

Resource Summary Report

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FindPeaks

RRID:SCR_010857

Type: Tool

Proper Citation

FindPeaks (RRID:SCR_010857)

Resource Information

URL: <http://sourceforge.net/apps/mediawiki/vancouvershorttr/index.php?title=FindPeaks>

Proper Citation: FindPeaks (RRID:SCR_010857)

Description: Software application that can be used for converting Eland, Maq (.map), BED or other files into WIG files and identifying areas of enrichment (ChIP-Seq analysis).

Abbreviations: FindPeaks

Resource Type: software resource

Keywords: chip-seq

Funding: BC Cancer Agency ;
Michael Smith Foundation for Health Research

Resource Name: FindPeaks

Resource ID: SCR_010857

Alternate IDs: OMICS_00440

Record Creation Time: 20220129T080301+0000

Record Last Update: 20260815T182410+0000

Ratings and Alerts

No rating or validation information has been found for FindPeaks.

No alerts have been found for FindPeaks.

Data and Source Information

Usage and Citation Metrics

We found 348 mentions in open access literature.

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

Kama Y, et al. (2026) Notch interaction with RUNX factors regulates initiation of the T-lineage program. *The Journal of experimental medicine*, 223(2).

Chen X, et al. (2026) FOXI3 establishes the ectodermal niche in pharyngeal arches for cranial neural crest cells and their lineages. *Bone research*, 14(1), 16.

Van de Velde S, et al. (2026) Med14 phosphorylation shapes genomic response to GLP-1 agonists. *Proceedings of the National Academy of Sciences of the United States of America*, 123(10), e2536772123.

Yang HJ, et al. (2026) SMARCA4 activation engages FOSL1 to drive enhancer reprogramming and tumorigenic phenotypes in SMARCA4-deficient LUAD cells. *Cell death discovery*, 12(1).

Liang J, et al. (2026) scDeepAPA: a deep learning framework for single-cell alternative polyadenylation identification. *Briefings in bioinformatics*, 27(3).

Kumar Y, et al. (2026) Acetylation of H3K115 is associated with fragile nucleosomes at CpG island promoters and active regulatory sites. *eLife*, 14.

You C, et al. (2026) Single-Nucleus Multi-Omics Reveals Hypoxia-Driven Angiogenic Programs and Their Epigenetic Control in Sinonasal Squamous Cell Carcinoma. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(12), e10302.

Sun X, et al. (2026) sc-rDSeq: a robust and cost-effective full-length total RNA sequencing method for single cells reveals multilayered heterogeneity in drug-resistant lung cancer cells. *Nucleic acids research*, 54(7).

Simmons SK, et al. (2026) Experimental and computational methods for allelic imbalance analysis from single-nucleus RNA-seq data. *Genome biology*, 27(1).

Chandrasekaran V, et al. (2026) Insulin enables acquisition of the IL7R+ memory phenotype in PD1+ T cells in RA tissues. *Cell death & disease*, 17(1).

Kumar A, et al. (2026) Transcription initiation profiling defines the regulatory logic of astrocyte gene regulation. *bioRxiv : the preprint server for biology*.

Janevska S, et al. (2026) Facultative heterochromatin mediated by core and accessory chromosome-encoded H3K27-specific methyltransferases controls virulence in a fungal phytopathogen. *Nucleic acids research*, 54(1).

Nanchira Abraham L, et al. (2026) Population-level Variability in Genome-wide Repressive Histone Marks in a Fungal Wheat Pathogen. *Genome biology and evolution*, 18(5).

Freire CF, et al. (2026) Comprehensive Schistosoma mansoni Hierarchical Transcriptome Assembly Points to Novel lncRNAs Associated with Sexual Dimorphism. *Non-coding RNA*, 12(2).

Geng R, et al. (2026) Stable maintenance of MERVL-positive embryonic stem cells reveals sustained transcriptional programs and enhancer remodeling. *The Journal of biological chemistry*, 302(7), 113166.

Erdmann H, et al. (2026) Repeat-associated ataxias in a German patient cohort analysed by targeted parallel long-read sequencing. *Brain : a journal of neurology*, 149(3), 993.

Boubou Y, et al. (2025) Rural-urban transformation shapes oasis agriculture in Morocco's High Atlas Mountains. *Scientific reports*, 15(1), 3433.

Ozturk H, et al. (2025) High PRMT5 levels, maintained by KEAP1 inhibition, drive chemoresistance in high-grade serous ovarian cancer. *The Journal of clinical investigation*, 135(6).

Wang G, et al. (2025) Machine learning-based prediction reveals kinase MAP4K4 regulates neutrophil differentiation through phosphorylating apoptosis-related proteins. *PLoS computational biology*, 21(3), e1012877.

Zhou Z, et al. (2025) GnRH pulse generator activity in mouse models of polycystic ovary syndrome. *eLife*, 13.