Resource Summary Report

Generated by NIF on Apr 19, 2025

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 hairpinassociated 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

Funding:

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: 20250410T070024+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 192 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>NIF</u>.

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.

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).

Kakoulidou I, et al. (2024) Mapping parental DMRs predictive of local and distal methylome remodeling in epigenetic F1 hybrids. Life science alliance, 7(4).

Kesidou D, et al. (2024) Extracellular vesicles from differentiated stem cells contain novel proangiogenic miRNAs and induce angiogenic responses at low doses. Molecular therapy: the journal of the American Society of Gene Therapy, 32(1), 185.

Zhan J, et al. (2024) Premeiotic 24-nt phasiRNAs are present in the Zea genus and unique in biogenesis mechanism and molecular function. Proceedings of the National Academy of Sciences of the United States of America, 121(21), e2402285121.

Sun MS, et al. (2024) Regulatory microRNAs and phasiRNAs of paclitaxel biosynthesis in Taxus chinensis. Frontiers in plant science, 15, 1403060.

de Oliveira AC, et al. (2024) MicroRNA Transcriptomes Reveal Prevalence of Rare and Species-Specific Arm Switching Events During Zebrafish Ontogenesis. Evolutionary bioinformatics online, 20, 11769343241263230.

Edelbroek B, et al. (2024) Chromosome-level genome assembly and annotation of the social amoeba Dictyostelium firmibasis. Scientific data, 11(1), 678.

Pakdel MH, et al. (2024) Machine learning-aided microRNA discovery for olive oil quality. PloS one, 19(10), e0311569.

Díez-Sainz E, et al. (2024) MicroRNAs from edible plants reach the human gastrointestinal tract and may act as potential regulators of gene expression. Journal of physiology and biochemistry, 80(3), 655.

Chen S, et al. (2024) PBOX-sRNA-seq uncovers novel features of miRNA modification and identifies selected 5'-tRNA fragments bearing 2'-O-modification. Nucleic acids research, 52(14), e65.

?ermák V, et al. (2024) SPT6L, a newly discovered ancestral component of the plant RNA-directed DNA methylation pathway. Frontiers in plant science, 15, 1372880.

Felgines L, et al. (2024) CLSY docking to Pol IV requires a conserved domain critical for small RNA biogenesis and transposon silencing. Nature communications, 15(1), 10298.

Zhan J, et al. (2024) Premeiotic 24-nt phasiRNAs are present in the Zea genus and unique in biogenesis mechanism and molecular function. bioRxiv: the preprint server for biology.

Cortesi A, et al. (2024) Activation of endogenous retroviruses and induction of viral mimicry by MEK1/2 inhibition in pancreatic cancer. Science advances, 10(13), eadk5386.

Gravot A, et al. (2024) Two adjacent NLR genes conferring quantitative resistance to clubroot disease in Arabidopsis are regulated by a stably inherited epiallelic variation. Plant communications, 5(5), 100824.

Edelbroek B, et al. (2024) Evolution of microRNAs in Amoebozoa and implications for the origin of multicellularity. Nucleic acids research, 52(6), 3121.

Gualdrini F, et al. (2024) An integrative epigenome-based strategy for unbiased functional profiling of clinical kinase inhibitors. Molecular systems biology, 20(6), 626.

Vega JM, et al. (2024) Chromosome-scale genome assembly and annotation of Paspalum

notatum Flüggé var. saurae. Scientific data, 11(1), 891.

Kumar D, et al. (2024) RiceMetaSys: Drought-miR, a one-stop solution for drought responsive miRNAs-mRNA module in rice. Database : the journal of biological databases and curation, 2024.