Resource Summary Report

Generated by dkNET on Aug 25, 2026

SpeedSeq

RRID:SCR_000469
Type: Tool

Proper Citation

SpeedSeq (RRID:SCR_000469)

Resource Information

URL: https://github.com/cc2qe/speedseq

Proper Citation: SpeedSeq (RRID:SCR_000469)

Description: Software for a lightweight, flexible, and open source pipeline that identifies genomic variation (single nucleotide variants (SNVs), indels, and structural variants (SVs)).

Resource Type: software resource

Keywords: standalone software

Availability: Free, Available for download, Freely available

Resource Name: SpeedSeq

Resource ID: SCR_000469

Alternate IDs: OMICS_04673

Record Creation Time: 20220129T080201+0000

Record Last Update: 20260815T182145+0000

Ratings and Alerts

No rating or validation information has been found for SpeedSeq.

No alerts have been found for SpeedSeq.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Chihab LY, et al. (2025) Comparative performance analysis of neoepitope prediction algorithms in head and neck cancer. Frontiers in immunology, 16, 1494453.

Lee LH, et al. (2025) Defining Non-small Cell Lung Cancer Tumor Microenvironment Changes at Primary and Acquired Immune Checkpoint Inhibitor Resistance Using Clinical and Real-World Data. Cancer research communications, 5(6), 1049.

Carpenter MA, et al. (2023) Mutational impact of APOBEC3A and APOBEC3B in a human cell line and comparisons to breast cancer. PLoS genetics, 19(11), e1011043.

Smith SD, et al. (2017) Lightning-fast genome variant detection with GROM. GigaScience, 6(10), 1.

DeBoever C, et al. (2017) Large-Scale Profiling Reveals the Influence of Genetic Variation on Gene Expression in Human Induced Pluripotent Stem Cells. Cell stem cell, 20(4), 533.

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

Chiang C, et al. (2015) SpeedSeq: ultra-fast personal genome analysis and interpretation. Nature methods, 12(10), 966.