

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 processing software, data analysis software, software application, software resource

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: 20260801T190410+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 [RRID](#).

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.

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.

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

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.

Inukai S, et al. (2018) A microRNA feedback loop regulates global microRNA abundance during aging. *RNA (New York, N.Y.)*, 24(2), 159.