Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Mar 31, 2025

phantompeakqualtools

RRID:SCR_005331
Type: Tool

Proper Citation

phantompeakqualtools (RRID:SCR_005331)

Resource Information

URL: https://code.google.com/p/phantompeakqualtools/

Proper Citation: phantompeakqualtools (RRID:SCR_005331)

Description: Software package that computes quick but highly informative enrichment and quality measures for ChIP-seq/DNase-seq/FAIRE-seq/MNase-seq data. It can also be used to obtain robust estimates of the predominant fragment length or characteristic tag shift values in these assays.

Abbreviations: phantompeakqualtools

Synonyms: phantompeakqualtools - Computes quick but highly informative enrichment and quality measures and fragment lengths for ChIP-seq/DNase-seq/FAIRE-seq/MNase-seq data

Resource Type: software resource

Keywords: chip-seq, dnase-seq, faire-seq, mnase-seq, dataquality, enrichment, phantompeak, cross-correlation, spppeakcaller, chipseq, dnaseseq, fairseq, mnaseseq, bio.tools

Funding:

Availability: MIT License

Resource Name: phantompeakqualtools

Resource ID: SCR_005331

Alternate IDs: biotools:phantompeakqualtools, OMICS_00431

Alternate URLs: https://bio.tools/phantompeakqualtools

Record Creation Time: 20220129T080229+0000

Record Last Update: 20250214T183037+0000

Ratings and Alerts

No rating or validation information has been found for phantompeakqualtools.

No alerts have been found for phantompeakqualtools.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 79 mentions in open access literature.

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

Zhu T, et al. (2024) Comprehensive mapping and modelling of the rice regulome landscape unveils the regulatory architecture underlying complex traits. Nature communications, 15(1), 6562.

Hu G, et al. (2024) Evolutionary Dynamics of Chromatin Structure and Duplicate Gene Expression in Diploid and Allopolyploid Cotton. Molecular biology and evolution, 41(5).

Silveira AB, et al. (2024) Base-excision repair pathway shapes 5-methylcytosine deamination signatures in pan-cancer genomes. Nature communications, 15(1), 9864.

Lyu P, et al. (2024) Chromatin profiling reveals TFAP4 as a critical transcriptional regulator of bovine satellite cell differentiation. BMC genomics, 25(1), 272.

Gao L, et al. (2024) Selective gene expression maintains human tRNA anticodon pools during differentiation. Nature cell biology, 26(1), 100.

Pham VC, et al. (2024) Epigenetic regulation by polycomb repressive complex 1 promotes cerebral cavernous malformations. EMBO molecular medicine, 16(11), 2827.

Puri D, et al. (2023) CTCF deletion alters the pluripotency and DNA methylation profile of human iPSCs. Frontiers in cell and developmental biology, 11, 1302448.

Yin L, et al. (2023) Transcription Factor Dynamics in Cross-Regulation of Plant Hormone Signaling Pathways. bioRxiv : the preprint server for biology.

Yazar V, et al. (2023) Impaired ATF3 signaling involves SNAP25 in SOD1 mutant ALS patients. Scientific reports, 13(1), 12019.

Quintela M, et al. (2023) In silico enhancer mining reveals SNS-032 and EHMT2 inhibitors as therapeutic candidates in high-grade serous ovarian cancer. British journal of cancer, 129(1), 163.

Spracklin G, et al. (2023) Diverse silent chromatin states modulate genome compartmentalization and loop extrusion barriers. Nature structural & molecular biology, 30(1), 38.

Alexandari AM, et al. (2023) De novo distillation of thermodynamic affinity from deep learning regulatory sequence models of in vivo protein-DNA binding. bioRxiv : the preprint server for biology.

Pelinski Y, et al. (2022) NF-?B signaling controls H3K9me3 levels at intronic LINE-1 and hematopoietic stem cell genes in cis. The Journal of experimental medicine, 219(8).

Diego-Martin B, et al. (2022) The TRIPLE PHD FINGERS proteins are required for SWI/SNF complex-mediated +1 nucleosome positioning and transcription start site determination in Arabidopsis. Nucleic acids research, 50(18), 10399.

Nadeu F, et al. (2022) Detection of early seeding of Richter transformation in chronic lymphocytic leukemia. Nature medicine, 28(8), 1662.

Li H, et al. (2022) YAP/TAZ drives cell proliferation and tumour growth via a polyamine-eIF5A hypusination-LSD1 axis. Nature cell biology, 24(3), 373.

Wang N, et al. (2022) Identification of crucial factors involved in Cynoglossus semilaevis sexual size dimorphism by GWAS and demonstration of zbed1 regulatory network by DAP-seq. Genomics, 114(3), 110376.

Seyres D, et al. (2022) Transcriptional, epigenetic and metabolic signatures in cardiometabolic syndrome defined by extreme phenotypes. Clinical epigenetics, 14(1), 39.

Cantilena S, et al. (2022) Direct targeted therapy for MLL-fusion-driven high-risk acute leukaemias. Clinical and translational medicine, 12(6), e933.

Vilarrasa-Blasi R, et al. (2021) Dynamics of genome architecture and chromatin function during human B cell differentiation and neoplastic transformation. Nature communications, 12(1), 651.