biotools:PASTEClassifier

Alternate URLs: <https://urgi.versailles.inra.fr/download/repet/PASTEClassifier-1.0.tar.gz>, <https://bio.tools/repet>, <https://bio.tools/PASTEClassifier>

Record Creation Time: 20220129T080336+0000

Record Last Update: 20260905T133054+0000

Ratings and Alerts

No rating or validation information has been found for PASTEClassifier.

No alerts have been found for PASTEClassifier.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 12 mentions in open access literature.

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

Ding D, et al. (2025) Genomic analysis of *Inonotus hispidus* provides insights into its medicinal properties and evolutionary dynamics. *Scientific reports*, 15(1), 23031.

Bhadauria V, et al. (2025) Near-complete genome and infection transcriptomes of the maize leaf and sheath spot pathogen *Epicoccum sorghinum*. *Scientific data*, 12(1), 261.

Zhang H, et al. (2024) The High-Quality Genome Sequencing and Analysis of Red Raspberry (*Rubus idaeus* L.). *International journal of genomics*, 2024, 9271183.

He J, et al. (2022) A chromosome-level genome assembly of *Artocarpus nanchuanensis* (Moraceae), an extremely endangered fruit tree. *GigaScience*, 11.

Zhang J, et al. (2021) The genome of *Cleistogenes songorica* provides a blueprint for functional dissection of dimorphic flower differentiation and drought adaptability. *Plant biotechnology journal*, 19(3), 532.

Pedro DLF, et al. (2021) An Atlas of Plant Transposable Elements. *F1000Research*, 10, 1194.

Ou M, et al. (2021) Chromosome-level genome assemblies of *Channa argus* and *Channa maculata* and comparative analysis of their temperature adaptability. *GigaScience*, 10(10).

Zhao T, et al. (2021) A chromosome-level reference genome of the hazelnut, *Corylus heterophylla* Fisch. *GigaScience*, 10(4).

Guo XM, et al. (2021) Chromosomal-level assembly of the *Leptodermis oblonga* (Rubiaceae) genome and its phylogenetic implications. *Genomics*, 113(5), 3072.

Jiang S, et al. (2020) Chromosome-level genome assembly and annotation of the loquat (*Eriobotrya japonica*) genome. *GigaScience*, 9(3).

Alonge M, et al. (2020) Major Impacts of Widespread Structural Variation on Gene Expression and Crop Improvement in Tomato. *Cell*, 182(1), 145.

Ou C, et al. (2019) A de novo genome assembly of the dwarfing pear rootstock Zhongai 1. *Scientific data*, 6(1), 281.