

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: 20260905T132648+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 235 mentions in open access literature.

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

Martinez-Ugalde I, et al. (2026) Comparative Transcriptomics Reveals an Extracellular Worm Argonaute as an Ancestral Regulator of LTR Retrotransposons. *Genome biology and evolution*, 18(5).

Hafner A, et al. (2026) Intragenic methylation repatterning is associated with alternative splicing and unique epigenetic phenotypes. *bioRxiv : the preprint server for biology*.

Neophytou K, et al. (2026) An Argonaute protein traffics from nematode to mouse and is a vaccine against parasitic nematodes. *EMBO reports*, 27(2), 311.

Quan C, et al. (2026) Genome-wide reprogramming of sRNA and lncRNA in the epigenetic regulation following interspecific hybridization in the Brassica species. *Molecular horticulture*, 6(1), 14.

Lang X, et al. (2026) FungiSNC: An integrated database for fungi small non-coding RNAs based on high-throughput sequencing. *Journal of advanced research*, 84, 187.

Lacroix M, et al. (2026) Cell-type-specific ablation of siRNAs by Arabidopsis RTL1 reveals a role of phloem companion cells in systemic post-transcriptional gene silencing. *Nucleic acids research*, 54(8).

Shin SY, et al. (2026) Genome-wide CG hypomethylation of the Arabidopsis ecotype Cvi linked to structural variation and RNAi at the VIM4-VIM2 locus. *Proceedings of the National Academy of Sciences of the United States of America*, 123(21), e2603682123.

Whitcomb SJ, et al. (2026) Post-Transcriptional Gene Regulation by MicroRNAs During Barley Malting. *Genes*, 17(6).

Jamnik K, et al. (2026) Limitations of Single Prediction Tools in miRNA Profiling of Grapevine Viral Coinfection. *Genes*, 17(2).

A Batista R, et al. (2026) Dominance modifiers at the Arabidopsis self-incompatibility locus retain proto-miRNA features and act through non-canonical pathways. *PLoS genetics*, 22(4), e1012127.

Wang L, et al. (2026) Effector gene silencing coordinated by histone methylation and small RNAs enhances host adaptation in a plant pathogen. *Nucleic acids research*, 54(1).

Vivek AT, et al. (2026) Integrative multi-omics analysis widens annotation and functional insights into long non-coding RNAs of Arabidopsis thaliana. *Biology direct*, 21(1), 14.

Dautt-Castro M, et al. (2026) Genome-wide analysis of conserved and novel miRNAs in mango mesocarp reveals early regulatory networks involved in postharvest heat stress response. *Scientific reports*, 16(1).

Zhang Y, et al. (2026) Telomere-to-telomere genome assembly and comprehensive mutation library facilitate bitter melon breeding and functional genomics research. *Plant communications*, 7(4), 101779.

Zhu J, et al. (2026) Long-distance transport of siRNAs with functional roles in pollen development. *Nature plants*, 12(2), 386.

Déctor MA, et al. (2026) An Exploratory Biomarker Study of First-Trimester Circulating miRNAs Associated with Later Gestational Diabetes Mellitus. *International journal of molecular sciences*, 27(4).

Rieger I, et al. (2026) Scavenger Cells Failure to Maintain Systemic RNA Homeostasis Causes Epigenetically Inherited Germline Tumors. *bioRxiv : the preprint server for biology*.

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.