Resource Summary Report

Generated by Kravitz on Sep 10, 2026

RUbioSeq

RRID:SCR_002508
Type: Tool

Proper Citation

RUbioSeq (RRID:SCR_002508)

Resource Information

URL: http://rubioseq.sourceforge.net/

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Description: Stand-alone and multiplatform application for the integrated analysis of NGS data. It implements pipelines for the analysis of single nucleotide and copy-number variation and bisulfite-seq and ChIP-seq experiments.

Synonyms: RUbioSeq+

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

Defining Citation: PMID:23630175

Keywords: resequencing analysis, exome variant detection, pipeline, bio.tools

Funding: BLUEPRINT Consortium FP7/2007-2013 282510;
Spanish Ministry of Economy and Competitiveness BIO2007-666855

Availability: Free, Available for download

Resource Name: RUbioSeq

Resource ID: SCR_002508

Alternate IDs: biotools:rubioseq, OMICS_00072

Alternate URLs: https://sourceforge.net/projects/rubioseq/files/, https://bio.tools/rubioseq

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Ratings and Alerts

No rating or validation information has been found for RUbioSeq.

No alerts have been found for RUbioSeq.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 12 mentions in open access literature.

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

Jodkowska K, et al. (2022) 3D chromatin connectivity underlies replication origin efficiency in mouse embryonic stem cells. Nucleic acids research, 50(21), 12149.

Richart L, et al. (2021) STAG2 loss-of-function affects short-range genomic contacts and modulates the basal-luminal transcriptional program of bladder cancer cells. Nucleic acids research, 49(19), 11005.

Monteagudo M, et al. (2021) Analysis of Telomere Maintenance Related Genes Reveals NOP10 as a New Metastatic-Risk Marker in Pheochromocytoma/Paraganglioma. Cancers, 13(19).

Marión RM, et al. (2019) TERRA regulate the transcriptional landscape of pluripotent cells through TRF1-dependent recruitment of PRC2. eLife, 8.

de Matos MR, et al. (2019) A Systematic Pan-Cancer Analysis of Genetic Heterogeneity Reveals Associations with Epigenetic Modifiers. Cancers, 11(3).

Fernández-Navarro P, et al. (2019) The use of PanDrugs to prioritize anticancer drug treatments in a case of T-ALL based on individual genomic data. BMC cancer, 19(1), 1005.

Zagorac I, et al. (2018) In vivo phosphoproteomics reveals kinase activity profiles that predict treatment outcome in triple-negative breast cancer. Nature communications, 9(1), 3501.

Mondejar R, et al. (2017) Molecular basis of targeted therapy in T/NK-cell lymphoma/leukemia: A comprehensive genomic and immunohistochemical analysis of a panel of 33 cell lines. PloS one, 12(5), e0177524.

Abascal F, et al. (2016) Extreme genomic erosion after recurrent demographic bottlenecks in the highly endangered Iberian lynx. Genome biology, 17(1), 251.

Calvete O, et al. (2015) A mutation in the POT1 gene is responsible for cardiac angiosarcoma in TP53-negative Li-Fraumeni-like families. Nature communications, 6,

8383.

Cuadrado A, et al. (2015) The contribution of cohesin-SA1 to gene expression and chromatin architecture in two murine tissues. Nucleic acids research, 43(6), 3056.

Sánchez-Guiu I, et al. (2014) Functional and molecular characterization of inherited platelet disorders in the Iberian Peninsula: results from a collaborative study. Orphanet journal of rare diseases, 9, 213.