

Resource Summary Report

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ShortStack

RRID:SCR_010834

Type: Tool

Proper Citation

ShortStack (RRID:SCR_010834)

Resource Information

URL: <http://sites.psu.edu/axtell/software/shortstack/>

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Description: A software tool developed to process and analyze small RNA-seq data with respect to a reference genome, and output a comprehensive and informative annotation of all discovered small RNA genes. ShortStack discovers small RNA "clusters" de novo, based on user-set thresholds, and annotates clusters with respect to small RNA size, orientation, and repetitiveness. ShortStack also discovers and annotates MIRNA genes, and other Hairpin-associated small RNA genes. In addition, ShortStack includes a robust method to detect genes producing small RNAs in a phased manner. It outputs a descriptive table of all results, useful genome browser tracks, a table describing the results of the hairpin / MIRNA analysis for each cluster, and detailed text-based alignments of all MIRNAs and hairpin-associated clusters. It can also be run in "count" mode, to quantify a set of input loci with genomic coordinates determined a priori by the user. ShortStack is a perl program. Besides perl, ShortStack also requires samtools and the RNALfold and RNAeval programs from the Vienna RNA Package to execute. When used to control the alignment of small RNA data to a reference genome, ShortStack also requires bowtie and bowtie-build. Finally, for optimal results, ShortStack uses a file of inverted repeats produced by the EMBOSS application einverted.

Synonyms: ShortStack : Comprehensive annotation and quantification of small RNA genes

Resource Type: software resource

Defining Citation: [PMID:24139974](#), [PMID:23610128](#)

Availability: Acknowledgement requested

Resource Name: ShortStack

Resource ID: SCR_010834

Alternate IDs: OMICS_00384

Old URLs: <http://axtell-lab-psu.weebly.com/shortstack.html>

Record Creation Time: 20220129T080301+0000

Record Last Update: 20260725T190703+0000

Ratings and Alerts

No rating or validation information has been found for ShortStack.

No alerts have been found for ShortStack.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 217 mentions in open access literature.

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

Quan C, et al. (2025) Interspecific hybridization in Brassica species leads to changes in agronomic traits through the regulation of gene expression by chromatin accessibility and DNA methylation. GigaScience, 14.

Wang H, et al. (2025) Ribosomes binding to TAS transcripts buffer ta-siRNA biogenesis in Arabidopsis thaliana. Frontiers in plant science, 16, 1561041.

Bélanger S, et al. (2025) DICER-LIKE 5 loss causes thermosensitive male sterility in durum wheat and reveals an AU-rich motif guiding 24-nt phasiRNA biogenesis. Proceedings of the National Academy of Sciences of the United States of America, 122(31), e2504349122.

Jouni R, et al. (2025) Distinct classes of 21- and 24-nt phasiRNAs suggests diverse mechanisms of biogenesis and function in rice anther development. The plant genome, 18(3), e70107.

Kolanchi P, et al. (2025) Genomic exploration of Bemisia tabaci microRNAs using predictive modeling and confirmation through experimental evidence. Scientific reports, 15(1), 34006.

Fang Y, et al. (2025) Epigenetic regulation modulates seasonal temperature-dependent growth of soybean in southern China. Plant biotechnology journal, 23(10), 4580.

Pal AK, et al. (2025) Loss of function of chromatin remodeler OsCLSY4 leads to RdDM-mediated mis-expression of endosperm-specific genes affecting grain qualities. PLoS genetics, 21(12), e1011956.

- Russell AC, et al. (2025) Secreted small RNAs of *Naegleria fowleri* are biomarkers for diagnosis of primary amoebic meningoencephalitis. *bioRxiv : the preprint server for biology*.
- Tavakol E, et al. (2025) Pleiotropic effects of barley BLADE-ON-PETIOLE gene *Uniculme4* on plant architecture and the jasmonic acid pathway. *Journal of experimental botany*, 76(8), 2177.
- Pérez-Arques C, et al. (2025) RNAi epimutations conferring antifungal drug resistance are inheritable. *Nature communications*, 16(1), 7293.
- Beltran-Sanz N, et al. (2025) Chromosome-level assembly of the 400-year-old Goethe's Palm (*Chamaerops humilis* L.). *Scientific data*, 12(1), 1542.
- Xian W, et al. (2025) TIPPO: A User-Friendly Tool for De Novo Assembly of Organellar Genomes with High-Fidelity Data. *Molecular biology and evolution*, 42(1).
- Ravet A, et al. (2025) Vesicular and non-vesicular extracellular small RNAs direct gene silencing in a plant-interacting bacterium. *Nature communications*, 16(1), 3533.
- Pérez-Lázaro S, et al. (2025) Dysregulated microRNAs in blood correlate with central nervous system neuropathology of prion disease. *Veterinary research*, 56(1), 132.
- Turek S, et al. (2025) Multi-omics integration of transcriptome, miRNA, and metabolome uncovers molecular mechanisms of male flower development in cucumber line B10 (*Cucumis sativus* L.). *Scientific reports*, 15(1), 45734.
- Miró-Pina C, et al. (2025) A histone methyltransferase-independent function of PRC2 controls small RNA dynamics during programmed DNA elimination in *Paramecium*. *Nucleic acids research*, 53(19).
- Cerda-Herrera JD, et al. (2025) Chromosome level assembly and annotation of *Cuscuta campestris* Yunck. ("field dodder"), a model parasitic plant. *G3 (Bethesda, Md.)*, 15(10).
- Elmayan T, et al. (2025) *Arabidopsis* SGS3 is recruited to chromatin by CHR11 to select RNA that initiate siRNA production. *Nature communications*, 16(1), 2978.
- Xue LJ, et al. (2025) Overexpression of plasma membrane SUT1 in poplar alters lateral sucrose partitioning in stem and promotes leaf necrosis. *Plant direct*, 9(3), e70023.
- Zhao H, et al. (2025) New insights into the salt-responsive regulation in eelgrass at transcriptional and post-transcriptional levels. *Frontiers in plant science*, 16, 1497064.