

Resource Summary Report

Generated by T1D on Jul 28, 2026

READSCAN

RRID:SCR_005204

Type: Tool

Proper Citation

READSCAN (RRID:SCR_005204)

Resource Information

URL: <http://cbrc.kaust.edu.sa/readscan/>

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Description: A highly scalable parallel software program to identify non-host sequences (of potential pathogen origin) and estimate their genome relative abundance in high-throughput sequence datasets.

Abbreviations: READSCAN

Resource Type: software resource

Defining Citation: [PMID:23193222](#)

Keywords: pathgen, genome, sequence, high-throughput sequence, align, read, host, microbe, virus, taxon, simulation, bio.tools

Resource Name: READSCAN

Resource ID: SCR_005204

Alternate IDs: OMICS_00222, biotools:readscan

Alternate URLs: <https://bio.tools/readscan>

Record Creation Time: 20220129T080228+0000

Record Last Update: 20260725T190603+0000

Ratings and Alerts

No rating or validation information has been found for READSCAN.

No alerts have been found for READSCAN.

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 [T1D](#) .

Reteng P, et al. (2021) A targeted approach with nanopore sequencing for the universal detection and identification of flaviviruses. Scientific reports, 11(1), 19031.

Yuan Z, et al. (2021) Presence of complete murine viral genome sequences in patient-derived xenografts. Nature communications, 12(1), 2031.

Yuan Z, et al. (2020) Virome assembly and annotation in brain tissue based on next-generation sequencing. Cancer medicine, 9(18), 6776.

Nooij S, et al. (2018) Overview of Virus Metagenomic Classification Methods and Their Biological Applications. Frontiers in microbiology, 9, 749.

Haglund F, et al. (2017) Inflammatory infiltrates in parathyroid tumors. European journal of endocrinology, 177(6), 445.