

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

IARC TP53 Database

RRID:SCR_007731

Type: Tool

Proper Citation

IARC TP53 Database (RRID:SCR_007731)

Resource Information

URL: <http://p53.iarc.fr/>

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Description: The IARC TP53 Mutation Database compiles all TP53 gene variations identified in human populations and tumor samples. Data are compiled from the peer-reviewed literature and from generalist databases. The following datasets are available: # TP53 somatic mutations in sporadic cancers # TP53 germline mutation in familial cancers # Common TP53 polymorphisms identified in human populations # Functional and structural properties of P53 mutant proteins # TP53 gene status in human cell-lines # Mouse-models with engineered TP53 The database includes various annotations on the predicted or experimentally assessed functional impact of mutations, clinicopathologic characteristics of tumors and demographic and life-style information on patients. The database is meant to be a source of information on TP53 mutations for a broad range of scientists and clinicians who work in different research areas: # Basic research, to study the structural and functional aspects of the p53 protein # Molecular pathology of cancer, to understand the clinical significance of mutations identified in cancer patients # Molecular epidemiology of cancer, to analyze the links between specific exposures and mutation patterns and to make inferences about possible causes of cancer # Molecular genetics, to analyze genotype/phenotype relationships

Abbreviations: IARC TP53 Database

Resource Type: data or information resource, database

Resource Name: IARC TP53 Database

Resource ID: SCR_007731

Alternate IDs: nif-0000-03006

Old URLs: <http://www-p53.iarc.fr/index.html>

Record Creation Time: 20220129T080243+0000

Record Last Update: 20260905T133144+0000

Ratings and Alerts

No rating or validation information has been found for IARC TP53 Database.

No alerts have been found for IARC TP53 Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 160 mentions in open access literature.

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

Li Y, et al. (2026) Progress in the research and development of oncolytic virus therapies. *Frontiers in pharmacology*, 17, 1751206.

Li S, et al. (2025) Potential application of the bulk RNA sequencing in routine MPN clinics. *BMC cancer*, 25(1), 746.

Perachino M, et al. (2025) Different activity and toxicity of immunotherapy in monozygotic twins diagnosed with early triple-negative breast cancer: a case report. *Therapeutic advances in medical oncology*, 17, 17588359241297565.

Fawaz S, et al. (2024) Evaluation of clonal hematopoiesis and mosaic loss of Y chromosome in cardiovascular risk: An analysis in prospective studies. *eLife*, 13.

Cordova RA, et al. (2024) Coordination between the eIF2 kinase GCN2 and p53 signaling supports purine metabolism and the progression of prostate cancer. *Science signaling*, 17(864), eadp1375.

Qi L, et al. (2024) Twenty years of Gendicine® rAd-p53 cancer gene therapy: The first-in-class human cancer gene therapy in the era of personalized oncology. *Genes & diseases*, 11(4), 101155.

Li C, et al. (2024) Unveiling correlations between aristolochic acids and liver cancer: spatiotemporal heterogeneity phenomenon. *Chinese medicine*, 19(1), 132.

Song R, et al. (2024) Clinical Features of Li-Fraumeni Syndrome in Korea. *Cancer research and treatment*, 56(1), 334.

Kibe Y, et al. (2024) Pediatric-type high-grade gliomas with PDGFRA amplification in adult patients with Li-Fraumeni syndrome: clinical and molecular characterization of three cases. *Acta neuropathologica communications*, 12(1), 57.

Thatikonda V, et al. (2023) Comprehensive analysis of mutational signatures reveals distinct patterns and molecular processes across 27 pediatric cancers. *Nature cancer*, 4(2), 276.

Huang Q, et al. (2023) Evaluating the prognostic significance of p53 and TP53 mutations in HPV-negative hypopharyngeal carcinoma patients: a 5-year follow-up retrospective study. *BMC cancer*, 23(1), 324.

Meirson T, et al. (2023) Systemic structural analysis of alterations reveals a common structural basis of driver mutations in cancer. *NAR cancer*, 5(1), zcac040.

Zheng E, et al. (2023) Exploration into Plasma Hsa_circ_0052184 as a New Biomarker of Colorectal Cancer Prognosis. *Pharmacogenomics and personalized medicine*, 16, 589.

Stružinská I, et al. (2023) A comprehensive molecular analysis of 113 primary ovarian clear cell carcinomas reveals common therapeutically significant aberrations. *Diagnostic pathology*, 18(1), 72.

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

Rana M, et al. (2022) A ferrocene-containing nucleoside analogue targets DNA replication in pancreatic cancer cells. *Metallomics : integrated biometal science*, 14(7).

d'Amati A, et al. (2022) NSD1 Mutations and Pediatric High-Grade Gliomas: A Comparative Genomic Study in Primary and Recurrent Tumors. *Diagnostics (Basel, Switzerland)*, 13(1).

Cafforio L, et al. (2022) Treatment with ibrutinib does not induce a TP53 clonal evolution in chronic lymphocytic leukemia. *Haematologica*, 107(1), 334.

Tong X, et al. (2021) Identification of a druggable protein-protein interaction site between mutant p53 and its stabilizing chaperone DNAJA1. *The Journal of biological chemistry*, 296, 100098.

Martinho MS, et al. (2021) Chaperones and Ubiquitin Ligases Balance Mutant p53 Protein Stability in Esophageal and Other Digestive Cancers. *Cellular and molecular gastroenterology and hepatology*, 11(2), 449.