Resource Summary Report

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RazerS

RRID:SCR_006889
Type: Tool

Proper Citation

RazerS (RRID:SCR_006889)

Resource Information

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

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Description: A read mapping software program with adjustable sensitivity based on counting q-grams. RazerS 3 supports shared-memory parallelism, an additional seed-based filter with adjustable sensitivity, a much faster, banded version of the Myers? bit-vector algorithm for verification, memory saving measures and support for the SAM output format. This leads to a much improved performance for mapping reads, in particular long reads with many errors.

Abbreviations: RazerS

Resource Type: software resource

Defining Citation: PMID:22923295, PMID:19592482

Keywords: next-generation sequencing, c++, openmp, linux, mac os x, windows

Funding:

Availability: GNU General Public License

Resource Name: RazerS

Resource ID: SCR_006889

Alternate IDs: OMICS_00679

Record Creation Time: 20220129T080238+0000

Record Last Update: 20250214T183057+0000

Ratings and Alerts

No rating or validation information has been found for RazerS.

No alerts have been found for RazerS.

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 FDI Lab - SciCrunch.org.

Holm JS, et al. (2022) Neoantigen-specific CD8 T cell responses in the peripheral blood following PD-L1 blockade might predict therapy outcome in metastatic urothelial carcinoma. Nature communications, 13(1), 1935.

Yu Y, et al. (2022) Neoantigen-reactive T cells exhibit effective anti-tumor activity against colorectal cancer. Human vaccines & immunotherapeutics, 18(1), 1.

Zytnicki M, et al. (2021) Finding differentially expressed sRNA-Seq regions with srnadiff. PloS one, 16(8), e0256196.

Westcott PMK, et al. (2021) Low neoantigen expression and poor T-cell priming underlie early immune escape in colorectal cancer. Nature cancer, 2(10), 1071.

Fehlmann T, et al. (2019) The sncRNA Zoo: a repository for circulating small noncoding RNAs in animals. Nucleic acids research, 47(9), 4431.

Kavagutti VS, et al. (2019) Phage-centric ecological interactions in aquatic ecosystems revealed through ultra-deep metagenomics. Microbiome, 7(1), 135.

?enbabao?lu Y, et al. (2016) Tumor immune microenvironment characterization in clear cell renal cell carcinoma identifies prognostic and immunotherapeutically relevant messenger RNA signatures. Genome biology, 17(1), 231.

Kalscheuer VM, et al. (2015) Novel Missense Mutation A789V in IQSEC2 Underlies X-Linked Intellectual Disability in the MRX78 Family. Frontiers in molecular neuroscience, 8, 85.

Cheng H, et al. (2015) BitMapper: an efficient all-mapper based on bit-vector computing. BMC bioinformatics, 16, 192.

Szolek A, et al. (2014) OptiType: precision HLA typing from next-generation sequencing data. Bioinformatics (Oxford, England), 30(23), 3310.

Li SC, et al. (2011) Interrogation of rabbit miRNAs and their isomiRs. Genomics, 98(6), 453.

Summerer D, et al. (2010) Targeted high throughput sequencing of a cancer-related exome subset by specific sequence capture with a fully automated microarray platform. Genomics, 95(4), 241.