Resource Summary Report

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Cancer Cell Map

RRID:SCR_006792
Type: Tool

Proper Citation

Cancer Cell Map (RRID:SCR_006792)

Resource Information

URL: http://cancer.cellmap.org

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Description: It is a collection of selected human-focused cellular pathways implicated in cancer that are linked to visualization and analysis tools. Biologists can browse and search the Cancer Cell Map pathways and view gene expression data on any pathway. All data is freely available. Computational biologists can download all pathways in BioPAX format for global analysis. Software developers can build software on top of the Cancer Cell Map using the web service API. Download and install the cPath pathway database software to create a local mirror of the Cancer Cell Map. Cancer Cell Map pathways were selected based on the scientific interests of research labs at Memorial Sloan-Kettering Cancer Center. Effort was made not to duplicate information in other public pathway databases. Available pathways include: Alpha6Beta4Integrin, AndrogenReceptor, EGFR1, Hedgehog, ID, KitReceptor, NOTCH, TGFBR, TNF alpha/NF-kB, Wnt. Each pathway has around 100-400 interactions.

Abbreviations: Cancer Cell Map

Synonyms: The Cancer Cell Map

Resource Type: analysis service resource, software resource, production service resource, data access protocol, data or information resource, data analysis service, database, service resource, web service

Keywords: cancer, cell map, cellular, human cancer pathway, homo sapiens, mus musculus, rattus norvegicus

Funding:

Resource Name: Cancer Cell Map

Resource ID: SCR_006792

Alternate IDs: nif-0000-20919

Record Creation Time: 20220129T080238+0000

Record Last Update: 20250422T055332+0000

Ratings and Alerts

No rating or validation information has been found for Cancer Cell Map.

No alerts have been found for Cancer Cell Map.

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 NIF.

Liu S, et al. (2021) ERBB1/2/3 Expression, Prognosis, and Immune Infiltration in Cutaneous Melanoma. Frontiers in genetics, 12, 602160.

Sharma N, et al. (2019) Differential Expression Profile of NLRs and AIM2 in Glioma and Implications for NLRP12 in Glioblastoma. Scientific reports, 9(1), 8480.

Wu Y, et al. (2016) Clinical significance of mitofusin-2 and its signaling pathways in hepatocellular carcinoma. World journal of surgical oncology, 14(1), 179.

Wang X, et al. (2016) A network-pathway based module identification for predicting the prognosis of ovarian cancer patients. Journal of ovarian research, 9(1), 73.

Jo BS, et al. (2016) Methylome analysis reveals alterations in DNA methylation in the regulatory regions of left ventricle development genes in human dilated cardiomyopathy. Genomics, 108(2), 84.

Lu H, et al. (2015) Gene target specificity of the Super Elongation Complex (SEC) family: how HIV-1 Tat employs selected SEC members to activate viral transcription. Nucleic acids research, 43(12), 5868.

Bonnet E, et al. (2013) BiNoM 2.0, a Cytoscape plugin for accessing and analyzing pathways using standard systems biology formats. BMC systems biology, 7, 18.

Carbonetto P, et al. (2013) Integrated enrichment analysis of variants and pathways in genome-wide association studies indicates central role for IL-2 signaling genes in type 1 diabetes, and cytokine signaling genes in Crohn's disease. PLoS genetics, 9(10), e1003770.

Chung FH, et al. (2013) ToP: a trend-of-disease-progression procedure works well for identifying cancer genes from multi-state cohort gene expression data for human colorectal cancer. PloS one, 8(6), e65683.

Chen G, et al. (2013) Characterization of a novel CRAC inhibitor that potently blocks human T cell activation and effector functions. Molecular immunology, 54(3-4), 355.

Raju R, et al. (2011) NetSlim: high-confidence curated signaling maps. Database : the journal of biological databases and curation, 2011, bar032.

Isserlin R, et al. (2010) Pathway analysis of dilated cardiomyopathy using global proteomic profiling and enrichment maps. Proteomics, 10(6), 1316.

Kandasamy K, et al. (2010) NetPath: a public resource of curated signal transduction pathways. Genome biology, 11(1), R3.

Demir E, et al. (2010) The BioPAX community standard for pathway data sharing. Nature biotechnology, 28(9), 935.

Wu G, et al. (2010) A human functional protein interaction network and its application to cancer data analysis. Genome biology, 11(5), R53.

Holford ME, et al. (2009) Semantic Web-based integration of cancer pathways and allele frequency data. Cancer informatics, 8, 19.

Zhang J, et al. (2009) A systems biology-based gene expression classifier of glioblastoma predicts survival with solid tumors. PloS one, 4(7), e6274.

Mathew JP, et al. (2007) From bytes to bedside: data integration and computational biology for translational cancer research. PLoS computational biology, 3(2), e12.

Tsui IF, et al. (2007) Public databases and software for the pathway analysis of cancer genomes. Cancer informatics, 3, 379.

Higgins ME, et al. (2007) CancerGenes: a gene selection resource for cancer genome projects. Nucleic acids research, 35(Database issue), D721.