Resource Summary Report

Generated by RRID on Aug 15, 2026

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 utiizing off-target reads.

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

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

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: 20260815T042920+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 29 mentions in open access literature.

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

Hollis RL, et al. (2026) Molecular Profiling and Tumor Biomarker Analysis of GOG281/LOGS: A Positive Late-Phase Trial of Trametinib for Recurrent/Persistent Low-Grade Serous Ovarian Carcinoma. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(4), 724.

Kim N, et al. (2026) Performance Evaluation of Whole-Genome Amplification Platforms for Clinical Next-Generation Sequencing with Minimal Nucleic Acid Input. Annals of laboratory medicine, 46(4), 476.

Jaehnig EJ, et al. (2025) Proteogenomic analysis of the CALGB 40601 (Alliance) HER2+ breast cancer neoadjuvant trial reveals resistance biomarkers. Cell reports. Medicine, 6(6), 102154.

Tedeschi A, et al. (2025) Pan-KRAS Inhibitors BI-2493 and BI-2865 Display Potent Antitumor Activity in Tumors with KRAS Wild-type Allele Amplification. Molecular cancer therapeutics, 24(4), 550.

Sharma S, et al. (2025) Functional genomics and tumor microenvironment analysis reveal prognostic biological subtypes in Mantle cell lymphoma. Nature communications, 16(1), 9762.

Sawant A, et al. (2025) Immune Checkpoint Blockade Delays Cancer Development and Extends Survival in DNA Polymerase Mutator Syndromes. Cancer research, 85(6), 1130.

Zekri Y, et al. (2025) Comprehensive functional annotation of ESR1-driven enhancers in breast cancer reveals hierarchical activity independent of genomic and epigenomic contexts. Genome research, 35(7), 1530.

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.

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.

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.

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.

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

Charmpi K, et al. (2020) Convergent network effects along the axis of gene expression during prostate cancer progression. Genome biology, 21(1), 302.

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.

de Matos MR, et al. (2019) A Systematic Pan-Cancer Analysis of Genetic Heterogeneity Reveals Associations with Epigenetic Modifiers. Cancers, 11(3).