



## **TE Hub: a community-oriented space for sharing and connecting tools, data, resources, and methods for transposable element annotation**

Tyler A. Elliott, Tony Heitkam, Robert Hubley, Hadi Quesneville, Alexander Suh, Travis J. Wheeler, . The Te Hub Consortium

### **► To cite this version:**

Tyler A. Elliott, Tony Heitkam, Robert Hubley, Hadi Quesneville, Alexander Suh, et al.. TE Hub: a community-oriented space for sharing and connecting tools, data, resources, and methods for transposable element annotation. The Mobile DNA Conference: Evolution, Diversity, and Impact, Jun 2021, Virtuel, France. 2021. hal-03357402

**HAL Id: hal-03357402**

**<https://hal.inrae.fr/hal-03357402>**

Submitted on 28 Sep 2021

**HAL** is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



# TE Hub: a community-oriented space for sharing and connecting tools, data, resources, and methods for transposable element annotation

Tyler A. Elliott<sup>1\*</sup>, Tony Heitkam<sup>2\*</sup>, Robert Hubley<sup>3\*</sup>, Hadi Quesneville<sup>4\*</sup>, Alexander Suh<sup>5\*</sup>, Travis J. Wheeler<sup>6\*</sup>, TE Hub Consortium



## Abstract

The diversity of available TE-related methods and resources raises compatibility concerns and can be overwhelming to researchers and communicators seeking straightforward guidance or materials. To address these challenges, we have initiated a new resource, TE Hub, that provides a space where members of the TE community can collaborate to document, create, and integrate resources and methods.

TE Hub consists of

- a website (<http://tehub.org>) organized with an open wiki framework
- a conversation framework via a Twitter account (@hub\_te) and a Slack channel (#te-hub) housed in the larger TransposonsWorldwide workspace
- bi-monthly Hub Update video chats on the platform's development

In addition to serving as a centralized repository and communication platform, TE Hub lays the foundation for improved integration, standardization, and effectiveness of diverse tools and protocols.



<http://tehub.org>  
(wiki)



@hub\_te



#te-hub  
(TransposonsWorldwide)

## Overarching classification schemes

- ▶ [Repbase: Jurka et al. \(2005\)](#)
- ▶ [Wicker et al. \(2007\)](#)
- ▶ [Piégu et al. \(2015\)](#)
- ▶ [Arkhipova \(2017\)](#)
- ▶ [Dfam Classification](#)

## Specific classification schemes

The TE orders can be classified further into lineages and clades. The

### Long Terminal Repeat (LTR) retrotransposons

- ▶ [Gypsy Database \(GyDB\) Classification](#)
- ▶ [ICTV LTR Taxonomy](#)

### Other systems

- ▶ [Group I Intron Classification](#)
- ▶ [ISfinder Classification](#)

## Individual TE lineages

Individual TE can be summarized into families and superfamilies.

## Contribute

We invite the TE community, both novices and experts in TE identification and analysis, to join us in expanding our community-oriented resource.



## Overview of repeat databases

| Resource  | DOI   | Taxonomic Group   | Repeat Types                          |
|---|---|-------------------|---------------------------------------|
| <a href="#">3'UTR-SIRF</a>  | <a href="https://doi.org/10.1186/1471-2105-8-274">https://doi.org/10.1186/1471-2105-8-274</a>     | Mammal            | SINE                                  |
| <a href="#">ACLAME</a>  | <a href="https://doi.org/10.1093/nar/gkp938">https://doi.org/10.1093/nar/gkp938</a>               | Archaea, Bacteria | Plasmid, Virus                        |
| <a href="#">alu_ontology</a>                                      | <a href="https://doi.org/10.1016/j.jbi.2016.01.010">https://doi.org/10.1016/j.jbi.2016.01.010</a> | Homo sapiens      | Alu, SINE                             |
| <a href="#">ARDB (Antibiotic Resistance Genes Database)</a>       | <a href="https://doi.org/10.1093/nar/gkn656">https://doi.org/10.1093/nar/gkn656</a>               | Archaea, Bacteria | AMR/Antibiotic Resistance             |
| <a href="#">ArTEDB (Arthropod Transposable Elements Database)</a> | <a href="https://doi.org/10.3390/genes10050338">https://doi.org/10.3390/genes10050338</a>         | Arthropod         | Eukaryotic Transposon                 |
| <a href="#">Bamboo Microsatellite Database</a>                    | <a href="https://doi.org/10.1038/srep08018">https://doi.org/10.1038/srep08018</a>                 | Phyllostachys     | Simple Sequence Repeat/Microsatellite |
| <a href="#">BanSatDB (Banana Satellite Database)</a>              | <a href="https://doi.org/10.1016/j.cj.2018.01.005">https://doi.org/10.1016/j.cj.2018.01.005</a>   | Musa              | Simple Sequence Repeat/Microsatellite |

