

Resource Summary Report

Generated by PRECISE-TBI on Jul 31, 2026

MMDiff

RRID:SCR_012692

Type: Tool

Proper Citation

MMDiff (RRID:SCR_012692)

Resource Information

URL: <http://bioconductor.org/packages/release/bioc/html/MMDiff.html>

Proper Citation: MMDiff (RRID:SCR_012692)

Description: Software package that detects statistically significant difference between read enrichment profiles in different ChIP-Seq samples.

Abbreviations: MMDiff

Synonyms: MMDiff - Statistical Testing for ChIP-Seq data sets

Resource Type: software resource

Availability: Free

Resource Name: MMDiff

Resource ID: SCR_012692

Alternate IDs: OMICS_00474

Record Creation Time: 20220129T080311+0000

Record Last Update: 20260725T190739+0000

Ratings and Alerts

No rating or validation information has been found for MMDiff.

No alerts have been found for MMDiff.

Data and Source Information

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Wang C, et al. (2022) Abnormal global alternative RNA splicing in COVID-19 patients. PLoS genetics, 18(4), e1010137.

Nemeth CL, et al. (2020) Neuronal ablation of mt-AspRS in mice induces immune pathway activation prior to severe and progressive cortical and behavioral disruption. Experimental neurology, 326, 113164.

Wong YL, et al. (2019) eIF2B activator prevents neurological defects caused by a chronic integrated stress response. eLife, 8.

Hilton HG, et al. (2019) Single-cell transcriptomics of the naked mole-rat reveals unexpected features of mammalian immunity. PLoS biology, 17(11), e3000528.

Waldron JA, et al. (2019) mRNA structural elements immediately upstream of the start codon dictate dependence upon eIF4A helicase activity. Genome biology, 20(1), 300.

Cartier J, et al. (2018) Investigation into the role of the germline epigenome in the transmission of glucocorticoid-programmed effects across generations. Genome biology, 19(1), 50.

Latos PA, et al. (2015) Fgf and Esrrb integrate epigenetic and transcriptional networks that regulate self-renewal of trophoblast stem cells. Nature communications, 6, 7776.

Modelska A, et al. (2015) The malignant phenotype in breast cancer is driven by eIF4A1-mediated changes in the translational landscape. Cell death & disease, 6(1), e1603.