

# Resource Summary Report

Generated by [ASWG](#) on Aug 2, 2026

## ExomePeak

RRID:SCR\_001076

Type: Tool

### Proper Citation

ExomePeak (RRID:SCR\_001076)

### Resource Information

**URL:** <http://www.bioconductor.org/packages/release/bioc/html/exomePeak.html>

**Proper Citation:** ExomePeak (RRID:SCR\_001076)

**Description:** THIS RESOURCE IS NO LONGER IN SERVICE. Documented on August 18, 2025. Software package developed for the analysis of affinity-based epitranscriptome shotgun sequencing data from MeRIP-seq (maA-seq). It was built on the basis of the exomePeak MATLAB package with new functions for differential analysis of two experimental conditions to unveil the dynamics in post-transcriptional regulation of the RNA methylome. The exomePeak R-package accepts and statistically supports multiple biological replicates, internally removes PCR artifacts and multi-mapping reads, outputs exome-based binding sites (RNA methylation sites) and detects differential post-transcriptional RNA modification sites between two experimental conditions in term of percentage rather the absolute amount.

**Abbreviations:** exomePeak

**Resource Type:** software resource

**Defining Citation:** [PMID:23589649](#)

**Keywords:** r, matlab

**Availability:** THIS RESOURCE IS NO LONGER IN SERVICE

**Resource Name:** ExomePeak

**Resource ID:** SCR\_001076

**Alternate IDs:** OMICS\_00570

**Record Creation Time:** 20220129T080205+0000

**Record Last Update:** 20260801T190122+0000

---

## Ratings and Alerts

No rating or validation information has been found for ExomePeak.

No alerts have been found for ExomePeak.

---

## Data and Source Information

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

---

## Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Li Z, et al. (2025) Metabolite-dependent m6A methylation driven by mechanotransduction-metabolism-epitranscriptomics axis promotes bone development and regeneration. Cell reports, 44(5), 115611.

Cheng Y, et al. (2023) Decoding m6A RNA methylome identifies PRMT6-regulated lipid transport promoting AML stem cell maintenance. Cell stem cell, 30(1), 69.

Wen J, et al. (2018) Zc3h13 Regulates Nuclear RNA m6A Methylation and Mouse Embryonic Stem Cell Self-Renewal. Molecular cell, 69(6), 1028.

Engel M, et al. (2018) The Role of m6A/m-RNA Methylation in Stress Response Regulation. Neuron, 99(2), 389.