

Resource Summary Report

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My Cancer Genome

RRID:SCR_004140

Type: Tool

Proper Citation

My Cancer Genome (RRID:SCR_004140)

Resource Information

URL: <http://www.mycancergenome.org/>

Proper Citation: My Cancer Genome (RRID:SCR_004140)

Description: A freely available online personalized cancer medicine knowledge resource for physicians, patients, caregivers and researchers that gives up-to-date information on what mutations make cancers grow and related therapeutic implications, including available clinical trials. It is a one-stop tool that matches tumor mutations to therapies, making information accessible and convenient for busy clinicians.

Abbreviations: MCG

Synonyms: MyCancerGenome.org

Resource Type: data or information resource, database

Defining Citation: [PMID:32483629](#)

Keywords: genome, disease, genome, medicine, clinical trial, mutation, therapy, FASEB list

Related Condition: Cancer, Tumor

Resource Name: My Cancer Genome

Resource ID: SCR_004140

Alternate IDs: OMICS_01552

Record Creation Time: 20220129T080223+0000

Record Last Update: 20260801T190922+0000

Ratings and Alerts

No rating or validation information has been found for My Cancer Genome.

No alerts have been found for My Cancer Genome.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 97 mentions in open access literature.

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

Zhou J, et al. (2025) Circulating tumour DNA in predicting and monitoring survival of patients with locally advanced rectal cancer undergoing multimodal treatment: long-term results from a prospective multicenter study. EBioMedicine, 112, 105548.

Yi ?? Y, et al. (2025) Biological Data Resources and Machine Learning Frameworks for Hematology Research. Genomics, proteomics & bioinformatics, 23(2).

Steenbock O, et al. (2025) [Next generation sequencing (NGS)-based molecular panel analysis for metastatic prostate cancer: how often can we detect druggable mutations? : NGS for metastatic adenocarcinoma of the prostate]. Urologie (Heidelberg, Germany), 64(3), 256.

Potonnier W, et al. (2025) Performance of the AmpliSeq NGS panel in thyroid nodules with indeterminate cytology. European thyroid journal, 14(1).

Lutz S, et al. (2025) Unveiling the Digital Evolution of Molecular Tumor Boards. Targeted oncology, 20(1), 27.

Srivastava R, et al. (2025) Advancing precision oncology with AI-powered genomic analysis. Frontiers in pharmacology, 16, 1591696.

Abdulkader-Nallib I, et al. (2025) Next-Generation Sequencing (NGS) in non-small cell lung carcinoma: A real-world experience in the public health system of Galicia (Northwest Spain). PloS one, 20(7), e0326336.

Kratz JD, et al. (2024) The Epidemiology of Biliary Tract Cancer and Associated Prevalence of MDM2 Amplification: A Targeted Literature Review. Targeted oncology, 19(6), 833.

Png CW, et al. (2024) DUSP6 regulates Notch1 signalling in colorectal cancer. Nature communications, 15(1), 10087.

Pervushin NV, et al. (2024) BH3-mimetics or DNA-damaging agents in combination with RG7388 overcome p53 mutation-induced resistance to MDM2 inhibition. Apoptosis : an international journal on programmed cell death, 29(11-12), 2197.

Kumar H, et al. (2024) FusionPDB: a knowledgebase of human fusion proteins. *Nucleic acids research*, 52(D1), D1289.

Karstensen S, et al. (2024) DNA alterations in ovarian adult granulosa cell tumours: A scoping review protocol. *PloS one*, 19(6), e0303989.

Gazola AA, et al. (2024) Precision oncology platforms: practical strategies for genomic database utilization in cancer treatment. *Molecular cytogenetics*, 17(1), 28.

Schmidt A, et al. (2024) The p21CIP1-CDK4-DREAM axis is a master regulator of genotoxic stress-induced cellular senescence. *Nucleic acids research*, 52(12), 6945.

Stahler A, et al. (2024) Negative Hyperselection of Resistance Mutations for Panitumumab Maintenance in RAS Wild-Type Metastatic Colorectal Cancer (PanaMa Phase II Trial, AIO KRK 0212). *Clinical cancer research : an official journal of the American Association for Cancer Research*, 30(7), 1256.

Wu K, et al. (2023) Analyses of canine cancer mutations and treatment outcomes using real-world clinico-genomics data of 2119 dogs. *NPJ precision oncology*, 7(1), 8.

Ade CM, et al. (2023) Identification of neoepitope reactive T-cell receptors guided by HLA-A*03:01 and HLA-A*11:01 immunopeptidomics. *Journal for immunotherapy of cancer*, 11(9).

Brown M, et al. (2023) Functional analysis reveals driver cooperativity and novel mechanisms in endometrial carcinogenesis. *EMBO molecular medicine*, 15(10), e17094.

Rae S, et al. (2023) Prevalence of mutations in common tumour types in Northern England and comparable utility of national and international Trial Finders. *Journal of cancer research and clinical oncology*, 149(18), 16355.

Wu J, et al. (2023) Cerebrospinal fluid circulating tumor DNA depicts profiling of brain metastasis in NSCLC. *Molecular oncology*, 17(5), 810.