

Resource Summary Report

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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: 20260815T182202+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 5 mentions in open access literature.

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

Monteagudo-García Ó, et al. (2026) ZC3H13 Loss Drives Cancer Metastatic Progression by Disrupting m6A RNA Methylation. Cancer research, 86(3), 622.

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.