

# Resource Summary Report

Generated by [SPARC SAWG](#) on Aug 9, 2026

## 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:** 20260808T185738+0000

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## Ratings and Alerts

No rating or validation information has been found for PeakAnalyzer.

No alerts have been found for PeakAnalyzer.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 3 mentions in open access literature.

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

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.