

Resource Summary Report

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CGH-Explorer

RRID:SCR_001283

Type: Tool

Proper Citation

CGH-Explorer (RRID:SCR_001283)

Resource Information

URL: <http://heim.ifi.uio.no/bioinf/Projects/CGHExplorer/>

Proper Citation: CGH-Explorer (RRID:SCR_001283)

Description: Software program for visualization and statistical analysis of microarray-based comparative genomic hybridization (array-CGH) data. The program has preprocessing facilities, tools for graphical exploration of individual arrays or groups of arrays, and tools for statistical identification of regions of amplification and deletion.

Abbreviations: CGH-Explorer

Resource Type: software resource

Defining Citation: [PMID:15531610](#)

Keywords: microarray, comparative genomic hybridization, visualization, statistics, java, windows

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: CGH-Explorer

Resource ID: SCR_001283

Alternate IDs: OMICS_02054

Record Creation Time: 20220129T080206+0000

Record Last Update: 20260815T182155+0000

Ratings and Alerts

No rating or validation information has been found for CGH-Explorer.

No alerts have been found for CGH-Explorer.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 15 mentions in open access literature.

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

Woo XY, et al. (2021) Conservation of copy number profiles during engraftment and passaging of patient-derived cancer xenografts. *Nature genetics*, 53(1), 86.

, et al. (2018) Assessment of established techniques to determine developmental and malignant potential of human pluripotent stem cells. *Nature communications*, 9(1), 1925.

Abdeen SK, et al. (2018) Somatic loss of WWOX is associated with TP53 perturbation in basal-like breast cancer. *Cell death & disease*, 9(8), 832.

Ben-David U, et al. (2017) Patient-derived xenografts undergo mouse-specific tumor evolution. *Nature genetics*, 49(11), 1567.

Lee JH, et al. (2017) ID3 regulates the MDC1-mediated DNA damage response in order to maintain genome stability. *Nature communications*, 8(1), 903.

Ben-David U, et al. (2016) The landscape of chromosomal aberrations in breast cancer mouse models reveals driver-specific routes to tumorigenesis. *Nature communications*, 7, 12160.

Sundaravinayagam D, et al. (2016) miR146a-mediated targeting of FANCM during inflammation compromises genome integrity. *Oncotarget*, 7(29), 45976.

Adamczyk J, et al. (2016) Adaptive response to chronic mild ethanol stress involves ROS, sirtuins and changes in chromosome dosage in wine yeasts. *Oncotarget*, 7(21), 29958.

Adamczyk J, et al. (2016) Copy number variations of genes involved in stress responses reflect the redox state and DNA damage in brewing yeasts. *Cell stress & chaperones*, 21(5), 849.

Weissbein U, et al. (2016) Analysis of chromosomal aberrations and recombination by allelic bias in RNA-Seq. *Nature communications*, 7, 12144.

Deregowska A, et al. (2015) Genome-wide array-CGH analysis reveals YRF1 gene copy number variation that modulates genetic stability in distillery yeasts. *Oncotarget*, 6(31), 30650.

Wei Q, et al. (2011) Derivation of rhesus monkey parthenogenetic embryonic stem cells and its microRNA signature. *PLoS one*, 6(9), e25052.

Lyng H, et al. (2008) GeneCount: genome-wide calculation of absolute tumor DNA copy numbers from array comparative genomic hybridization data. *Genome biology*, 9(5), R86.

Yang S, et al. (2007) Identification of genes with correlated patterns of variations in DNA copy number and gene expression level in gastric cancer. *Genomics*, 89(4), 451.

Han W, et al. (2006) Genomic alterations identified by array comparative genomic hybridization as prognostic markers in tamoxifen-treated estrogen receptor-positive breast cancer. *BMC cancer*, 6, 92.