

Resource Summary Report

Generated by [Kravitz](#) on Sep 16, 2026

ScanNeo

RRID:SCR_019253

Type: Tool

Proper Citation

ScanNeo (RRID:SCR_019253)

Resource Information

URL: <https://github.com/ylab-hi/ScanNeo>

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Description: Open software pipeline for analyzing RNA-seq to predict neoepitopes derived from small to large sized indels. Used for identifying indel derived neoantigens using RNA-Seq data.

Resource Type: data analysis software, data processing software, sequence analysis software, software application, software resource

Defining Citation: [PMID:30887025](#)

Keywords: RNA-Seq, neoepitopes, indel, indel derived neoantigen, RNA-Seq data, neoantigen identification

Availability: Free, Available for download, Freely available

Resource Name: ScanNeo

Resource ID: SCR_019253

License: NPOSL-3.0

Record Creation Time: 20220129T080344+0000

Record Last Update: 20260912T195911+0000

Ratings and Alerts

No rating or validation information has been found for ScanNeo.

No alerts have been found for ScanNeo.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

Listed below are recent publications. The full list is available at [Kravitz](#) .

Bulashevskaya A, et al. (2024) Artificial intelligence and neoantigens: paving the path for precision cancer immunotherapy. *Frontiers in immunology*, 15, 1394003.

Huang J, et al. (2024) Bioinformatics tools and resources for cancer and application. *Chinese medical journal*, 137(17), 2052.

Wang TY, et al. (2021) A pan-cancer transcriptome analysis of exon splicing identifies novel cancer driver genes and neoepitopes. *Molecular cell*, 81(10), 2246.

Wang TY, et al. (2021) Integrated protocol for exon and exon-derived neoantigen identification using human RNA-seq data with ScanExon and ScanNeo. *STAR protocols*, 2(3), 100788.