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

Tyler A. Elliott^{1*}, Tony Heitkam^{2*}, Robert Hubley^{3*}, Hadi Quesneville^{4*}, Alexander Suh^{5*}, Travis J. Wheeler^{6*}, 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.



TE Hub

- Home
- Classification
- Databases
- Tools
- Protocols
- Conferences
- Journals
- Teaching Resources
- Outreach
- Volunteering
- Working Group
- About

Overview of repeat databases

Resource	DOI	Taxonomic Group	Repeat Types
3'UTR-SIRF	https://doi.org/10.1186/1471-2105-8-274	Mammal	SINE
ACLAME	https://doi.org/10.1093/nar/gkn938	Archaea, Bacteria	Plasmid, Virus
alu_ontology	https://doi.org/10.1016/j.jbi.2016.01.010	Homo sapiens	Alu, SINE
ARDB (Antibiotic Resistance Genes Database)	https://doi.org/10.1093/nar/gkn656	Archaea, Bacteria	AMR/Antibiotic Resistance
ARTEDB (Arthropod Transposable Elements Database)	https://doi.org/10.3390/genes10050338	Arthropod	Eukaryotic Transposon
Bamboo Microsatellite Database	https://doi.org/10.1038/srep08018	Phyllostachys	Simple Sequence Repeat/Microsatellite
BanSatDB (Banana Satellite Database)	https://doi.org/10.1016/j.cj.2018.01.005	Musa	Simple Sequence Repeat/Microsatellite

Overview of tools for repeat analysis

Tool	DOI	Alternate URL	Keywords
2 piRNApred	https://doi.org/10.1080/15476286.2020.1734382		piRNA
AAARF (Assisted Automated Assembler of Repeat Families)	https://doi.org/10.1186/1471-2105-9-235		Homology, Alignment
AgIn	https://doi.org/10.1093/bioinformatics/btw360		PacBio, Methylation
AlbaTrADIS	https://doi.org/10.1371/journal.pcbi.1007980		Tr-Seq, Transposon Mutagenesis
Alien_Hunter	https://doi.org/10.1093/bioinformatics/btl369		Genomic Island, HMM
alu-detect	https://doi.org/10.1093/nar/gkt612		Alu, SINE, Genotype, Polymorphism, NGS/HTS, Paired-End
AluMine	https://doi.org/10.1101/588434		Alu, SINE, Genotype,

▼ <Any>

- All
- Animal
- Archaea
- Arthropod
- Bacteria
- Beta vulgaris
- Boechea
- Bombyx mori
- Brassica oleracea
- Brassica rapa
- Bubalis bubalis
- Cajanus cajan
- Carica papaya
- Cicer arietinum
- Cucumis melo
- Cyanobacteria
- Cynara cardunculus
- Diocleous Plant
- Drosophila
- Drosophila melanogaster
- Eukaryote
- Fish
- Fungi
- Glycine
- Gossypium
- Gossypium raimondii

▼ Keywords <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