# **Resource Summary Report**

Generated by dkNET on Apr 30, 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:** 20250420T014640+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 dkNET.

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.