

Resource Summary Report

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SKY/M-FISH/CGH

RRID:SCR_007933

Type: Tool

Proper Citation

SKY/M-FISH/CGH (RRID:SCR_007933)

Resource Information

URL: <http://www.ncbi.nlm.nih.gov/sky/>

Proper Citation: SKY/M-FISH/CGH (RRID:SCR_007933)

Description: The SKY/M-FISH and CGH databases provide a public platform for investigators to share and compare their molecular cytogenetic data. The database is open to everyone and all users can view an individual investigator's public data or compare public cases from different investigators. Those wishing to contribute their own data must register and can choose to keep their data private for a period not to exceed two years. Spectral Karyotyping (SKY), Multiplex Fluorescence In Situ Hybridization (M-FISH) and Comparative Genomic Hybridization (CGH) are complementary fluorescent molecular cytogenetic techniques. SKY/M-FISH permits the simultaneous visualization of each human or mouse chromosome in a different color, facilitating the identification of chromosomal aberrations. CGH utilizes the hybridization of differentially labeled tumor and reference DNA to generate a map of DNA copy number changes in tumor genomes.

Synonyms: SKY/M-FISH/CGH

Resource Type: data or information resource, database

Resource Name: SKY/M-FISH/CGH

Resource ID: SCR_007933

Record Creation Time: 20220129T080244+0000

Record Last Update: 20260919T195713+0000

Ratings and Alerts

No rating or validation information has been found for SKY/M-FISH/CGH.

No alerts have been found for SKY/M-FISH/CGH.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 10 mentions in open access literature.

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

Wu P, et al. (2017) 3D genome of multiple myeloma reveals spatial genome disorganization associated with copy number variations. Nature communications, 8(1), 1937.

Kakizaki F, et al. (2016) Expression of metastasis suppressor gene AES driven by a Yin Yang (YY) element in a CpG island promoter and transcription factor YY2. Cancer science, 107(11), 1622.

Weiskirchen R, et al. (2013) Genetic characteristics of the human hepatic stellate cell line LX-2. PloS one, 8(10), e75692.

Case CM, et al. (2013) CKAP2 ensures chromosomal stability by maintaining the integrity of microtubule nucleation sites. PloS one, 8(5), e64575.

Caputo M, et al. (2013) The CSB repair factor is overexpressed in cancer cells, increases apoptotic resistance, and promotes tumor growth. DNA repair, 12(4), 293.

Kong F, et al. (2011) dbCRID: a database of chromosomal rearrangements in human diseases. Nucleic acids research, 39(Database issue), D895.

Shankavaram UT, et al. (2009) CellMiner: a relational database and query tool for the NCI-60 cancer cell lines. BMC genomics, 10, 277.

Abdel-Rahman WM, et al. (2008) Truncation of MBD4 predisposes to reciprocal chromosomal translocations and alters the response to therapeutic agents in colon cancer cells. DNA repair, 7(2), 321.

Bayani J, et al. (2007) Application and interpretation of FISH in biomarker studies. Cancer letters, 249(1), 97.

Galperin MY, et al. (2005) The Molecular Biology Database Collection: 2005 update. Nucleic acids research, 33(Database issue), D5.