

Resource Summary Report

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

MeRIP-PF

RRID:SCR_010904

Type: Tool

Proper Citation

MeRIP-PF (RRID:SCR_010904)

Resource Information

URL: <http://software.big.ac.cn/MeRIP-PF.html>

Proper Citation: MeRIP-PF (RRID:SCR_010904)

Description: A high-efficiency and easy-to-use analysis pipeline for MeRIP-Seq peak-finding at high resolution, which compares distributions of reads between immunoprecipitation sample and control sample.

Abbreviations: MeRIP-PF

Synonyms: MeRIP-Seq Peak-Finding Program

Resource Type: software resource

Keywords: bio.tools

Resource Name: MeRIP-PF

Resource ID: SCR_010904

Alternate IDs: biotools:merip-pf, OMICS_00571

Alternate URLs: <https://bio.tools/merip-pf>

Record Creation Time: 20220129T080301+0000

Record Last Update: 20260801T190400+0000

Ratings and Alerts

No rating or validation information has been found for MeRIP-PF.

No alerts have been found for MeRIP-PF.

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 [RRID](#) .

Yang Y, et al. (2023) Analysis approaches for the identification and prediction of N6-methyladenosine sites. *Epigenetics*, 18(1), 2158284.

Wang L, et al. (2022) m6A RNA methylation impairs gene expression variability and reproductive thermotolerance in Arabidopsis. *Genome biology*, 23(1), 244.

Liu L, et al. (2020) Bioinformatics approaches for deciphering the epitranscriptome: Recent progress and emerging topics. *Computational and structural biotechnology journal*, 18, 1587.