

Resource Summary Report

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CytoSure Interpret Software

RRID:SCR_010926

Type: Tool

Proper Citation

CytoSure Interpret Software (RRID:SCR_010926)

Resource Information

URL: http://www.ogt.co.uk/products/246_cytosure_interpret_software

Proper Citation: CytoSure Interpret Software (RRID:SCR_010926)

Description: A powerful and easy-to-use software package for the analysis of aCGH data, offering an impressive combination of features.

Abbreviations: CytoSure Interpret Software

Resource Type: commercial organization, software resource

Availability: Commercial license

Resource Name: CytoSure Interpret Software

Resource ID: SCR_010926

Alternate IDs: OMICS_00718

Record Creation Time: 20220129T080301+0000

Record Last Update: 20260728T043350+0000

Ratings and Alerts

No rating or validation information has been found for CytoSure Interpret Software.

No alerts have been found for CytoSure Interpret Software.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 10 mentions in open access literature.

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

Madritsch S, et al. (2024) Aneuploidy detection in pooled polar bodies using rapid nanopore sequencing. *Journal of assisted reproduction and genetics*, 41(5), 1261.

Kinnart I, et al. (2024) Elevated α -synuclein levels inhibit mitophagic flux. *NPJ Parkinson's disease*, 10(1), 80.

Nordenskjöld A, et al. (2023) Copy number variants suggest different molecular pathways for the pathogenesis of bladder exstrophy. *American journal of medical genetics. Part A*, 191(2), 378.

Dell'Edera D, et al. (2021) Mayer-Rokitansky-Küster-Hauser syndrome with 22q11.21 microduplication: a case report. *Journal of medical case reports*, 15(1), 208.

Kutkowska-Kaźmierczak A, et al. (2021) Wide Fontanels, Delayed Speech Development and Hoarse Voice as Useful Signs in the Diagnosis of KBG Syndrome: A Clinical Description of 23 Cases with Pathogenic Variants Involving the ANKRD11 Gene or Submicroscopic Chromosomal Rearrangements of 16q24.3. *Genes*, 12(8).

Colley E, et al. (2020) Cell-Free DNA in the Investigation of Miscarriage. *Journal of clinical medicine*, 9(11).

Lindstrand A, et al. (2019) From cytogenetics to cytogenomics: whole-genome sequencing as a first-line test comprehensively captures the diverse spectrum of disease-causing genetic variation underlying intellectual disability. *Genome medicine*, 11(1), 68.

Vincent-Chong VK, et al. (2017) Genome wide profiling in oral squamous cell carcinoma identifies a four genetic marker signature of prognostic significance. *PloS one*, 12(4), e0174865.

Barnes DJ, et al. (2016) A germline mutation of CDKN2A and a novel RPLP1-C19MC fusion detected in a rare melanotic neuroectodermal tumor of infancy: a case report. *BMC cancer*, 16, 629.

Baskin B, et al. (2014) Complex genomic rearrangements in the dystrophin gene due to replication-based mechanisms. *Molecular genetics & genomic medicine*, 2(6), 539.