Resource Summary Report

Generated by Kravitz on Sep 10, 2026

Genome Alteration Print

RRID:SCR_012016
Type: Tool

Proper Citation

Genome Alteration Print (RRID:SCR_012016)

Resource Information

URL: http://bioinfo-out.curie.fr/projects/snp_gap/

Proper Citation: Genome Alteration Print (RRID:SCR_012016)

Description: Software for automatic detection of absolute segmental copy numbers and genotype status in complex cancer genome profiles measured by single-nucleotide polymorphism (SNP) arrays. The method is based on pattern recognition of segmented and smoothed copy number and allelic imbalance profiles. The method performs well even for poor-quality data, low tumor content, and highly rearranged tumor genomes.

Abbreviations: GAP

Synonyms: Genome Alteration Print (GAP): Mining complex cancer genomic profiles

Resource Type: software resource

Defining Citation: PMID:19903341

Keywords: genome, segmental copy number, genotype, genome profile, copy number, single-nucleotide polymorphism, array

Related Condition: Cancer, Tumor

Resource Name: Genome Alteration Print

Resource ID: SCR_012016

Alternate IDs: OMICS_02119

Record Creation Time: 20220129T080308+0000

Record Last Update: 20260905T132718+0000

Ratings and Alerts

No rating or validation information has been found for Genome Alteration Print.

No alerts have been found for Genome Alteration Print.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Liu J, et al. (2021) A high-risk retinoblastoma subtype with stemness features, dedifferentiated cone states and neuronal/ganglion cell gene expression. Nature communications, 12(1), 5578.

Montaudon E, et al. (2020) PLK1 inhibition exhibits strong anti-tumoral activity in CCND1-driven breast cancer metastases with acquired palbociclib resistance. Nature communications, 11(1), 4053.

Neou M, et al. (2020) Pangenomic Classification of Pituitary Neuroendocrine Tumors. Cancer cell, 37(1), 123.

Chalign?? R, et al. (2015) The inactive X chromosome is epigenetically unstable and transcriptionally labile in breast cancer. Genome research, 25(4), 488.