

Resource Summary Report

Generated by [dkNET](#) on May 18, 2025

PeakSeq

RRID:SCR_005349

Type: Tool

Proper Citation

PeakSeq (RRID:SCR_005349)

Resource Information

URL: <http://info.gersteinlab.org/PeakSeq>

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Description: A software program for identifying and ranking peak regions in ChIP-Seq experiments. It takes as input, mapped reads from a ChIP-Seq experiment, mapped reads from a control experiment and outputs a file with peak regions ranked with increasing Q-values.

Abbreviations: PeakSeq

Resource Type: software resource

Defining Citation: [PMID:19122651](#)

Keywords: bio.tools

Funding:

Resource Name: PeakSeq

Resource ID: SCR_005349

Alternate IDs: biotools:peakseq, OMICS_00453

Alternate URLs: <https://bio.tools/peakseq>

Record Creation Time: 20220129T080229+0000

Record Last Update: 20250420T014249+0000

Ratings and Alerts

No rating or validation information has been found for PeakSeq.

No alerts have been found for PeakSeq.

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 [dkNET](#).

Alexander KD, et al. (2023) The homeodomain transcriptional regulator DVE-1 directs a program for synapse elimination during circuit remodeling. *Nature communications*, 14(1), 7520.

Coda DM, et al. (2022) A network of transcription factors governs the dynamics of NODAL/Activin transcriptional responses. *Journal of cell science*, 135(8).

Wei X, et al. (2022) Redistribution of lamina-associated domains reshapes binding of pioneer factor FOXA2 in development of nonalcoholic fatty liver disease. *Genome research*, 32(11-12), 1981.

Wang Y, et al. (2022) Psychiatric risk gene transcription factor 4 preferentially regulates cortical interneuron neurogenesis during early brain development. *Journal of biomedical research*, 36(4), 242.

Corvaisier M, et al. (2021) The γ -tubulin meshwork assists in the recruitment of PCNA to chromatin in mammalian cells. *Communications biology*, 4(1), 767.

Kain J, et al. (2021) Pioneer factor Foxa2 enables ligand-dependent activation of type II nuclear receptors FXR and LXR?. *Molecular metabolism*, 53, 101291.

Xiao Y, et al. (2021) HBO1 is a versatile histone acyltransferase critical for promoter histone acylations. *Nucleic acids research*, 49(14), 8037.

Jeon H, et al. (2020) Comparative analysis of commonly used peak calling programs for ChIP-Seq analysis. *Genomics & informatics*, 18(4), e42.

Price AJ, et al. (2020) Hdac3, Setdb1, and Kap1 mark H3K9me3/H3K14ac bivalent regions in young and aged liver. *Aging cell*, 19(2), e13092.

Eales JM, et al. (2019) Human Y Chromosome Exerts Pleiotropic Effects on Susceptibility to

Atherosclerosis. *Arteriosclerosis, thrombosis, and vascular biology*, 39(11), 2386.

Moumi NA, et al. (2019) Quartet-based inference of cell differentiation trees from ChIP-Seq histone modification data. *PloS one*, 14(9), e0221270.

Annunziata I, et al. (2019) MYC competes with MiT/TFE in regulating lysosomal biogenesis and autophagy through an epigenetic rheostat. *Nature communications*, 10(1), 3623.

Fujiwara S, et al. (2019) High Quality ATAC-Seq Data Recovered from Cryopreserved Breast Cell Lines and Tissue. *Scientific reports*, 9(1), 516.

Zhou L, et al. (2018) Prioritization and functional assessment of noncoding variants associated with complex diseases. *Genome medicine*, 10(1), 53.

Whitton H, et al. (2018) Changes at the nuclear lamina alter binding of pioneer factor Foxa2 in aged liver. *Aging cell*, 17(3), e12742.

Girdhar K, et al. (2018) Cell-specific histone modification maps in the human frontal lobe link schizophrenia risk to the neuronal epigenome. *Nature neuroscience*, 21(8), 1126.

Fleming KE, et al. (2018) An RpaA-Dependent Sigma Factor Cascade Sets the Timing of Circadian Transcriptional Rhythms in *Synechococcus elongatus*. *Cell reports*, 25(11), 2937.

Dardalhon-Cuménal D, et al. (2018) Cyclin G and the Polycomb Repressive complexes PRC1 and PR-DUB cooperate for developmental stability. *PLoS genetics*, 14(7), e1007498.

Shihab HA, et al. (2017) HIPred: an integrative approach to predicting haploinsufficient genes. *Bioinformatics (Oxford, England)*, 33(12), 1751.

Rosenberg M, et al. (2017) Denaturing CLIP, dCLIP, Pipeline Identifies Discrete RNA Footprints on Chromatin-Associated Proteins and Reveals that CBX7 Targets 3' UTRs to Regulate mRNA Expression. *Cell systems*, 5(4), 368.