Resource Summary Report

Generated by NIF on May 20, 2025

MicroRazerS

RRID:SCR_013316
Type: Tool

Proper Citation

MicroRazerS (RRID:SCR_013316)

Resource Information

URL: http://www.seqan.de/projects/microrazers/

Proper Citation: MicroRazerS (RRID:SCR_013316)

Description: A software tool optimized for mapping short RNAs onto a reference genome.

Abbreviations: MicroRazerS

Resource Type: software resource

Defining Citation: PMID:19880369

Funding:

Resource Name: MicroRazerS

Resource ID: SCR_013316

Alternate IDs: OMICS_00371

Record Creation Time: 20220129T080315+0000

Record Last Update: 20250519T203804+0000

Ratings and Alerts

No rating or validation information has been found for MicroRazerS.

No alerts have been found for MicroRazerS.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 5 mentions in open access literature.

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

King SE, et al. (2025) Prenatal maternal stress in rats alters the epigenetic and transcriptomic landscape of the maternal-fetal interface across four generations. Communications biology, 8(1), 38.

Ambeskovic M, et al. (2020) Ancestral stress programs sex-specific biological aging trajectories and non-communicable disease risk. Aging, 12(4), 3828.

Ambeskovic M, et al. (2019) Ancestral Stress Alters Lifetime Mental Health Trajectories and Cortical Neuromorphology via Epigenetic Regulation. Scientific reports, 9(1), 6389.

Ziemann M, et al. (2016) Evaluation of microRNA alignment techniques. RNA (New York, N.Y.), 22(8), 1120.

Thangam M, et al. (2015) CRCDA--Comprehensive resources for cancer NGS data analysis. Database : the journal of biological databases and curation, 2015.