Resource Summary Report

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Mitelman Database of Chromosome Aberrations in Cancer

RRID:SCR_012877
Type: Tool

Proper Citation

Mitelman Database of Chromosome Aberrations in Cancer (RRID:SCR_012877)

Resource Information

URL: http://cgap.nci.nih.gov/Chromosomes/Mitelman

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Description: The web site includes genomic data for humans and mice, including transcript sequence, gene expression patterns, single-nucleotide polymorphisms, clone resources, and cytogenetic information. Descriptions of the methods and reagents used in deriving the CGAP datasets are also provided. An extensive suite of informatics tools facilitates queries and analysis of the CGAP data by the community. One of the newest features of the CGAP web site is an electronic version of the Mitelman Database of Chromosome Aberrations in Cancer. The data in the Mitelman Database is manually culled from the literature and subsequently organized into three distinct sub-databases, as follows: -The sub-database of cases contains the data that relates chromosomal aberrations to specific tumor characteristics in individual patient cases. It can be searched using either the Cases Quick Searcher or the Cases Full Searcher. -The sub-database of molecular biology and clinical associations contains no data from individual patient cases. Instead, the data is pulled from studies with distinct information about: -Molecular biology associations that relate chromosomal aberrations and tumor histologies to genomic sequence data, typically genes rearranged as a consequence of structural chromosome changes. -Clinical associations that relate chromosomal aberrations and/or gene rearrangements and tumor histologies to clinical variables, such as prognosis, tumor grade, and patient characteristics. It can be searched using the Molecular Biology and Clinical (MBC) Associations Searcher -The reference sub-database contains all the references culled from the literature i.e., the sum of the references from the cases and the molecular biology and clinical associations. It can be searched using the Reference Searcher. CGAP has developed six web search tools to help you analyze the information within the Mitelman Database: -The Cases Quick Searcher allows you to query the individual patient cases using the four major fields: aberration, breakpoint, morphology, and topography. -The Cases Full Searcher permits a more detailed search of the same

individual patient cases as above, by including more cytogenetic field choices and adding search fields for patient characteristics and references. -The Molecular Biology Associations Searcher does not search any of the individual patient cases. It searches studies pertaining to gene rearrangements as a consequence of cytogenetic aberrations. -The Clinical Associations Searcher does not search any of the individual patient cases. It searches studies pertaining to clinical associations of cytogenetic aberrations and/or gene rearrangements. -The Recurrent Chromosome Aberrations Searcher provides a way to search for structural and numerical abnormalities that are recurrent, i.e., present in two or more cases with the same morphology and topography. -The Reference Searcher queries only the references themselves, i.e., the references from the individual cases and the molecular biology and clinical associations. Sponsors: This database is sponsored by the University of Lund, Sweden and have support from the Swedish Cancer Society and the Swedish Children"s Cancer Foundation

Synonyms: Mitelman Database

Resource Type: database, data or information resource

Keywords: expression, gene, aberration, abnormality, biology, breakpoint, cancer, cancer databases, characteristic, chromosomal, chromosome, clinical, clone, cytogenetic, genomic, grade, hisotology, human, mice, molecular, morphology, nucleotide, patient, pattern, polymorphism, prognosis, reagent, rearrangement, sequence, single, structural, topography, transcript, tumor, FASEB list

Resource Name: Mitelman Database of Chromosome Aberrations in Cancer

Resource ID: SCR_012877

Alternate IDs: nif-0000-21268

Record Creation Time: 20220129T080312+0000

Record Last Update: 20260805T044306+0000

Ratings and Alerts

No rating or validation information has been found for Mitelman Database of Chromosome Aberrations in Cancer.

No alerts have been found for Mitelman Database of Chromosome Aberrations in Cancer.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 114 mentions in open access literature.

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

García R, et al. (2025) Distinct structural and numerical chromosome abnormalities determine the MYC status in diffuse large B-Cell lymphoma and help differentiate from Burkitt lymphoma: a cytogenetic data analysis using unsupervised and AI-driven prediction models. Annals of hematology, 104(7), 3763.

Koczkodaj D, et al. (2021) Prognostic significance of isochromosome 17q in hematologic malignancies. Oncotarget, 12(7), 708.

Chen Y, et al. (2019) Overdosage of Balanced Protein Complexes Reduces Proliferation Rate in Aneuploid Cells. Cell systems, 9(2), 129.

Tamura R, et al. (2018) Novel MXD4-NUTM1 fusion transcript identified in primary ovarian undifferentiated small round cell sarcoma. Genes, chromosomes & cancer, 57(11), 557.

Heng HH, et al. (2018) A Postgenomic Perspective on Molecular Cytogenetics. Current genomics, 19(3), 227.

Vihinen M, et al. (2018) Systematics for types and effects of DNA variations. BMC genomics, 19(1), 974.

Thomas R, et al. (2018) Whole chromosome loss and associated breakage-fusion-bridge cycles transform mouse tetraploid cells. The EMBO journal, 37(2), 201.

Agostini A, et al. (2018) Identification of novel cyclin gene fusion transcripts in endometrioid ovarian carcinomas. International journal of cancer, 143(6), 1379.

Brunetti M, et al. (2018) RNA-sequencing identifies novel GREB1-NCOA2 fusion gene in a uterine sarcoma with the chromosomal translocation t(2;8)(p25;q13). Genes, chromosomes & cancer, 57(4), 176.

Xu T, et al. (2018) Gene Fusion in Malignant Glioma: An Emerging Target for Next-Generation Personalized Treatment. Translational oncology, 11(3), 609.

Panagopoulos I, et al. (2017) Loss of chromosome 13 material in cellular angiofibromas indicates pathogenetic similarity with spindle cell lipomas. Diagnostic pathology, 12(1), 17.

, et al. (2017) The 150 most important questions in cancer research and clinical oncology series: questions 67-75 : Edited by Chinese Journal of Cancer. Chinese journal of cancer, 36(1), 86.

Torres-Ruiz R, et al. (2017) Efficient Recreation of t(11;22) EWSR1-FLI1+ in Human Stem Cells Using CRISPR/Cas9. Stem cell reports, 8(5), 1408.

Collado R, et al. (2017) Chronic lymphocytic leukemia with isochromosome 17q: An aggressive subgroup associated with TP53 mutations and complex karyotypes. Cancer letters, 409, 42.

Qiu Z, et al. (2017) Generation of Gross Chromosomal Rearrangements by a Single Engineered DNA Double Strand Break. Scientific reports, 7, 43156.

Brunetti M, et al. (2017) Recurrent fusion transcripts in squamous cell carcinomas of the vulva. Oncotarget, 8(10), 16843.

Tabbò F, et al. (2016) Oncogenic kinase fusions: an evolving arena with innovative clinical opportunities. Oncotarget, 7(18), 25064.

Demeulemeester J, et al. (2016) Tracing the origin of disseminated tumor cells in breast cancer using single-cell sequencing. Genome biology, 17(1), 250.

Staege MS, et al. (2016) Gene Expression Music Algorithm-Based Characterization of the Ewing Sarcoma Stem Cell Signature. Stem cells international, 2016, 7674824.

Slot LM, et al. (2016) B-Lymphoblastic Lymphomas Evolving from Follicular Lymphomas Co-Express Surrogate Light Chains and Mutated Gamma Heavy Chains. The American journal of pathology, 186(12), 3273.