Resource Summary Report

Generated by <u>NIF</u> on Apr 19, 2025

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

Funding:

Resource Name: DROMPA

Resource ID: SCR_012928

Alternate IDs: OMICS_00438

Record Creation Time: 20220129T080313+0000

Record Last Update: 20250410T070317+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 13 mentions in open access literature.

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

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 IncRNA 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.