Resource Summary Report

Generated by RRID on Apr 29, 2025

RobiNA

RRID:SCR_011908
Type: Tool

Proper Citation

RobiNA (RRID:SCR_011908)

Resource Information

URL: http://mapman.gabipd.org/web/guest/robin

Proper Citation: RobiNA (RRID:SCR_011908)

Description: Software package for RNA-Seq-based transcriptomics. Used to analyse Illumina/Solexa-based RNA-Seq data, Affymetrix data and generic tabular two color or single channel array data. Offers variety of quality control methods that can be used to gain overview of experimental data technical quality and structure.

Abbreviations: RobiNA

Resource Type: software resource

Defining Citation: PMID:22684630

Keywords: analyse Illumina/Solexa-based RNA-Seq data, data quality control,

Funding:

Resource Name: RobiNA

Resource ID: SCR_011908

Alternate IDs: OMICS_01411

License: GNU GPL v3

Record Creation Time: 20220129T080307+0000

Record Last Update: 20250420T014602+0000

Ratings and Alerts

No rating or validation information has been found for RobiNA.

No alerts have been found for RobiNA.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 19 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID.

Pignocchi C, et al. (2021) Restriction of cytosolic sucrose hydrolysis profoundly alters development, metabolism, and gene expression in Arabidopsis roots. Journal of experimental botany, 72(5), 1850.

Afzal M, et al. (2020) Legume genomics and transcriptomics: From classic breeding to modern technologies. Saudi journal of biological sciences, 27(1), 543.

Diretto G, et al. (2020) Manipulation of ?-carotene levels in tomato fruits results in increased ABA content and extended shelf life. Plant biotechnology journal, 18(5), 1185.

Kim JH, et al. (2019) Effect of growth rate on transcriptomic responses to immune stimulation in wild-type, domesticated, and GH-transgenic coho salmon. BMC genomics, 20(1), 1024.

Fares MA, et al. (2017) Genome Mutational and Transcriptional Hotspots Are Traps for Duplicated Genes and Sources of Adaptations. Genome biology and evolution, 9(5), 1229.

de Oliveira LS, et al. (2017) Short- and long-term changes in sugarbeet (Beta vulgaris L.) gene expression due to postharvest jasmonic acid treatment - Data. Data in brief, 11, 165.

Mattenberger F, et al. (2017) The Phenotypic Plasticity of Duplicated Genes in Saccharomyces cerevisiae and the Origin of Adaptations. G3 (Bethesda, Md.), 7(1), 63.

Mattenberger F, et al. (2017) Expression properties exhibit correlated patterns with the fate of duplicated genes, their divergence, and transcriptional plasticity in Saccharomycotina. DNA research : an international journal for rapid publication of reports on genes and genomes, 24(6), 559.

Park CJ, et al. (2017) Overexpression of Rice Auxilin-Like Protein, XB21, Induces Necrotic Lesions, up-Regulates Endocytosis-Related Genes, and Confers Enhanced Resistance to Xanthomonas oryzae pv. oryzae. Rice (New York, N.Y.), 10(1), 27.

Shah M, et al. (2017) HOXC8 regulates self-renewal, differentiation and transformation of breast cancer stem cells. Molecular cancer, 16(1), 38.

Pagter M, et al. (2017) Rapid transcriptional and metabolic regulation of the deacclimation process in cold acclimated Arabidopsis thaliana. BMC genomics, 18(1), 731.

Parfitt GJ, et al. (2016) Transcriptome analysis of aging mouse meibomian glands. Molecular vision, 22, 518.

Graeff M, et al. (2016) MicroProtein-Mediated Recruitment of CONSTANS into a TOPLESS Trimeric Complex Represses Flowering in Arabidopsis. PLoS genetics, 12(3), e1005959.

Villarino A, et al. (2016) Signal transducer and activator of transcription 5 (STAT5) paralog dose governs T cell effector and regulatory functions. eLife, 5.

Jung H, et al. (2016) Optimizing Hybrid de Novo Transcriptome Assembly and Extending Genomic Resources for Giant Freshwater Prawns (Macrobrachium rosenbergii): The Identification of Genes and Markers Associated with Reproduction. International journal of molecular sciences, 17(5).

Foster AJ, et al. (2015) Transcriptome Analysis of Poplar during Leaf Spot Infection with Sphaerulina spp. PloS one, 10(9), e0138162.

Papadimou E, et al. (2015) Direct reprogramming of human bone marrow stromal cells into functional renal cells using cell-free extracts. Stem cell reports, 4(4), 685.

Ocaña S, et al. (2015) Large-Scale Transcriptome Analysis in Faba Bean (Vicia faba L.) under Ascochyta fabae Infection. PloS one, 10(8), e0135143.

Debat HJ, et al. (2014) Exploring the genes of yerba mate (Ilex paraguariensis A. St.-Hil.) by NGS and de novo transcriptome assembly. PloS one, 9(10), e109835.