Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 8, 2025

RINS

RRID:SCR_003652
Type: Tool

Proper Citation

RINS (RRID:SCR_003652)

Resource Information

URL: http://khavarilab.stanford.edu/resources.html

Proper Citation: RINS (RRID:SCR_003652)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on January 6, 2023. An intersection-based pathogen detection workflow that utilizes a user-provided custom reference genome set for identification of nonhuman sequences in deep sequencing datasets. This is a package recommended for advanced users only.

Abbreviations: RINS

Resource Type: software resource

Defining Citation: PMID:22377895

Keywords: virus, rna-seq, dna-seq, viral integration, clipped-sequence, paired-end, reconstruction, fusion transcript, sequence, perl

Funding:

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: RINS

Resource ID: SCR_003652

Alternate IDs: OMICS_00223

Record Creation Time: 20220129T080220+0000

Record Last Update: 20250214T183009+0000

Ratings and Alerts

No rating or validation information has been found for RINS.

No alerts have been found for RINS.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 26 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Dwivedi AK, et al. (2025) High-resolution multimodal profiling of human epileptic brain activity via explanted depth electrodes. JCI insight, 10(1).

Li GX, et al. (2024) Comprehensive proteogenomic characterization of rare kidney tumors. Cell reports. Medicine, 5(5), 101547.

Dryzer M, et al. (2024) Neural mechanisms underlying the effects of cognitive fatigue on physical effort-based choice. bioRxiv : the preprint server for biology.

Riva F, et al. (2023) Age-related differences in interference control in the context of a finger-lifting task: an fMRI study. Social cognitive and affective neuroscience, 18(1).

Coelho R, et al. (2022) Computer Simulations of Silicide-Tetrahedrite Thermoelectric Generators. Micromachines, 13(11).

Naik P, et al. (2022) Methicillin resistance in Staphylococcus aureus modulates the transcriptome and disease pathology in a murine model of endophthalmitis. Experimental eye research, 218, 109016.

Gadd S, et al. (2022) Genetic changes associated with relapse in favorable histology Wilms tumor: A Children's Oncology Group AREN03B2 study. Cell reports. Medicine, 3(6), 100644.

Guennewig B, et al. (2021) Defining early changes in Alzheimer's disease from RNA sequencing of brain regions differentially affected by pathology. Scientific reports, 11(1), 4865.

Herrera-Uribe J, et al. (2021) Reference Transcriptomes of Porcine Peripheral Immune Cells Created Through Bulk and Single-Cell RNA Sequencing. Frontiers in genetics, 12, 689406.

Wozniak EAL, et al. (2021) Cholecystokinin 1 receptor activation restores normal mTORC1 signaling and is protective to Purkinje cells of SCA mice. Cell reports, 37(2), 109831.

Martín-Montañez E, et al. (2021) Insulin-like growth factor II prevents oxidative and neuronal damage in cellular and mice models of Parkinson's disease. Redox biology, 46, 102095.

Streefkerk N, et al. (2020) A detailed insight in the high risks of hospitalizations in long-term childhood cancer survivors-A Dutch LATER linkage study. PloS one, 15(5), e0232708.

Giannuzzi D, et al. (2020) A First NGS Investigation Suggests No Association Between Viruses and Canine Cancers. Frontiers in veterinary science, 7, 365.

Drake J, et al. (2020) Assessing the Role of Long Noncoding RNA in Nucleus Accumbens in Subjects With Alcohol Dependence. Alcoholism, clinical and experimental research, 44(12), 2468.

Vornholt E, et al. (2020) Network preservation reveals shared and unique biological processes associated with chronic alcohol abuse in NAc and PFC. PloS one, 15(12), e0243857.

Fraser VN, et al. (2020) Metabolomics analysis reveals both plant variety and choice of hormone treatment modulate vinca alkaloid production in Catharanthus roseus. Plant direct, 4(9), e00267.

Ethier SP, et al. (2020) Development and implementation of the SUM breast cancer cell line functional genomics knowledge base. NPJ breast cancer, 6, 30.

Xia Y, et al. (2019) Detecting virus integration sites based on multiple related sequencing data by VirTect. BMC medical genomics, 12(Suppl 1), 19.

Hendee KE, et al. (2018) PITX2 deficiency and associated human disease: insights from the zebrafish model. Human molecular genetics, 27(10), 1675.

Liang Y, et al. (2017) Frequency Specific Effects of ApoE ?4 Allele on Resting-State Networks in Nondemented Elders. BioMed research international, 2017, 9823501.