

Resource Summary Report

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[phantompeakqualtools](#)

RRID:SCR_005331

Type: Tool

Proper Citation

phantompeakqualtools (RRID:SCR_005331)

Resource Information

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

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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

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: 20260808T185837+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 87 mentions in open access literature.

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

Mukherjee S, et al. (2025) Tumor-associated neutrophil precursors impair homologous DNA repair and promote sensitivity to PARP inhibition. *Nature communications*, 16(1), 6999.

Bresnahan ST, et al. (2025) Intragenomic conflict associated with extreme phenotypic plasticity in queen-worker caste determination in honey bees (*Apis mellifera*). *Genome biology*, 26(1), 171.

Kanduri M, et al. (2025) IER3: exploring its dual function as an oncogene and tumor suppressor. *Cancer gene therapy*, 32(4), 450.

Palma LG, et al. (2025) Chromatin activity of I?B? mediates the exit from naïve pluripotency. *eLife*, 14.

Severson TM, et al. (2025) Epigenetic profiling identifies markers of endocrine resistance and therapeutic options for metastatic castration-resistant prostate cancer. *Cell reports. Medicine*, 6(7), 102215.

Cheng CCY, et al. (2025) Multi-omic analysis of hepatocellular carcinoma reveals aberrant cis-regulatory changes and dysregulated retrotransposons with prognostic potential. *Communications biology*, 8(1), 1792.

Budkina A, et al. (2025) Functional characterization of DNAAF3-AS1 in chromatin remodeling and H3K36me3 distribution. *bioRxiv : the preprint server for biology*.

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.

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.

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

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

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

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.

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

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

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

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.

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.

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