Resource Summary Report

Generated by RRID on Aug 12, 2026

Cancer Genome Interpreter

RRID:SCR_023752
Type: Tool

Proper Citation

Cancer Genome Interpreter (RRID:SCR_023752)

Resource Information

URL: https://www.cancergenomeinterpreter.org/home

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Description: Platform that systematizes interpretation of cancer genomes and makes it automatic. Web tool to annotate genomic alterations and interpret their possible role in tumorigenesis and in response to anti cancer therapies. Used to support identification of tumor alterations that drive disease and/or which may be therapeutically actionable. Analyses mutations including single nucleotide changes and small insertions/deletions, copy number alterations including gene amplifications and deletions and translocations.

Abbreviations: CGI

Resource Type: web service, software resource, data access protocol

Defining Citation: DOI:10.1101/140475

Keywords: cancer genomes, annotate genomic alterations, tumor alterations identification, mutations analysis, single nucleotide change, copy number alteration, gene amplifications, gene deletions, gene translocation,

Funding: European Union Horizon 2020 ;
European Research Council ;
Spanish Ministry of Economy and Competitiveness ;
CERCA

Availability: Free, Freely available

Resource Name: Cancer Genome Interpreter

Resource ID: SCR_023752

Record Creation Time: 20230706T050207+0000

Record Last Update: 20260812T044430+0000

Ratings and Alerts

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

No alerts have been found for Cancer Genome Interpreter.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 21 mentions in open access literature.

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

Notini G, et al. (2026) Pan-cancer multi-omic integration of Trop2 reveals biological determinants and translational implications for ADC therapy. NPJ precision oncology, 10(1).

Jang H, et al. (2026) Oncogenic PI3K? variants reveal graded conformational spectrum with mutation-specific cryptic pockets. Communications chemistry, 9(1).

You T, et al. (2025) A highly annotated drug combination resource for catalyzing precision combinatorial therapy. Scientific data, 12(1), 1284.

Zhang T, et al. (2025) APOBEC affects tumor evolution and age at onset of lung cancer in smokers. Nature communications, 16(1), 4711.

Jang H, et al. (2025) Oncogenic PI3K? variants reveal graded conformational spectrum with mutation-specific cryptic pockets. bioRxiv : the preprint server for biology.

Parra A, et al. (2025) Genomic Profiling of Highly Aggressive Musculoskeletal Sarcomas Identifies Potential Therapeutic Targets: A Single-Center Experience. Cancers, 18(1).

Erices JI, et al. (2025) The mutational landscape and actionable targets of gallbladder cancer: an ancestry-informed and comparative analysis of a Chilean population. Frontiers in oncology, 15, 1658528.

Cerrato-Izaguirre D, et al. (2024) Genomic landscape of early-stage prostate adenocarcinoma in Mexican patients: an exploratory study. Discover oncology, 15(1), 378.

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

Zhang T, et al. (2024) APOBEC shapes tumor evolution and age at onset of lung cancer in smokers. bioRxiv : the preprint server for biology.

Zhu S, et al. (2024) Pan-cancer association of a mitochondrial function score with genomic alterations and clinical outcome. Scientific reports, 14(1), 31430.

Koka H, et al. (2024) Genomic profiles and clinical presentation of chordoma. Acta neuropathologica communications, 12(1), 129.

Pérez-Villa A, et al. (2023) Integrated multi-omics analysis reveals the molecular interplay between circadian clocks and cancer pathogenesis. Scientific reports, 13(1), 14198.

van de Weijer LL, et al. (2023) A novel patient-derived meningioma spheroid model as a tool to study and treat epithelial-to-mesenchymal transition (EMT) in meningiomas. Acta neuropathologica communications, 11(1), 198.

Yavuz BR, et al. (2023) Neurodevelopmental disorders and cancer networks share pathways, but differ in mechanisms, signaling strength, and outcome. NPJ genomic medicine, 8(1), 37.

Sobahy TM, et al. (2022) Clinically actionable cancer somatic variants (CACSV): a tumor interpreted dataset for analytical workflows. BMC medical genomics, 15(1), 95.

Sabatier R, et al. (2022) Whole-genome/exome analysis of circulating tumor DNA and comparison to tumor genomics from patients with heavily pre-treated ovarian cancer: subset analysis of the PERMED-01 trial. Frontiers in oncology, 12, 946257.

Lee BCH, et al. (2022) Mutational landscape of normal epithelial cells in Lynch Syndrome patients. Nature communications, 13(1), 2710.

Neron M, et al. (2022) Investigation of Molecular Features Involved in Clinical Responses and Survival in Advanced Endometrial Carcinoma Treated by Hormone Therapy. Journal of personalized medicine, 12(5).

Vellichirammal NN, et al. (2020) Pan-Cancer Analysis Reveals the Diverse Landscape of Novel Sense and Antisense Fusion Transcripts. Molecular therapy. Nucleic acids, 19, 1379.