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RepetDB: A TE database

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Transposable elements (TEs) are major players of structure and evolution of eukaryote genomes. Thanks to their ability to move around and to replicate within genomes, they are probably the most important contributors to genome plasticity. **Their detection and annotation are considered essential and must be undertaken in any genome sequencing project.**

To annotate transposable elements in genome, consensus are needed and RepetDB aims to make available these sequence to make easier the annotation of closely related genomes. You can select consensus of interest in the database and download fasta sequence.

- I wish to make an annotation of a Brassicaceae species close from *Arabidopsis thaliana*. - I go to repetdb website and check the related species of interest <https://urgi.versailles.inrae.fr/repetdb>

- I can also select multiple species, from example all *Brassicaceae* or just one close related species like *Arabidopsis thaliana*

- Selection of specifics class, order or superfamily is also available to refine a search

Consensus search result

Back to home screen

Search criteria: Taxon group: Arabidopsis thaliana

Showing 1 to 25 of 406 rows

| Consensus Identifier | Consensus Copies | Consensus Full-length copies | Consensus Length | Consensus TE classification code | Consensus Manual validation | Consensus Confused | Consensus Comments |
|---|------------------|------------------------------|------------------|----------------------------------|-----------------------------|--------------------|--------------------|
| MCL102_AthaCol0_TEdenovo-B-G1208-Map3 | 20 | 9 | 471 | Class I : LINE : ? | classification | no | NO VALUE |
| MCL102_AthaCol0_TEdenovo-B-R178-Map3 | 122 | 8 | 2017 | Class I : LINE : ? | classification | no | NO VALUE |
| MCL103_AthaCol0_TEdenovo-B-G1214-Map20 | 23 | 11 | 449 | Class II : Helitron : ? | classification | no | NO VALUE |
| MCL103_AthaCol0_TEdenovo-B-P161.100-Map16 | 21 | 11 | 452 | Class II : Helitron : ? | classification | no | NO VALUE |

- I can obtain statistics and filter some values out or download my result and consensus **fasta sequences**

- I have an interesting sequence that I suspect is a transposable element and I wish to check if a match exist in the database. I go to PlantbioinfoPF blast services <https://urgi.versailles.inrae.fr/blast/> and select in group « Repeats » a close related species

- If a match is found I get a direct link to the consensus card

By selecting one consensus I can access a consensus card describing its classification