

Resource Summary Report

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DROMPA

RRID:SCR_012928

Type: Tool

Proper Citation

DROMPA (RRID:SCR_012928)

Resource Information

URL: <http://www.iam.u-tokyo.ac.jp/chromosomeinformatics/rnakato/drompa/>

Proper Citation: DROMPA (RRID:SCR_012928)

Description: A software program for peak-calling and visualization for ChIP-seq analysis.

Abbreviations: DROMPA

Synonyms: DROMPA - Peak-calling and Visualization Tool for Multiple ChIP-seq Data

Resource Type: software resource

Resource Name: DROMPA

Resource ID: SCR_012928

Alternate IDs: OMICS_00438

Record Creation Time: 20220129T080313+0000

Record Last Update: 20260801T190443+0000

Ratings and Alerts

No rating or validation information has been found for DROMPA.

No alerts have been found for DROMPA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Nguyen SA, et al. (2025) Regulation of pericentromeric DNA loop size via Scc2-cohesin interaction. *iScience*, 28(5), 112322.

Machino H, et al. (2022) The metabolic stress-activated checkpoint LKB1-MARK3 axis acts as a tumor suppressor in high-grade serous ovarian carcinoma. *Communications biology*, 5(1), 39.

Fujiwara Y, et al. (2021) Preparation of optimized concanavalin A-conjugated Dynabeads® magnetic beads for CUT&Tag. *PloS one*, 16(11), e0259846.

Nakato R, et al. (2019) Comprehensive epigenome characterization reveals diverse transcriptional regulation across human vascular endothelial cells. *Epigenetics & chromatin*, 12(1), 77.

Fujita Y, et al. (2017) Decreased cohesin in the brain leads to defective synapse development and anxiety-related behavior. *The Journal of experimental medicine*, 214(5), 1431.

Pakchuen S, et al. (2016) Physical Association of *Saccharomyces cerevisiae* Polo-like Kinase Cdc5 with Chromosomal Cohesin Facilitates DNA Damage Response. *The Journal of biological chemistry*, 291(33), 17228.

Izumi K, et al. (2015) Germline gain-of-function mutations in *AFF4* cause a developmental syndrome functionally linking the super elongation complex and cohesin. *Nature genetics*, 47(4), 338.

Leonard J, et al. (2015) Condensin Relocalization from Centromeres to Chromosome Arms Promotes Top2 Recruitment during Anaphase. *Cell reports*, 13(11), 2336.

Liao Q, et al. (2015) Identification and functional annotation of lncRNA genes with hypermethylation in colorectal cancer. *Gene*, 572(2), 259.

Liao Q, et al. (2015) DNA methylation patterns of protein-coding genes and long non-coding RNAs in males with schizophrenia. *Molecular medicine reports*, 12(5), 6568.

Sakashita A, et al. (2015) Sex Specification and Heterogeneity of Primordial Germ Cells in Mice. *PloS one*, 10(12), e0144836.

Sutani T, et al. (2015) Condensin targets and reduces unwound DNA structures associated with transcription in mitotic chromosome condensation. *Nature communications*, 6, 7815.

Tran NT, et al. (2014) A survey of motif finding Web tools for detecting binding site motifs in ChIP-Seq data. *Biology direct*, 9, 4.

Nakato R, et al. (2013) DROMPA: easy-to-handle peak calling and visualization software for the computational analysis and validation of ChIP-seq data. *Genes to cells : devoted to molecular & cellular mechanisms*, 18(7), 589.