

# Resource Summary Report

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## [maftools](#)

RRID:SCR\_024519

Type: Tool

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### Proper Citation

maftools (RRID:SCR\_024519)

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### Resource Information

**URL:** <https://github.com/PoisonAlien/Maftools>

**Proper Citation:** maftools (RRID:SCR\_024519)

**Description:** Software R package offers multitude of analysis and visualization modules that are commonly used in cancer genomic studies, including driver gene identification, pathway, signature, enrichment, and association analyses. Maftools requires somatic variants in Mutation Annotation Format (MAF) and is independent of larger alignment files.

**Resource Type:** software resource, software toolkit

**Defining Citation:** [PMID:30341162](#)

**Keywords:** MAF summarize, MAF analyze, MAF visualize, Mutation Annotation Format files, driver gene identification, pathway, signature, enrichment, association analyses, somatic variants in Mutation Annotation Format, MAF

**Availability:** Free, Available for download, Freely available

**Resource Name:** maftools

**Resource ID:** SCR\_024519

**Alternate URLs:** <https://bioconductor.org/packages/maftools/>

**License:** MIT license

**Record Creation Time:** 20231002T161337+0000

**Record Last Update:** 20260808T190341+0000

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### Ratings and Alerts

No rating or validation information has been found for maftools.

No alerts have been found for maftools.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 233 mentions in open access literature.

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

Brodsky AL, et al. (2026) Combination Therapy with Copanlisib and Niraparib in Patients with Recurrent Endometrial and Ovarian Cancer (COPANIRA): Efficacy, Toxicity, and Translational Insights. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(7), 1234.

Wang A, et al. (2026) Identification and validation of prognostic genes related to glycolysis and M2 macrophage in hepatocellular carcinoma: an integrated analysis of bulk RNA sequencing and single-cell RNA sequencing. *Frontiers in immunology*, 17, 1710411.

Hwang J, et al. (2026) Development of K-CORE: a web-based platform for integrated clinico-genomic analysis. *Life science alliance*, 9(8).

Zheng H, et al. (2026) Deciphering Angiogenic Drivers in Hepatocellular Carcinoma: From Prognostic Signature Construction to Genistein-Mediated Inhibition. *Journal of cellular and molecular medicine*, 30(10), e71203.

Bai Y, et al. (2026) Prognostic significance and immune landscape of anoikis-related genes in hepatocellular carcinoma: a multi-omics analysis of subtypes and cellular communication. *Clinical and experimental medicine*, 26(1), 122.

Kim D, et al. (2026) Molecular determinants of outcome to gemcitabine, cisplatin, and nab-paclitaxel in patients with advanced biliary tract cancer. *Clinical and molecular hepatology*, 32(2), 721.

Zaj?c AE, et al. (2026) Integrated Immune and Molecular Profiling Identifies Prognostic Subgroups and Therapeutic Targets in Chondrosarcoma. *International journal of molecular sciences*, 27(4).

Diao X, et al. (2026) Exploring and experimental validation of SLC7A11 and ferroptosis related prognostic genes in non-small cell lung cancer using bulk RNA sequencing and single-cell RNA sequencing. *Biology direct*, 21(1).

Yeh CM, et al. (2026) A New CA19-9 Cutoff Value Identifies Lewis Antigen Status and Refines Prognostic Stratification in PDAC. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 32(13), 2722.

Gárate-Calderón V, et al. (2026) Geographic and genetic diversity in gallbladder cancer mutation profiles: insights from a worldwide exome analysis. *EBioMedicine*, 128, 106305.

Kordowitzki P, et al. (2026) Deciphering the Pleiotropic Role of ARID1a and RIF1 in Endometrioid Ovarian Cancer. *Cells*, 15(11).

Shen P, et al. (2026) High RMI1 expression is associated with cancer cell progression and poor prognosis in prostate cancer. *Oncology reports*, 55(4).

Lee H, et al. (2026) Multimodal antigenic escape to GPRC5D-targeted T cell engagers in multiple myeloma. *Nature medicine*, 32(3), 964.

Cottu P, et al. (2026) Molecular and cellular composition changes after neoadjuvant letrozole and palbociclib in early luminal breast cancer. *Cell reports. Medicine*, 102544.

Xun Y, et al. (2026) Integrative analysis of a novel snoRNA-based prognostic signature in patients with breast cancer. *Frontiers in oncology*, 16, 1779697.

Zhang Q, et al. (2026) A novel mitochondrial-associated risk score reveals a potential link between pancreatic ductal adenocarcinoma and chemotherapy resistance as well as poor response to immunotherapy. *Discover oncology*, 17(1).

Frimer M, et al. (2026) Comprehensive Molecular Characterization of High-Grade Endometrial Cancer in an Ancestrally Diverse Cohort. *bioRxiv : the preprint server for biology*.

Siga H, et al. (2026) Resolving the Haplotype Complexity of Colorectal Cancer Genomes with Droplet Barcode Sequencing. *Life (Basel, Switzerland)*, 16(6).

Shi Y, et al. (2026) The role of DNAJC3 in enhancing glioma progression and regulating the tumor immune microenvironment. *The Journal of biological chemistry*, 302(2), 111059.

Miyabe M, et al. (2026) Deciphering RNA and protein expression discordance identifies TOP2A as a prognostic biomarker and potential therapeutic target in lung adenocarcinoma. *Discover oncology*, 17(1), 170.