## Overview of tools for repeat analysis

| Tool  | DOI   | Alternate URL | Keywords   |
|---|---|---------------|--|
| <a href="#">2ipiRNApred</a>   | <a href="https://doi.org/10.1080/15476286.2020.1734382">https://doi.org/10.1080/15476286.2020.1734382</a> |               | piRNA  |
| <a href="#">AAARF (Assisted Automated Assembler of Repeat Families)</a> | <a href="https://doi.org/10.1186/1471-2105-9-235">https://doi.org/10.1186/1471-2105-9-235</a>             |               | Homology, Alignment                                    |
| <a href="#">AgIn</a>  | <a href="https://doi.org/10.1093/bioinformatics/btw360">https://doi.org/10.1093/bioinformatics/btw360</a> |               | PacBio, Methylation                                    |
| <a href="#">AlbaTraDIS</a>  | <a href="https://doi.org/10.1371/journal.pcbi.1007980">https://doi.org/10.1371/journal.pcbi.1007980</a>   |               | Tr-Seq, Transposon Mutagenesis                         |
| <a href="#">Alien_Hunter</a>  | <a href="https://doi.org/10.1093/bioinformatics/bti369">https://doi.org/10.1093/bioinformatics/bti369</a> |               | Genomic Island, HMM                                    |
| <a href="#">alu-detect</a>  | <a href="https://doi.org/10.1093/nar/gkt612">https://doi.org/10.1093/nar/gkt612</a>                       |               | Alu, SINE, Genotype, Polymorphism, NGS/HTS, Paired-End |
| <a href="#">AluMine</a>   | <a href="https://doi.org/10.1101/588434">https://doi.org/10.1101/588434</a>                               |               | Alu, SINE, Genotype,                                   |

| Taxonomic Group         | Repeat Types |
|-------------------------|--------------|
| All                     | <Any>        |
| Animal                  |              |
| Archaea                 |              |
| Arthropod               |              |
| Bacteria                |              |
| Beta vulgaris           |              |
| Boechera                |              |
| Bombyx mori             |              |
| Brassica oleracea       |              |
| Brassica rapa           |              |
| Bubalis bubalis         |              |
| Cajanus cajan           |              |
| Carica papaya           |              |
| Cicer arietinum         |              |
| Cucumis melo            |              |
| Cyanobacteria           |              |
| Cynara cardunculus      |              |
| Dioecious Plant         |              |
| Drosophila              |              |
| Drosophila melanogaster |              |
| Eukaryote               |              |
| Fish                    |              |
| Fungi                   |              |
| Glycine                 |              |
| Gossypium               |              |
| Gossypium raimondii     |              |

| Keywords                     | Repeat Types |
|------------------------------|--------------|
| <Any>                        | <Any>        |
| AMR/Antibiotic Resistance    |              |
| Abundance                    |              |
| Active TEs                   |              |
| Activity                     |              |
| Aegilops                     |              |
| Age                          |              |
| Alignment                    |              |
| Alu                          |              |
| Analysis                     |              |
| Ancestral Reconstruction     |              |
| Annotation                   |              |
| Annotation Parsing           |              |
| Annotation Track             |              |
| Archaea                      |              |
| Archaea/Bacterial Transposon |              |
| Assembly                     |              |
| Assembly Polishing           |              |
| BLAST                        |              |
| BLAT                         |              |
| Bacteria                     |              |
| Bayesian                     |              |
| Bayesian MCMC                |              |