

Resource Summary Report

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PeakAnalyzer

RRID:SCR_001194

Type: Tool

Proper Citation

PeakAnalyzer (RRID:SCR_001194)

Resource Information

URL: <http://www.bioinformatics.org/peakanalyzer/wiki/>

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Description: A set of standalone software programs for the automated processing of any genomic loci, with an emphasis on datasets consisting of ChIP-derived signal peaks. The software is able to identify individual binding / modification sites from enrichment loci, retrieve peak region sequences for motif discovery, and integrate experimental data with different classes of annotated elements throughout the genome. PeakAnalyzer requires a peak file and a feature annotation file in BED or GTF format. Complete annotation files for the current builds of the human (HG19) and mouse (MM9) genomes are provided with the software distribution.

Abbreviations: PeakAnalyzer

Resource Type: software resource

Defining Citation: [PMID:20691053](#)

Keywords: genome, chip, signal peak, binding site, modification site, enrichment loci, peak region, sequence, motif, chip-seq, chip-chip, c++, java, linux, mac os x, windows, bed, gtf, annotation, r, high-throughput sequencing, chromatin binding, modification loci, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: PeakAnalyzer

Resource ID: SCR_001194

Alternate IDs: biotools:peakanalyzer, OMICS_02156

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

Record Creation Time: 20220129T080206+0000

Record Last Update: 20260912T195521+0000

Ratings and Alerts

No rating or validation information has been found for PeakAnalyzer.

No alerts have been found for PeakAnalyzer.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Rogers D, et al. (2021) Pre-existing chromatin accessibility and gene expression differences among naive CD4+ T cells influence effector potential. Cell reports, 37(9), 110064.

Falcão AM, et al. (2019) PAD2-Mediated Citrullination Contributes to Efficient Oligodendrocyte Differentiation and Myelination. Cell reports, 27(4), 1090.

Revote J, et al. (2017) Development of a cloud-based Bioinformatics Training Platform. Briefings in bioinformatics, 18(3), 537.