

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

PeakRanger

RRID:SCR_010863

Type: Tool

Proper Citation

PeakRanger (RRID:SCR_010863)

Resource Information

URL: <http://ranger.sourceforge.net/>

Proper Citation: PeakRanger (RRID:SCR_010863)

Description: Software for a multi-purpose ChIP Seq peak caller.

Abbreviations: PeakRanger

Resource Type: software resource

Defining Citation: [PMID:21554709](#)

Keywords: mapreduce/hadoop, bio.tools

Resource Name: PeakRanger

Resource ID: SCR_010863

Alternate IDs: OMICS_00451, biotools:peakranger

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

Record Creation Time: 20220129T080301+0000

Record Last Update: 20260905T132648+0000

Ratings and Alerts

No rating or validation information has been found for PeakRanger.

No alerts have been found for PeakRanger.

Data and Source Information

Usage and Citation Metrics

We found 21 mentions in open access literature.

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

Huynh D, et al. (2025) Effective in vivo binding energy landscape illustrates kinetic stability of RBPJ-DNA binding. *Nature communications*, 16(1), 1259.

Fracassi C, et al. (2024) PML is a constitutive component of chromatin domains enriched in repetitive elements and duplicated gene clusters in cancer cells. *Heliyon*, 10(17), e36499.

Yang N, et al. (2023) A hyper-quiescent chromatin state formed during aging is reversed by regeneration. *Molecular cell*, 83(10), 1659.

López C, et al. (2022) The key role of differential broad H3K4me3 and H3K4ac domains in breast cancer. *Gene*, 826, 146463.

Tock AJ, et al. (2021) Crossover-active regions of the wheat genome are distinguished by DMC1, the chromosome axis, H3K27me3, and signatures of adaptation. *Genome research*, 31(9), 1614.

Du Q, et al. (2021) DNA methylation is required to maintain both DNA replication timing precision and 3D genome organization integrity. *Cell reports*, 36(12), 109722.

Wu C, et al. (2018) Clustering-local-unique-enriched-signals (CLUES) promotes identification of novel regulators of ES cell self-renewal and pluripotency. *PloS one*, 13(11), e0206844.

Roquis D, et al. (2018) Histone methylation changes are required for life cycle progression in the human parasite *Schistosoma mansoni*. *PLoS pathogens*, 14(5), e1007066.

Cencioni C, et al. (2018) Zeb1-Hdac2-eNOS circuitry identifies early cardiovascular precursors in naive mouse embryonic stem cells. *Nature communications*, 9(1), 1281.

Valdés-Mora F, et al. (2017) Acetylated histone variant H2A.Z is involved in the activation of neo-enhancers in prostate cancer. *Nature communications*, 8(1), 1346.

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.

Jox T, et al. (2017) *Drosophila* CP190- and dCTCF-mediated enhancer blocking is augmented by SUMOylation. *Epigenetics & chromatin*, 10, 32.

Mateos JL, et al. (2017) Divergence of regulatory networks governed by the orthologous transcription factors FLC and PEP1 in Brassicaceae species. *Proceedings of the National Academy of Sciences of the United States of America*, 114(51), E11037.

Picard MA, et al. (2016) Sex-Biased Transcriptome of *Schistosoma mansoni*: Host-Parasite Interaction, Genetic Determinants and Epigenetic Regulators Are Associated with Sexual Differentiation. *PLoS neglected tropical diseases*, 10(9), e0004930.

Roquis D, et al. (2015) The Epigenome of *Schistosoma mansoni* Provides Insight about How Cercariae Poise Transcription until Infection. *PLoS neglected tropical diseases*, 9(8), e0003853.

Cieřlik M, et al. (2015) Genome-wide predictors of NF- κ B recruitment and transcriptional activity. *BioData mining*, 8, 37.

McGann JC, et al. (2014) Polycomb- and REST-associated histone deacetylases are independent pathways toward a mature neuronal phenotype. *eLife*, 3, e04235.

Tran NT, et al. (2014) A survey of motif finding Web tools for detecting binding site motifs in ChIP-Seq data. *Biology direct*, 9, 4.

van Heeringen SJ, et al. (2014) Principles of nucleation of H3K27 methylation during embryonic development. *Genome research*, 24(3), 401.

Lin YC, et al. (2013) Enabling large-scale biomedical analysis in the cloud. *BioMed research international*, 2013, 185679.