

Resource Summary Report

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Cancer Genome Anatomy Project

RRID:SCR_003072

Type: Tool

Proper Citation

Cancer Genome Anatomy Project (RRID:SCR_003072)

Resource Information

URL: <http://cgap.nci.nih.gov/>

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Description: Project to determine the gene expression profiles of normal, precancer, and cancer cells, whose generated resources are available to the cancer community. Interconnected modules provide access to all CGAP data, bioinformatic analysis tools, and biological resources allowing the user to find in silico answers to biological questions in a fraction of the time it once took in the laboratory. * Genes * Tissues * Pathways * RNAi * Chromosomes * SAGE Genie * Tools

Abbreviations: CGAP

Synonyms: Cancer Genome Anatomy Project (CGAP)

Resource Type: data or information resource, portal, topical portal

Keywords: gene, gene expression, normal cell, precancer cell, cancer cell, cell, genome, anatomy, gene expression profile, tissue, pathway, rnai, chromosome, bio.tools

Related Condition: Cancer, Normal, Precancer

Funding: NCI

Availability: Free, download Freely available

Resource Name: Cancer Genome Anatomy Project

Resource ID: SCR_003072

Alternate IDs: biotools:cgap, nif-0000-30468

Alternate URLs: https://mitelmandatabase.isb-cgc.org/mb_search

Record Creation Time: 20220129T080217+0000

Record Last Update: 20260903T234557+0000

Ratings and Alerts

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

No alerts have been found for Cancer Genome Anatomy Project.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 108 mentions in open access literature.

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

Tsai HW, et al. (2023) A combined bioinformatics and experimental approach identifies RMI2 as a Wnt/?-catenin signaling target gene related to hepatocellular carcinoma. BMC cancer, 23(1), 1025.

Lee H, et al. (2022) Human Retrotransposons and Effective Computational Detection Methods for Next-Generation Sequencing Data. Life (Basel, Switzerland), 12(10).

Roy T, et al. (2019) Analysis of cancer gene attributes using electrical sensor. Gene, 685, 62.

Lee KH, et al. (2017) Znf179 induces differentiation and growth arrest of human primary glioblastoma multiforme in a p53-dependent cell cycle pathway. Scientific reports, 7(1), 4787.

Oppelt SA, et al. (2017) Specific regions of the brain are capable of fructose metabolism. Brain research, 1657, 312.

Kim YR, et al. (2017) Identification of tumor antigens in malignant mesothelioma. Oncology letters, 14(4), 4557.

Cipollini M, et al. (2016) Polymorphisms within base and nucleotide excision repair pathways and risk of differentiated thyroid carcinoma. DNA repair, 41, 27.

Lin S, et al. (2016) Immortalization of human AE pre-leukemia cells by hTERT allows leukemic transformation. Oncotarget, 7(35), 55939.

Morrison CD, et al. (2016) c-Abl inhibits breast cancer tumorigenesis through reactivation of p53-mediated p21 expression. Oncotarget, 7(45), 72777.

Sextius P, et al. (2015) Analysis of gene expression dynamics revealed delayed and abnormal epidermal repair process in aged compared to young skin. Archives of dermatological research, 307(4), 351.

Pavlopoulou A, et al. (2015) Human cancer databases (review). Oncology reports, 33(1), 3.

Shahryari A, et al. (2015) Long non-coding RNA SOX2OT: expression signature, splicing patterns, and emerging roles in pluripotency and tumorigenesis. Frontiers in genetics, 6, 196.

Giulietti M, et al. (2014) How much do we know about the coupling of G-proteins to serotonin receptors? Molecular brain, 7, 49.

Roy T, et al. (2014) A behavioral study of healthy and cancer genes by modeling electrical network. Gene, 550(1), 81.

Soloviev M, et al. (2013) Elevated transcription of the gene QSOX1 encoding quiescin Q6 sulfhydryl oxidase 1 in breast cancer. PloS one, 8(2), e57327.

Kern JB, et al. (2013) A Novel del(20q) in Aggressive Nodal Marginal Zone Lymphoma. Case reports in pathology, 2013, 784176.

Binder ZA, et al. (2013) Podocalyxin-like protein is expressed in glioblastoma multiforme stem-like cells and is associated with poor outcome. PloS one, 8(10), e75945.

Teshiba R, et al. (2013) Identification of a KEAP1 germline mutation in a family with multinodular goitre. PloS one, 8(5), e65141.

DeBoever C, et al. (2013) Whole transcriptome sequencing enables discovery and analysis of viruses in archived primary central nervous system lymphomas. PloS one, 8(9), e73956.

Sribenja S, et al. (2013) Suppression of thymosin β 10 increases cell migration and metastasis of cholangiocarcinoma. BMC cancer, 13, 430.