

Resource Summary Report

Generated by [NIF](#) on Sep 8, 2026

MeTPeak

RRID:SCR_026533

Type: Tool

Proper Citation

MeTPeak (RRID:SCR_026533)

Resource Information

URL: <https://github.com/compgenomics/MeTPeak>

Proper Citation: MeTPeak (RRID:SCR_026533)

Description: Software package for finding the location of m6A sites in MeRIP-seq data.

Resource Type: software resource, software toolkit, source code

Defining Citation: [PMID:27307641](#)

Keywords: finding location of m6A sites, MeRIP-seq data

Funding: Natural Science Foundation of China ;
NCI P30CA54174;
NCI U54 CA113001;
NIGMS R01 GM113245;
NSF

Availability: Free, Available for download, Freely available

Resource Name: MeTPeak

Resource ID: SCR_026533

License: GNU GPL v3

Record Creation Time: 20250307T060316+0000

Record Last Update: 20260905T133525+0000

Ratings and Alerts

No rating or validation information has been found for MeTPeak.

No alerts have been found for MeTPeak.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 11 mentions in open access literature.

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

Chopra A, et al. (2026) The epitranscriptomic m6A RNA modification modulates the synapse in ageing and in a mouse model of synucleinopathy. NPJ Parkinson's disease, 12(1).

Tan Y, et al. (2025) The RNA N6-methyladenosine methylome coordinates long non-coding RNAs to mediate cancer drug resistance by activating PI3K signaling. Cell death & disease, 16(1), 804.

Zhang Y, et al. (2025) M6Allele: a toolkit for detection of allele-specific RNA N6-methyladenosine modifications. GigaScience, 14.

Annamalai K, et al. (2025) Deregulation of m6A-RNA methylation impairs adaptive hypertrophic response and drives maladaptation via mTORC1-S6K1-hyperactivation and autophagy impairment. Cell communication and signaling : CCS, 23(1), 522.

Perlegos AE, et al. (2024) Cell type-specific regulation of m6 A modified RNAs in the aging Drosophila brain. Aging cell, 23(3), e14076.

Liu S, et al. (2024) The RNA N6-Methyladenosine MethylomeCoordinates Long Non-Coding RNAs to MediateCancer Drug Resistance by Activating PI3KSignaling. Research square.

Castro-Hernandez R, et al. (2023) Conserved reduction of m6A RNA modifications during aging and neurodegeneration is linked to changes in synaptic transcripts. Proceedings of the National Academy of Sciences of the United States of America, 120(9), e2204933120.

Le Franc L, et al. (2023) m6A Profile Dynamics Indicates Regulation of Oyster Development by m6A-RNA Epitranscriptomes. Genomics, proteomics & bioinformatics, 21(4), 742.

Zhang ZW, et al. (2023) The role of m6A demethylase FTO in chemotherapy resistance mediating acute myeloid leukemia relapse. Cell death discovery, 9(1), 225.

Su H, et al. (2020) Transcriptome-wide map of m6A circRNAs identified in a rat model of hypoxia mediated pulmonary hypertension. BMC genomics, 21(1), 39.

Yan F, et al. (2018) A dynamic N6-methyladenosine methylome regulates intrinsic and acquired resistance to tyrosine kinase inhibitors. Cell research, 28(11), 1062.