Resource Summary Report

Generated by RRID on Apr 29, 2025

ERANGE

RRID:SCR_005240
Type: Tool

Proper Citation

ERANGE (RRID:SCR_005240)

Resource Information

URL: http://woldlab.caltech.edu/rnaseq

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Description: Software for Mapping and Quantifying Mammalian Transcriptomes by RNA-Seq. Its functions are to (i) assign reads that map uniquely in the genome to their site of origin and, for reads that match equally well to several sites ("multireads"), assign them to their most likely site(s) of origin; (ii) detect splice-crossing reads and assign them to their gene of origin; (iii) organize reads that cluster together, but do not map to an already known exon, into candidate exons or parts of exons; and (iv) calculate the prevalence of transcripts from each known or newly proposed RNA, based on normalized counts of unique reads, spliced reads and multireads. The new candidate RNA regions produced can be thought of as ESTs, and, like ESTs, some are provisionally appended to existing gene models if they meet several additional criteria. Remaining unassigned candidate transcribed regions (labeled RNAFAR features) can then be used in conjunction with other confirming data to develop new or revised gene models.

Abbreviations: ERANGE

Synonyms: Enhanced Read Analysis of Gene Expression

Resource Type: software resource

Defining Citation: PMID:18516045

Keywords: transcriptome, rna-seq, bio.tools

Funding:

Resource Name: ERANGE

Resource ID: SCR_005240

Alternate IDs: OMICS_01274, biotools:erange

Alternate URLs: https://bio.tools/erange

Record Creation Time: 20220129T080229+0000

Record Last Update: 20250420T014246+0000

Ratings and Alerts

No rating or validation information has been found for ERANGE.

No alerts have been found for ERANGE.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 30 mentions in open access literature.

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

Kasahara Y, et al. (2021) TMC4 is a novel chloride channel involved in high-concentration salt taste sensation. The journal of physiological sciences : JPS, 71(1), 23.

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

Zhao N, et al. (2020) Systematic Analysis of Differential H3K27me3 and H3K4me3 Deposition in Callus and Seedling Reveals the Epigenetic Regulatory Mechanisms Involved in Callus Formation in Rice. Frontiers in genetics, 11, 766.

Ben Zouari Y, et al. (2019) ChiCMaxima: a robust and simple pipeline for detection and visualization of chromatin looping in Capture Hi-C. Genome biology, 20(1), 102.

Yan H, et al. (2019) Chromatin State-Based Analysis of Epigenetic H3K4me3 Marks of Arabidopsis in Response to Dark Stress. Frontiers in genetics, 10, 306.

Liu Y, et al. (2018) PCSD: a plant chromatin state database. Nucleic acids research, 46(D1), D1157.

Wei J, et al. (2018) ER-associated ubiquitin ligase HRD1 programs liver metabolism by targeting multiple metabolic enzymes. Nature communications, 9(1), 3659.

Ozawa R, et al. (2017) Intraspecific variation among Tetranychid mites for ability to detoxify and to induce plant defenses. Scientific reports, 7, 43200.

Vaughan CA, et al. (2017) Gain-of-function p53 activates multiple signaling pathways to induce oncogenicity in lung cancer cells. Molecular oncology, 11(6), 696.

Berná L, et al. (2017) Transcriptomic analysis reveals metabolic switches and surface remodeling as key processes for stage transition in Trypanosoma cruzi. PeerJ, 5, e3017.

Hasegawa T, et al. (2017) Transient inflammatory response mediated by interleukin-1? is required for proper regeneration in zebrafish fin fold. eLife, 6.

Hsueh YP, et al. (2017) Nematophagous fungus Arthrobotrys oligospora mimics olfactory cues of sex and food to lure its nematode prey. eLife, 6.

Zhang Y, et al. (2016) Transcriptome Analysis Highlights Defense and Signaling Pathways Mediated by Rice pi21 Gene with Partial Resistance to Magnaporthe oryzae. Frontiers in plant science, 7, 1834.

Li M, et al. (2016) Exploration of rice pistil responses during early post-pollination through a combined proteomic and transcriptomic analysis. Journal of proteomics, 131, 214.

Bai Y, et al. (2016) Read-Split-Run: an improved bioinformatics pipeline for identification of genome-wide non-canonical spliced regions using RNA-Seq data. BMC genomics, 17 Suppl 7(Suppl 7), 503.

Chen X, et al. (2016) Comparative RNA-sequencing profiling reveals novel Delta-class glutathione S-transferases relative genes expression patterns in Tribolium castaneum. Gene, 593(1), 13.

de Dieuleveult M, et al. (2016) Genome-wide nucleosome specificity and function of chromatin remodellers in ES cells. Nature, 530(7588), 113.

Wu Y, et al. (2015) Gene Expression Profiles in Rice Developing Ovules Provided Evidence for the Role of Sporophytic Tissue in Female Gametophyte Development. PloS one, 10(10), e0141613.

Davis RV, et al. (2015) Transcriptome analysis of post-hatch breast muscle in legacy and modern broiler chickens reveals enrichment of several regulators of myogenic growth. PloS one, 10(3), e0122525.

Wang J, et al. (2015) Transcriptomic profiling of the salt-stress response in the halophyte Halogeton glomeratus. BMC genomics, 16(1), 169.