Resource Summary Report

Generated by NIF on Sep 8, 2026

NGSCheckMate

RRID:SCR_022994
Type: Tool

Proper Citation

NGSCheckMate (RRID:SCR_022994)

Resource Information

URL: https://github.com/parklab/NGSCheckMate

Proper Citation: NGSCheckMate (RRID:SCR_022994)

Description: Software package for validating sample identity in next generation sequencing studies within and across data types. Used for identifying next generation sequencing data files from the same individual. Used for checking sample matching for NGS data.

Resource Type: software resource, software toolkit

Defining Citation: PMID:28369524

Keywords: Next Generation sequencing data file, identifying next generation sequencing data files, next generation sequencing, same individual data files, checking sample matching, NGS data.

Funding: Harvard Medical School Eleanor and Miles Shore Fellowship ;
Korean Health Technology ;
NEI R01EY024230;
NIA K01AG051791;
NIMH 1P50MH106933;
NIMH 1U01MH106883;
Randolph Hearst Fund

Availability: Free, Available for download, Freely available

Resource Name: NGSCheckMate

Resource ID: SCR_022994

License: MIT license

Record Creation Time: 20221124T050201+0000

Record Last Update: 20260905T133312+0000

Ratings and Alerts

No rating or validation information has been found for NGSCheckMate.

No alerts have been found for NGSCheckMate.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Valentín López JC, et al. (2026) Evolution of AR and Non-AR Alterations in ctDNA of Patients with Metastatic Prostate Cancer Treated in the Phase III Alliance A031201 Trial. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(12), 2413.

Patte C, et al. (2025) Comprehensive molecular portrait reveals genetic diversity and distinct molecular subtypes of small intestinal neuroendocrine tumors. Nature communications, 16(1), 2197.

Xu Z, et al. (2025) PISAD: reference-free intraspecies sample anomalies detection tool based on k-mer counting. GigaScience, 14.

Parida P, et al. (2025) Precise identification of viral-host integration events in HPV-positive cervical cancers by targeted long-read sequencing. Tumour virus research, 20, 200325.

Alcala N, et al. (2024) Multi-omic dataset of patient-derived tumor organoids of neuroendocrine neoplasms. GigaScience, 13.

Di Genova A, et al. (2022) A molecular phenotypic map of malignant pleural mesothelioma. GigaScience, 12.

Grant RA, et al. (2021) Circuits between infected macrophages and T cells in SARS-CoV-2 pneumonia. Nature, 590(7847), 635.

Amin SB, et al. (2020) Comparative Molecular Life History of Spontaneous Canine and Human Gliomas. Cancer cell, 37(2), 243.