Resource Summary Report

Generated by PRECISE-TBI on Sep 19, 2026

BioDiscovery Nexus Copy Number

RRID:SCR_004557
Type: Tool

Proper Citation

BioDiscovery Nexus Copy Number (RRID:SCR_004557)

Resource Information

URL: https://www.biodiscovery.com/products/nexus-copy-number?hsLang=en

Proper Citation: BioDiscovery Nexus Copy Number (RRID:SCR_004557)

Description: Software package provides statistical tools. Derives copy number and BAF from variety of NGS data including WES, WGS, targeted panel, and shallow sequencing as well as Microarray data. Multifaceted desktop software for rapid discovery of genomic alterations. Accepts data from various manufacturers and technologies including Infinium GSA and CytoScan XON.

Abbreviations: BioDiscovery

Synonyms: Nexus Copy Number

Resource Type: data analysis software, data analytics software, data processing software, software application, software resource

Keywords: Derives copy number, BAF, NGS data, WES, WGS, targeted panel, shallow sequencing, microarray data

Availability: Commercially available

Resource Name: BioDiscovery Nexus Copy Number

Resource ID: SCR_004557

Alternate IDs: OMICS_01122

Old URLs: http://www.biodiscovery.com/software/nexus-expression/

Record Creation Time: 20220129T080225+0000

Record Last Update: 20260912T195614+0000

Ratings and Alerts

No rating or validation information has been found for BioDiscovery Nexus Copy Number.

No alerts have been found for BioDiscovery Nexus Copy Number.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 168 mentions in open access literature.

Listed below are recent publications. The full list is available at PRECISE-TBI .

Chen J, et al. (2026) A Genomically Tailored Multiagent Precision Medicine Clinical Trial for Adults with Recurrent Glioblastoma. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(9), 1652.

Yuan CH, et al. (2026) High VRK2 expression level predicts unfavorable survival outcomes in nasopharyngeal carcinoma. BMC cancer, 26(1).

Hung MY, et al. (2026) Exploring XDH expression as a prognostic marker for urothelial carcinoma. Discover oncology, 17(1).

Jiang Y, et al. (2026) Prenatal Exome Sequencing Analysis in Fetuses With Structural Anomalies: A Multicenter Prospective Cohort Study With Practical Implications. Prenatal diagnosis, 46(1), 46.

Wong NKY, et al. (2026) Establishment and characterization of preclinical models of human gynecologic tract carcinosarcomas demonstrates targetable FGFR1 alterations. Translational oncology, 63, 102591.

Rodemann MM, et al. (2025) Identification of a Growth-Promoting Gene Cluster in the Region 2q24 as a Driver of Tumorigenesis in Childhood Hepatoblastoma. The American journal of pathology, 195(8), 1553.

Ewert W, et al. (2025) Structure and function of the geldanamycin amide synthase from Streptomyces hygroscopicus. Nature communications, 16(1), 2464.

Arbet J, et al. (2025) The Landscape of Prostate Tumour Methylation. bioRxiv : the preprint server for biology.

Apfelbaum AA, et al. (2025) A diverse landscape of FGFR alterations and co-mutations suggests potential therapeutic strategies in pediatric low-grade gliomas. Nature communications, 16(1), 7018.

Nakatochi M, et al. (2025) Copy number variations in RNF216 and postsynaptic membrane-associated genes are associated with bipolar disorder: a case-control study in the Japanese population. Psychiatry and clinical neurosciences, 79(1), 12.

Durgin JS, et al. (2025) Role of single-nucleotide polymorphism microarray in the classification of BAP1-inactivated melanocytic tumours. Histopathology, 87(1), 110.

Petersson A, et al. (2025) Reliable on-treatment prognostication and target identification with a customized assay for circulating tumor DNA in patients with newly diagnosed pancreatic cancer. Scientific reports, 15(1), 34481.

Posthoorn-Verheul C, et al. (2025) Optimized culturing yields high success rates and preserves molecular heterogeneity, enabling personalized screening for high-grade gliomas. NPJ precision oncology, 9(1), 156.

Ross CR, et al. (2025) Genetic background and oncogenic driver determines the genomic evolution and transcriptomics of mammary tumor metastasis. Communications biology, 8(1), 1224.

Sikta N, et al. (2025) Improving genetic diagnostic yield in familial and sporadic cerebral cavernous malformations: detection of copy number and deep Intronic variants. Human molecular genetics, 34(15), 1286.

Goschzik T, et al. (2025) Recurrent genetic alterations in epigenetically defined pineoblastoma subtypes. Acta neuropathologica communications, 13(1), 241.

Mensah GA, et al. (2025) Effect of Kinases in Extracellular Vesicles from HIV-1-Infected Cells on Bystander Cells. Cells, 14(2).

Thompson D, et al. (2025) Robust molecular subgrouping and reference-free aneuploidy detection in medulloblastoma using low-depth whole genome bisulfite sequencing. Acta neuropathologica communications, 13(1), 132.

Ye JL, et al. (2025) Development of a microarray based telomerase binding assay reveals unusual binding of a cytochalasin derivative. Scientific reports, 15(1), 19515.

De Bellis C, et al. (2024) Genomic, epigenomic and transcriptomic inter- and intra-tumor heterogeneity in desmoid tumors. Clinical cancer research : an official journal of the American Association for Cancer Research.