Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 14, 2025

Ringo

RRID:SCR_012973
Type: Tool

Proper Citation

Ringo (RRID:SCR_012973)

Resource Information

URL: http://www.bioconductor.org/packages/2.12/bioc/html/Ringo.html

Proper Citation: Ringo (RRID:SCR_012973)

Description: Software package that facilitates the primary analysis of ChIP-chip data.

Abbreviations: Ringo

Resource Type: software resource

Funding:

Resource Name: Ringo

Resource ID: SCR_012973

Alternate IDs: OMICS_00809

Record Creation Time: 20220129T080313+0000

Record Last Update: 20250410T070320+0000

Ratings and Alerts

No rating or validation information has been found for Ringo.

No alerts have been found for Ringo.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 38 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Zhang N, et al. (2025) Deciphering the molecular logic of WOX5 function in the root stem cell organizer. The EMBO journal, 44(1), 281.

Le MNU, et al. (2023) ChIP-chip data for identifying target genes and consensus binding sequences of mutant p53 in MDA-MB-468 breast cancer cells. Data in brief, 50, 109499.

Martin LJ, et al. (2022) Aberrant DNA and RNA Methylation Occur in Spinal Cord and Skeletal Muscle of Human SOD1 Mouse Models of ALS and in Human ALS: Targeting DNA Methylation Is Therapeutic. Cells, 11(21).

Dard RF, et al. (2022) The rapid developmental rise of somatic inhibition disengages hippocampal dynamics from self-motion. eLife, 11.

Wang X, et al. (2021) Maternal folic acid impacts DNA methylation profile in male rat offspring implicated in neurodevelopment and learning/memory abilities. Genes & nutrition, 16(1), 1.

Preising GA, et al. (2021) Correspondence of aCGH and long-read genome assembly for detection of copy number differences: A proof-of-concept with cichlid genomes. PloS one, 16(10), e0258193.

Noreen F, et al. (2019) DNA methylation instability by BRAF-mediated TET silencing and lifestyle-exposure divides colon cancer pathways. Clinical epigenetics, 11(1), 196.

Gobé C, et al. (2019) Dual role of DMXL2 in olfactory information transmission and the first wave of spermatogenesis. PLoS genetics, 15(2), e1007909.

Huang Y, et al. (2019) Developmental features of DNA methylation in CpG islands of human gametes and preimplantation embryos. Experimental and therapeutic medicine, 17(6), 4447.

Wang J, et al. (2018) Integrated analysis of DNA methylation profiling and gene expression profiling identifies novel markers in lung cancer in Xuanwei, China. PloS one, 13(10), e0203155.

Buckle A, et al. (2018) Polymer Simulations of Heteromorphic Chromatin Predict the 3D Folding of Complex Genomic Loci. Molecular cell, 72(4), 786.

Danks GB, et al. (2018) Distinct core promoter codes drive transcription initiation at key developmental transitions in a marine chordate. BMC genomics, 19(1), 164.

Hua BL, et al. (2018) Dynamic changes in ORC localization and replication fork progression during tissue differentiation. BMC genomics, 19(1), 623.

Chan SKK, et al. (2017) Role of co-repressor genomic landscapes in shaping the Notch response. PLoS genetics, 13(11), e1007096.

El-Sharnouby S, et al. (2017) Regions of very low H3K27me3 partition the Drosophila genome into topological domains. PloS one, 12(3), e0172725.

Ngollo M, et al. (2017) Global analysis of H3K27me3 as an epigenetic marker in prostate cancer progression. BMC cancer, 17(1), 261.

Karsli-Ceppioglu S, et al. (2017) The Epigenetic Landscape of Promoter Genome-wide Analysis in Breast Cancer. Scientific reports, 7(1), 6597.

Chater-Diehl EJ, et al. (2016) Alteration of Gene Expression, DNA Methylation, and Histone Methylation in Free Radical Scavenging Networks in Adult Mouse Hippocampus following Fetal Alcohol Exposure. PloS one, 11(5), e0154836.

Song M, et al. (2016) Combined analysis of DNA methylome and transcriptome reveal novel candidate genes with susceptibility to bovine Staphylococcus aureus subclinical mastitis. Scientific reports, 6, 29390.

Wang J, et al. (2016) DNA methylation is critical for tooth agenesis: implications for sporadic non-syndromic anodontia and hypodontia. Scientific reports, 6, 19162.