

Resource Summary Report

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PePr

RRID:SCR_005759

Type: Tool

Proper Citation

PePr (RRID:SCR_005759)

Resource Information

URL: <https://code.google.com/p/pepr-chip-seq/>

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Description: A ChIP-Seq peak calling or differential binding analysis tool that is primarily designed for data with biological replicates. It uses a negative binomial distribution to model the read counts among the samples in the same group, and look for consistent differences between ChIP and control group or two ChIP groups run under different conditions.

Abbreviations: PePr

Synonyms: pepr-chip-seq, Peak Prioritization Pipeline, pepr-chip-seq: A ChIP-Seq analyzing program for biological replicates

Resource Type: software resource

Defining Citation: [PMID:24894502](#)

Keywords: python, bio.tools

Availability: GNU General Public License, v3

Resource Name: PePr

Resource ID: SCR_005759

Alternate IDs: OMICS_04058, biotools:pepr

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

Record Creation Time: 20220129T080232+0000

Record Last Update: 20260912T195631+0000

Ratings and Alerts

No rating or validation information has been found for PePr.

No alerts have been found for PePr.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 55 mentions in open access literature.

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

Shtolz N, et al. (2026) Hypoxia leads to reduced mito-nuclear gene expression and increased mtDNA transcriptional pausing in human cells. *Communications biology*, 9(1), 180.

Kliver TA, et al. (2026) Differential Wnt/??-catenin signaling via TCF7L2/LEF1 binding specificity shapes cellular and tumor phenotypes. *Proceedings of the National Academy of Sciences of the United States of America*, 123(24), e2528450123.

Shi L, et al. (2025) CRISPRepi: a multi-omic atlas for CRISPR-based epigenome editing. *Nucleic acids research*, 53(D1), D901.

Nordin A, et al. (2025) Wnt signaling activation induces CTCF binding and loop formation at cis-regulatory elements of target genes. *Genome research*, 35(8), 1701.

Cao N, et al. (2025) OsGATA7 and SMOS1 cooperatively determine rice taste quality by repressing OsGluA2 expression and protein biosynthesis. *Nature communications*, 16(1), 3513.

Liu XD, et al. (2025) DNA methylation confers a cerebellum-specific identity in non-human primates. *Zoological research*, 46(2), 414.

Sala-Hamrick KE, et al. (2025) Sex-stratified piRNA expression analysis reveals shared functional impacts of perinatal lead (Pb) exposure in murine hearts. *Epigenetics*, 20(1), 2542879.

Tong X, et al. (2024) 5-Hydroxymethylcytosine in circulating cell-free DNA as a potential diagnostic biomarker for SLE. *Lupus science & medicine*, 11(2).

Suresh V, et al. (2024) PRDM16 co-operates with LHX2 to shape the human brain. *Oxford open neuroscience*, 3, kvae001.

Jyoti , et al. (2024) Comprehensive analysis of computational approaches in plant transcription factors binding regions discovery. *Heliyon*, 10(20), e39140.

Kayahashi K, et al. (2024) Androgen-responsive FOXP4 is a target for endometrial carcinoma. *Communications biology*, 7(1), 740.

Haghani V, et al. (2024) Improving rigor and reproducibility in chromatin immunoprecipitation assay data analysis workflows with Rocketchip. *bioRxiv : the preprint server for biology*.

Wang K, et al. (2024) piOxi database: a web resource of germline and somatic tissue piRNAs identified by chemical oxidation. *Database : the journal of biological databases and curation*, 2024.

Maggonage MHU, et al. (2024) Identifying the potential of ovalbumin and its' hydrolysates to be used in a liquid food system to develop functional beverages. *Poultry science*, 104(1), 104515.

Beauvais V, et al. (2023) Tho2 is critical for the recruitment of Rrp6 to chromatin in response to perturbed mRNP biogenesis. *RNA (New York, N.Y.)*, 30(1), 89.

Suresh V, et al. (2023) Regulation of chromatin accessibility and gene expression in the developing hippocampal primordium by LIM-HD transcription factor LHX2. *PLoS genetics*, 19(8), e1010874.

Sumimoto H, et al. (2023) Oncogenic epidermal growth factor receptor signal-induced histone deacetylation suppresses chemokine gene expression in human lung adenocarcinoma. *Scientific reports*, 13(1), 5087.

Batugedara G, et al. (2023) Novel insights into the role of long non-coding RNA in the human malaria parasite, *Plasmodium falciparum*. *Nature communications*, 14(1), 5086.

Dhat R, et al. (2023) Epigenetic modifier alpha-ketoglutarate modulates aberrant gene body methylation and hydroxymethylation marks in diabetic heart. *Epigenetics & chromatin*, 16(1), 12.

Wang L, et al. (2022) Cell-cell contact-driven EphB1 cis- and trans- signalings regulate cancer stem cells enrichment after chemotherapy. *Cell death & disease*, 13(11), 980.