Resource Summary Report

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SeqBuster

RRID:SCR_009616
Type: Tool

Proper Citation

SeqBuster (RRID:SCR_009616)

Resource Information

URL: https://github.com/lpantano/seqbuster

Proper Citation: SeqBuster (RRID:SCR_009616)

Description: Software tool for processing and analysis of small RNAs datasets.Reveals ubiquitous miRNA modifications in human embryonic cells.

Resource Type: data analysis software, software application, software resource, data processing software

Defining Citation: PMID:20008100

Keywords: small RNAs datasets, ubiquitous miRNA modifications, human embryonic cells, bio.tools

Funding: Spanish Ministry of Health ;
CIBERESP ;
Sixth Framework Programme of the European Commission ;
Spanish Ministry of Science and Innovation

Availability: Free, Available for download, Freely available

Resource Name: SeqBuster

Resource ID: SCR_009616

Alternate IDs: OMICS_00367, biotools:seqbuster

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

Record Creation Time: 20220129T080253+0000

Record Last Update: 20250412T055427+0000

Ratings and Alerts

No rating or validation information has been found for SeqBuster.

No alerts have been found for SeqBuster.

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 FDI Lab - SciCrunch.org.

Stawiski K, et al. (2024) Validation of miRNA signatures for ovarian cancer earlier detection in the pre-diagnosis setting using machine learning approaches. Frontiers in oncology, 14, 1389066.

Asghar S, et al. (2023) Epithelial senescence in idiopathic pulmonary fibrosis is propagated by small extracellular vesicles. Respiratory research, 24(1), 51.

Loganathan T, et al. (2023) Non-coding RNAs in human health and disease: potential function as biomarkers and therapeutic targets. Functional & integrative genomics, 23(1), 33.

Umu SU, et al. (2022) Serum RNAs can predict lung cancer up to 10 years prior to diagnosis. eLife, 11.

Smith MD, et al. (2021) Large-scale transcriptome-wide profiling of microRNAs in human placenta and maternal plasma at early to mid gestation. RNA biology, 18(sup1), 507.

Espeso-Gil S, et al. (2021) Environmental Enrichment Induces Epigenomic and Genome Organization Changes Relevant for Cognition. Frontiers in molecular neuroscience, 14, 664912.

Bencurova P, et al. (2021) Dynamic miRNA changes during the process of epileptogenesis in an infantile and adult-onset model. Scientific reports, 11(1), 9649.

Giassa IC, et al. (2021) Bioinformatics and Machine Learning Approaches to Understand the Regulation of Mobile Genetic Elements. Biology, 10(9).

Solé C, et al. (2020) The Urinary Transcriptome as a Source of Biomarkers for Prostate Cancer. Cancers, 12(2).

Burton J, et al. (2020) Serum RNA Profiling in the 10-Years Period Prior to Diagnosis of Testicular Germ Cell Tumor. Frontiers in oncology, 10, 574977.

Baloun J, et al. (2020) Epilepsy miRNA Profile Depends on the Age of Onset in Humans and Rats. Frontiers in neuroscience, 14, 924.

Umu SU, et al. (2020) A 10-year prediagnostic follow-up study shows that serum RNA signals are highly dynamic in lung carcinogenesis. Molecular oncology, 14(2), 235.

Shukla V, et al. (2019) Enumeration of deregulated miRNAs in liquid and tissue biopsies of cervical cancer. Gynecologic oncology, 155(1), 135.

Solé C, et al. (2019) The Circulating Transcriptome as a Source of Biomarkers for Melanoma. Cancers, 11(1).

Brovkina O, et al. (2019) Role of MicroRNAs in the Regulation of Subcutaneous White Adipose Tissue in Individuals With Obesity and Without Type 2 Diabetes. Frontiers in endocrinology, 10, 840.

Cornell L, et al. (2019) MicroRNA-Mediated Suppression of the TGF-? Pathway Confers Transmissible and Reversible CDK4/6 Inhibitor Resistance. Cell reports, 26(10), 2667.

Pallarès-Albanell J, et al. (2019) A High-Throughput Screening Identifies MicroRNA Inhibitors That Influence Neuronal Maintenance and/or Response to Oxidative Stress. Molecular therapy. Nucleic acids, 17, 374.

Trontti K, et al. (2018) Strong conservation of inbred mouse strain microRNA loci but broad variation in brain microRNAs due to RNA editing and isomiR expression. RNA (New York, N.Y.), 24(5), 643.

Kang W, et al. (2018) miRTrace reveals the organismal origins of microRNA sequencing data. Genome biology, 19(1), 213.

Umu SU, et al. (2018) A comprehensive profile of circulating RNAs in human serum. RNA biology, 15(2), 242.