

Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

TIGR Plant Transcript Assembly database

RRID:SCR_005470

Type: Tool

Proper Citation

TIGR Plant Transcript Assembly database (RRID:SCR_005470)

Resource Information

URL: <http://plantta.jcvi.org/>

Proper Citation: TIGR Plant Transcript Assembly database (RRID:SCR_005470)

Description: The TIGR database is a collection of plant transcript sequences. Transcript assemblies are searchable using BLAST and accession number. The construction of plant transcript assemblies (TAs) is similar to the TIGR gene indices. The sequences that are used to build the plant TAs are expressed transcripts collected from dbEST (ESTs) and the NCBI GenBank nucleotide database (full length and partial cDNAs). "Virtual" transcript sequences derived from whole genome annotation projects are not included. All plant species for which more than 1,000 ESTs or cDNA sequences are available are included in this project. TAs are clustered and assembled using the TGICL tool (Perteza et al., 2003), Megablast (Zhang et al., 2000) and the CAP3 assembler (Huang and Madan, 1999). TGICL is a wrapper script which invokes Megablast and CAP3. Sequences are initially clustered based on an all-against-all comparisons using Megablast. The initial clusters are assembled to generate consensus sequences using CAP3. Assembly criteria include a 50 bp minimum match, 95% minimum identity in the overlap region and 20 bp maximum unmatched overhangs. Any EST/cDNA sequences that are not assembled into TAs are included as singletons. All singletons retain their GenBank accession numbers as identifiers. Plant TA identifiers are of the form TAnumber_taxonID, where number is a unique numerical identifier of the transcript assembly and taxonID represents the NCBI taxon id. In order to provide annotation for the TAs, each TA/singleton was aligned to the UniProt Uniref database. For release 1 TAs, a masked version of the Uniref90 database was used. For release 2 and onwards, a masked version of the UniRef100 database is used. Alignments were required to have at least 20% identity and 20% coverage. The annotation for the protein with the best alignment to each TA or singleton was used as the annotation for that sequence. Additionally, the relative orientation of each TA/singleton to the best matching protein sequence was used to determine the orientation of each TA/singleton. Some sequences did not have alignments to the protein database that met our quality criteria, and those sequences have neither annotation nor orientation assignments. The release number for the plant TAs refers to the release version for a particular species. For the initial build, all TA sets are of version 1. Subsequent TA

updates for new releases will be carried out when the percentage increase of the EST and cDNA counts exceeds 10% of the previous release and when the increase contains more than 1,000 new sequences. New releases will also include additional plant species with more than 1,000 EST or cDNA sequences that have become publicly available.

Synonyms: TIGR

Resource Type: database, data or information resource

Keywords: FASEB list

Resource Name: TIGR Plant Transcript Assembly database

Resource ID: SCR_005470

Alternate IDs: nif-0000-03559

Record Creation Time: 20220129T080230+0000

Record Last Update: 20260725T191140+0000

Ratings and Alerts

No rating or validation information has been found for TIGR Plant Transcript Assembly database.

No alerts have been found for TIGR Plant Transcript Assembly database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 825 mentions in open access literature.

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

Faure G, et al. (2025) TIGR-Tas: A family of modular RNA-guided DNA-targeting systems in prokaryotes and their viruses. *Science* (New York, N.Y.), 388(6746), eadv9789.

Hosseini Pouya HS, et al. (2025) Decoding the CBL gene family in durum wheat: Insights into dual ABA signaling pathways and calcium-mediated drought tolerance. *The plant genome*, 18(3), e70062.

Zhang K, et al. (2025) Genome-wide identification of the TIFY gene family in *Helianthus annuus* and expression analysis in response to drought and salt stresses. *Scientific reports*, 15(1), 15138.

Fan G, et al. (2024) Generation of Two-Line Restorer Line with Low Chalkiness Using Knockout of Chalk5 through CRISPR/Cas9 Editing. *Biology*, 13(8).

- Wang C, et al. (2024) Data-Driven Engineering of Phages with Tunable Capsule Tropism for *Klebsiella pneumoniae*. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 11(33), e2309972.
- Luo X, et al. (2024) Curcumin improves atrial fibrillation susceptibility by regulating tsRNA expression in aging mouse atrium. *PeerJ*, 12, e17495.
- Degrelle SA, et al. (2024) Understanding bovine embryo elongation: a transcriptomic study of trophoblastic vesicles. *Frontiers in physiology*, 15, 1331098.
- Nye-Wood MG, et al. (2023) Low Gluten Beers Contain Variable Gluten and Immunogenic Epitope Content. *Foods* (Basel, Switzerland), 12(17).
- Singh BK, et al. (2023) Meta-Analysis of Microarray Data and Their Utility in Dissecting the Mapped QTLs for Heat Acclimation in Rice. *Plants* (Basel, Switzerland), 12(8).
- Zhao H, et al. (2023) Genome-wide analysis of the CML gene family and its response to melatonin in common bean (*Phaseolus vulgaris* L.). *Scientific reports*, 13(1), 1196.
- Del Campo EM, et al. (2023) Comparative Transcriptomic and Proteomic Analyses Provide New Insights into the Tolerance to Cyclic Dehydration in a Lichen Phycobiont. *Microbial ecology*, 86(3), 1725.
- Guo B, et al. (2023) Comprehensive Analysis of BR Receptor Expression under Hormone Treatment in the Rubber Tree (*Hevea brasiliensis* Muell. Arg.). *Plants* (Basel, Switzerland), 12(6).
- Dong C, et al. (2023) A Small Subunit of Geranylgeranyl Diphosphate Synthase Functions as an Active Regulator of Carotenoid Synthesis in *Nicotiana tabacum*. *International journal of molecular sciences*, 24(2).
- Tao J, et al. (2022) Genome-wide identification and characterization of the TIFY gene family in kiwifruit. *BMC genomics*, 23(1), 179.
- Godoy F, et al. (2021) The role of auxin during early berry development in grapevine as revealed by transcript profiling from pollination to fruit set. *Horticulture research*, 8(1), 140.
- Changwal C, et al. (2021) Regulation of Postharvest Tomato Fruit Ripening by Endogenous Salicylic Acid. *Frontiers in plant science*, 12, 663943.
- Milner DS, et al. (2021) A functional bacteria-derived restriction modification system in the mitochondrion of a heterotrophic protist. *PLoS biology*, 19(4), e3001126.
- Bourhim T, et al. (2021) Elucidation of Melanogenesis-Associated Signaling Pathways Regulated by Argan Press Cake in B16 Melanoma Cells. *Nutrients*, 13(8).
- Khatun K, et al. (2021) Genome-wide identification, genomic organization, and expression profiling of the CONSTANS-like (COL) gene family in petunia under multiple stresses. *BMC genomics*, 22(1), 727.
- Divya D, et al. (2021) RNA-Sequencing Reveals Differentially Expressed Rice Genes Functionally Associated with Defense against BPH and WBPH in RILs Derived from a Cross between RP2068 and TN1. *Rice* (New York, N.Y.), 14(1), 27.