

Resource Summary Report

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[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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Record Last Update: 20260829T182115+0000

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 [NIF](#) .

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.