Resource Summary Report

Generated by RRID on Apr 29, 2025

MSIsensor

RRID:SCR_006418
Type: Tool

Proper Citation

MSIsensor (RRID:SCR_006418)

Resource Information

URL: https://github.com/ding-lab/msisensor

Proper Citation: MSIsensor (RRID:SCR_006418)

Description: A C++ software program for automatically detecting somatic and germline variants at microsatellite regions. It computes length distributions of microsatellites per site in paired tumor and normal sequence data, subsequently using these to statistically compare observed distributions in both samples.

Abbreviations: MSIsensor

Resource Type: software resource

Defining Citation: PMID:24371154

Keywords: c++, somatic variant, germline variant, microsatellite, bio.tools

Related Condition: Tumor, Normal

Funding:

Availability: Copyrighted, See LICENSE

Resource Name: MSIsensor

Resource ID: SCR_006418

Alternate IDs: biotools:msisensor, OMICS_02192

Alternate URLs: https://bio.tools/msisensor

Record Creation Time: 20220129T080236+0000

Record Last Update: 20250420T014326+0000

Ratings and Alerts

No rating or validation information has been found for MSIsensor.

No alerts have been found for MSIsensor.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 138 mentions in open access literature.

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

Rekhtman N, et al. (2025) Chromothripsis-Mediated Small Cell Lung Carcinoma. Cancer discovery, 15(1), 83.

Unger M, et al. (2025) Deep Learning for Biomarker Discovery in Cancer Genomes. bioRxiv : the preprint server for biology.

Zhou B, et al. (2025) A novel algorithm for the detection of microsatellite instability in endometrial cancer using next?generation sequencing data. Oncology letters, 29(2), 86.

Egea-Rodriguez S, et al. (2025) RECQL4 affects MHC class II-mediated signalling and favours an immune-evasive signature that limits response to immune checkpoint inhibitor therapy in patients with malignant melanoma. Clinical and translational medicine, 15(1), e70094.

Ziegler J, et al. (2025) A deep multiple instance learning framework improves microsatellite instability detection from tumor next generation sequencing. Nature communications, 16(1), 136.

Mariella E, et al. (2024) Transcriptome-wide gene expression outlier analysis pinpoints therapeutic vulnerabilities in colorectal cancer. Molecular oncology, 18(6), 1460.

Friedman CF, et al. (2024) Nivolumab for mismatch-repair-deficient or hypermutated gynecologic cancers: a phase 2 trial with biomarker analyses. Nature medicine, 30(5), 1330.

Jonchère V, et al. (2024) Microsatellite instability at U2AF-binding polypyrimidic tract sites perturbs alternative splicing during colorectal cancer initiation. Genome biology, 25(1), 210.

Seligson ND, et al. (2024) A multicenter, randomized, non-comparative, phase II study of nivolumab ± ipilimumab for patients with metastatic sarcoma (Alliance A091401): expansion cohorts and correlative analyses. Journal for immunotherapy of cancer, 12(9).

Haugh AM, et al. (2024) Targeted DNA Sequencing of Cutaneous Melanoma Identifies Prognostic and Predictive Alterations. Cancers, 16(7).

Kayhanian H, et al. (2024) Homopolymer switches mediate adaptive mutability in mismatch repair-deficient colorectal cancer. Nature genetics, 56(7), 1420.

Ding W, et al. (2024) Unraveling EGFR-TKI resistance in lung cancer with high PD-L1 or TMB in EGFR-sensitive mutations. Respiratory research, 25(1), 40.

Zhu YC, et al. (2024) Camrelizumab plus apatinib for previously treated advanced adrenocortical carcinoma: a single-arm phase 2 trial. Nature communications, 15(1), 10371.

Xu S, et al. (2024) Whole-exome sequencing reveals novel genomic signatures and potential therapeutic targets during the progression of rectal neuroendocrine neoplasm. Cell death & disease, 15(11), 833.

Kim R, et al. (2024) Clinical application of whole-genome sequencing of solid tumors for precision oncology. Experimental & molecular medicine, 56(8), 1856.

Liu B, et al. (2024) Immune landscape and heterogeneity of cervical squamous cell carcinoma and adenocarcinoma. Aging, 16(1), 568.

Petralia F, et al. (2024) Pan-cancer proteogenomics characterization of tumor immunity. Cell, 187(5), 1255.

Guerrini-Rousseau L, et al. (2024) Neurofibromatosis type 1 mosaicism in patients with constitutional mismatch repair deficiency. Journal of medical genetics, 61(2), 158.

Gordhandas S, et al. (2024) Molecular profiling of primary endometrioid endometrial cancer and matched lung metastases: CTNNB1 mutation as a potential driver. Gynecologic oncology reports, 53, 101391.

Li RQ, et al. (2024) Genomic characterization reveals distinct mutational landscapes and therapeutic implications between different molecular subtypes of triple-negative breast cancer. Scientific reports, 14(1), 12386.