

Resource Summary Report

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CopywriteR

RRID:SCR_025864

Type: Tool

Proper Citation

CopywriteR (RRID:SCR_025864)

Resource Information

URL: <https://github.com/PeeperLab/CopywriteR>

Proper Citation: CopywriteR (RRID:SCR_025864)

Description: Software R package for DNA copy number detection from off-target sequence data. Used to extract DNA copy number information from targeted sequencing by utilizing off-target reads.

Resource Type: data analysis software, source code, software resource, software application, data processing software

Keywords: DNA copy number detection, DNA copy number, targeted sequencing, off-target reads,

Funding:

Availability: Free, Available for download, Freely available

Resource Name: CopywriteR

Resource ID: SCR_025864

Alternate URLs: <https://bioconductor.org/packages/CopywriteR/>

License: GNU GPL v3

Record Creation Time: 20241008T053255+0000

Record Last Update: 20250506T062132+0000

Ratings and Alerts

No rating or validation information has been found for CopywriteR.

No alerts have been found for CopywriteR.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 22 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Shim Y, et al. (2024) Comparison of Optical Genome Mapping With Conventional Diagnostic Methods for Structural Variant Detection in Hematologic Malignancies. *Annals of laboratory medicine*, 44(4), 324.

Herrington CS, et al. (2024) Compartment-specific multiomic profiling identifies SRC and GNAS as candidate drivers of epithelial-to-mesenchymal transition in ovarian carcinosarcoma. *British journal of cancer*, 130(2), 327.

Hollis RL, et al. (2023) Distinct histopathological features are associated with molecular subtypes and outcome in low grade serous ovarian carcinoma. *Scientific reports*, 13(1), 7681.

Warrick JI, et al. (2022) A transcriptional network of cell cycle dysregulation in noninvasive papillary urothelial carcinoma. *Scientific reports*, 12(1), 16538.

Anurag M, et al. (2022) Proteogenomic Markers of Chemotherapy Resistance and Response in Triple-Negative Breast Cancer. *Cancer discovery*, 12(11), 2586.

Li N, et al. (2021) Evaluation of the association of heterozygous germline variants in NTHL1 with breast cancer predisposition: an international multi-center study of 47,180 subjects. *NPJ breast cancer*, 7(1), 52.

Gonzalez Bosquet J, et al. (2021) Creation and validation of models to predict response to primary treatment in serous ovarian cancer. *Scientific reports*, 11(1), 5957.

Mueller S, et al. (2020) Linkage of genetic drivers and strain-specific germline variants confound mouse cancer genome analyses. *Nature communications*, 11(1), 4474.

Benvenuti S, et al. (2020) Cancer of Unknown Primary (CUP): genetic evidence for a novel nosological entity? A case report. *EMBO molecular medicine*, 12(7), e11756.

- Badhai J, et al. (2020) Combined deletion of Bap1, Nf2, and Cdkn2ab causes rapid onset of malignant mesothelioma in mice. *The Journal of experimental medicine*, 217(6).
- Satpathy S, et al. (2020) Microscaled proteogenomic methods for precision oncology. *Nature communications*, 11(1), 532.
- Charnpi K, et al. (2020) Convergent network effects along the axis of gene expression during prostate cancer progression. *Genome biology*, 21(1), 302.
- de Matos MR, et al. (2019) A Systematic Pan-Cancer Analysis of Genetic Heterogeneity Reveals Associations with Epigenetic Modifiers. *Cancers*, 11(3).
- Kim B, et al. (2019) Targeted next generation sequencing can serve as an alternative to conventional tests in myeloid neoplasms. *PloS one*, 14(3), e0212228.
- Rim JH, et al. (2018) Efficient strategy for the molecular diagnosis of intractable early-onset epilepsy using targeted gene sequencing. *BMC medical genomics*, 11(1), 6.
- Cioni B, et al. (2018) Loss of androgen receptor signaling in prostate cancer-associated fibroblasts (CAFs) promotes CCL2- and CXCL8-mediated cancer cell migration. *Molecular oncology*, 12(8), 1308.
- Stelloo S, et al. (2018) Integrative epigenetic taxonomy of primary prostate cancer. *Nature communications*, 9(1), 4900.
- Jiménez-Sánchez A, et al. (2017) Heterogeneous Tumor-Immune Microenvironments among Differentially Growing Metastases in an Ovarian Cancer Patient. *Cell*, 170(5), 927.
- Semenova EA, et al. (2016) Transcription Factor NFIB Is a Driver of Small Cell Lung Cancer Progression in Mice and Marks Metastatic Disease in Patients. *Cell reports*, 16(3), 631.
- Bruna A, et al. (2016) A Biobank of Breast Cancer Explants with Preserved Intra-tumor Heterogeneity to Screen Anticancer Compounds. *Cell*, 167(1), 260.