

Resource Summary Report

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MSIsensor

RRID:SCR_006418

Type: Tool

Proper Citation

MSIsensor (RRID:SCR_006418)

Resource Information

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

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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

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: 20260801T190308+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 156 mentions in open access literature.

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

Kim K, et al. (2025) Molecular Heterogeneity and Immune Infiltration Drive Clinical Outcomes in Upper Tract Urothelial Carcinoma. *European urology*, 87(3), 342.

Domenico D, et al. (2025) Enabling whole genome sequencing analysis from FFPE specimens in clinical oncology. *Nature communications*, 16(1), 10649.

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*.

Yazaki S, et al. (2025) AlphaMissense for Identifying Pathogenic Missense Mutations in DNA Damage Repair Genes in Cancer. *JCO precision oncology*, 9, e2400908.

Kyung SM, et al. (2025) Delineating molecular mechanisms on the acquisition of in vitro-adapted colistin-resistant *Klebsiella pneumoniae* by transcriptomic analysis. *Microbiology spectrum*, 13(12), e0342824.

van Opijnen MP, et al. (2025) Whole genome sequencing-based analysis of genetic predisposition to adult glioblastoma. *NPJ genomic medicine*, 10(1), 70.

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.

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.

Li J, et al. (2025) The Expression Characteristics of the RBFOX1 Gene in Colorectal Cancer. *Technology in cancer research & treatment*, 24, 15330338251333695.

Huo ??? X, et al. (2025) Genome-wide Genetic Mutations Accumulated in Pigs Genome-edited for Xenotransplantation and Their Filial Generation. *Genomics, proteomics & bioinformatics*, 23(4).

Joly F, et al. (2025) Maintenance olaparib after platinum-based chemotherapy for advanced/metastatic endometrial cancer: GINECO randomized phase IIb UTOLA trial. *Nature communications*, 16(1), 7950.

Yoo SK, et al. (2025) Prediction of checkpoint inhibitor immunotherapy efficacy for cancer using routine blood tests and clinical data. *Nature medicine*, 31(3), 869.

Omer DM, et al. (2025) Clinical and Genomic Characterization of Secondary Rectal Cancer After Radiotherapy for Prostate Cancer. *JAMA network open*, 8(3), e251039.

Brooksbank K, et al. (2025) The DNA mismatch repair protein, MSH6 is a novel regulator of PD-L1 expression. *Neoplasia (New York, N.Y.)*, 67, 101207.

Hwang S, et al. (2025) Identifying predictive markers of head and neck squamous cell carcinoma in an umbrella trial (KCSG HN 15-16 TRIUMPH trial). *ESMO open*, 10(10), 105772.

Höppener DJ, et al. (2025) The colorectal liver metastasis growth pattern phenotype is not dependent on genotype. *British journal of cancer*, 133(7), 945.

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.

Varghese AM, et al. (2025) Clinicogenomic landscape of pancreatic adenocarcinoma identifies KRAS mutant dosage as prognostic of overall survival. *Nature medicine*, 31(2), 466.

Chikaishi Y, et al. (2025) Mutation Analysis of TMB-High Colorectal Cancer: Insights Into Molecular Pathways and Clinical Implications. *Cancer science*, 116(4), 1082.