Resource Summary Report

Generated by dkNET on Apr 24, 2025

RIPSeeker

RRID:SCR_006810
Type: Tool

Proper Citation

RIPSeeker (RRID:SCR_006810)

Resource Information

URL: http://www.bioconductor.org/packages/2.12/bioc/html/RIPSeeker.html

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Description: A statistical software package for identifying protein-associated transcripts from RIP-seq experiments. Infer and discriminate RIP peaks from RIP-seq alignments using two-state HMM with negative binomial emission probability. While RIPSeeker is specifically tailored for RIP-seq data analysis, it also provides a suite of bioinformatics tools integrated within this self-contained software package comprehensively addressing issues ranging from post-alignments processing to visualization and annotation.

Abbreviations: RIPSeeker

Synonyms: RIPSeeker: a statistical package for identifying protein-associated transcripts from RIP-seq experiments

Resource Type: software resource

Keywords: rip-seq

Funding:

Availability: GNU General Public License, v2

Resource Name: RIPSeeker

Resource ID: SCR_006810

Alternate IDs: OMICS_00569

Record Creation Time: 20220129T080238+0000

Record Last Update: 20250420T014347+0000

Ratings and Alerts

No rating or validation information has been found for RIPSeeker.

No alerts have been found for RIPSeeker.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Liu P, et al. (2023) Noncanonical contribution of microglial transcription factor NR4A1 to post-stroke recovery through TNF mRNA destabilization. PLoS biology, 21(7), e3002199.

Li S, et al. (2023) The Role of PRRC2B in Cerebral Vascular Remodeling Under Acute Hypoxia in Mice. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 10(25), e2300892.

Du Z, et al. (2021) Chromatin lncRNA Platr10 controls stem cell pluripotency by coordinating an intrachromosomal regulatory network. Genome biology, 22(1), 233.

Wang S, et al. (2021) Splicing factor USP39 promotes ovarian cancer malignancy through maintaining efficient splicing of oncogenic HMGA2. Cell death & disease, 12(4), 294.

Yu L, et al. (2020) MTR4 drives liver tumorigenesis by promoting cancer metabolic switch through alternative splicing. Nature communications, 11(1), 708.

Grossi E, et al. (2020) A lncRNA-SWI/SNF complex crosstalk controls transcriptional activation at specific promoter regions. Nature communications, 11(1), 936.

Boudreault S, et al. (2019) The Epstein-Barr virus EBNA1 protein modulates the alternative splicing of cellular genes. Virology journal, 16(1), 29.

Skariah G, et al. (2017) Mov10 suppresses retroelements and regulates neuronal development and function in the developing brain. BMC biology, 15(1), 54.