

Resource Summary Report

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REPCLASS

RRID:SCR_014654

Type: Tool

Proper Citation

REPCLASS (RRID:SCR_014654)

Resource Information

URL: <https://github.com/feschottelab/REPCLASS>

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Description: Tool for the classification of known transposable elements in eukaryotic genomes. It can be combined with ab initio repeat finding in order to recover contrasting transposable element landscapes between species.

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

Defining Citation: [DOI:10.1093/gbe/evp023](https://doi.org/10.1093/gbe/evp023)

Keywords: transposable element, eukaryotic genome, eukaryote, genome, ab initio, repeat, software, source code, sequence analysis software, data analysis software

Availability: Available for download

Resource Name: REPCLASS

Resource ID: SCR_014654

Record Creation Time: 20220129T080321+0000

Record Last Update: 20260819T044411+0000

Ratings and Alerts

No rating or validation information has been found for REPCLASS.

No alerts have been found for REPCLASS.

Data and Source Information

Usage and Citation Metrics

We found 10 mentions in open access literature.

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

Xu MR, et al. (2023) Maternal dominance contributes to subgenome differentiation in allopolyploid fishes. *Nature communications*, 14(1), 8357.

Zhang Y, et al. (2020) The genome of opportunistic fungal pathogen *Fusarium oxysporum* carries a unique set of lineage-specific chromosomes. *Communications biology*, 3(1), 50.

Shao F, et al. (2019) Evolution and diversity of transposable elements in fish genomes. *Scientific reports*, 9(1), 15399.

Shao F, et al. (2018) FishTEDB: a collective database of transposable elements identified in the complete genomes of fish. *Database : the journal of biological databases and curation*, 2018.

Holt C, et al. (2018) Improved Genome Assembly and Annotation for the Rock Pigeon (*Columba livia*). *G3 (Bethesda, Md.)*, 8(5), 1391.

Hiraki H, et al. (2017) Genome analysis of *Diploscapter coronatus*: insights into molecular peculiarities of a nematode with parthenogenetic reproduction. *BMC genomics*, 18(1), 478.

Hamilton EP, et al. (2016) Structure of the germline genome of *Tetrahymena thermophila* and relationship to the massively rearranged somatic genome. *eLife*, 5.

Sun C, et al. (2012) LTR retrotransposons contribute to genomic gigantism in plethodontid salamanders. *Genome biology and evolution*, 4(2), 168.

de la Chaux N, et al. (2012) The predominantly selfing plant *Arabidopsis thaliana* experienced a recent reduction in transposable element abundance compared to its outcrossing relative *Arabidopsis lyrata*. *Mobile DNA*, 3(1), 2.

Feschotte C, et al. (2009) Exploring repetitive DNA landscapes using REPCCLASS, a tool that automates the classification of transposable elements in eukaryotic genomes. *Genome biology and evolution*, 1, 205.