

Resource Summary Report

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rMAT

RRID:SCR_001583

Type: Tool

Proper Citation

rMAT (RRID:SCR_001583)

Resource Information

URL: <http://www.bioconductor.org/packages/2.4/bioc/html/rMAT.html>

Proper Citation: rMAT (RRID:SCR_001583)

Description: Software package for normalizing and analyzing tiling arrays and ChIP-chip data. It is the R-version of a MAT program.

Resource Type: data analysis software, data processing software, software application, software resource, source code

Defining Citation: [PMID:20089513](#)

Keywords: chip-seq, normalize data, tiling array, mat, r

Availability: Free, Available for download, Freely available

Resource Name: rMAT

Resource ID: SCR_001583

Alternate IDs: OMICS_00810

Alternate URLs: <http://www.rglab.org>

License: Artistic-2.0

Record Creation Time: 20220129T080208+0000

Record Last Update: 20260829T182057+0000

Ratings and Alerts

No rating or validation information has been found for rMAT.

No alerts have been found for rMAT.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 16 mentions in open access literature.

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

Germano DPJ, et al. (2023) Free and Interfacial Boundaries in Individual-Based Models of Multicellular Biological systems. *Bulletin of mathematical biology*, 85(11), 111.

Hanaizi Z, et al. (2023) Considering Global Development? Insights from Applications for FDA Breakthrough Therapy and EMA PRIME Designations. *Therapeutic innovation & regulatory science*, 57(2), 321.

Ye R, et al. (2023) Capture RIC-seq reveals positional rules of PTBP1-associated RNA loops in splicing regulation. *Molecular cell*, 83(8), 1311.

Li Y, et al. (2022) Evaluating the activity of nonsense-mediated RNA decay via Nanopore direct RNA sequencing. *Biochemical and biophysical research communications*, 621, 67.

Carey RM, et al. (2020) The virome of HPV-positive tonsil squamous cell carcinoma and neck metastasis. *Oncotarget*, 11(3), 282.

Matlani M, et al. (2020) Severe vivax malaria trends in the last two years: a study from a tertiary care centre, Delhi, India. *Annals of clinical microbiology and antimicrobials*, 19(1), 49.

Chang EY, et al. (2019) MRE11-RAD50-NBS1 promotes Fanconi Anemia R-loop suppression at transcription-replication conflicts. *Nature communications*, 10(1), 4265.

Chang EY, et al. (2017) RECQ-like helicases Sgs1 and BLM regulate R-loop-associated genome instability. *The Journal of cell biology*, 216(12), 3991.

Rathmann H, et al. (2017) Reconstructing human population history from dental phenotypes. *Scientific reports*, 7(1), 12495.

Kawakami E, et al. (2016) Weighted enrichment method for prediction of transcription regulators from transcriptome and global chromatin immunoprecipitation data. *Nucleic acids research*, 44(11), 5010.

Aristizabal MJ, et al. (2015) The RNAPII-CTD Maintains Genome Integrity through Inhibition of Retrotransposon Gene Expression and Transposition. *PLoS genetics*, 11(10), e1005608.

Lorenzi LE, et al. (2015) Fission yeast Cactin restricts telomere transcription and elongation by controlling Rap1 levels. *The EMBO journal*, 34(1), 115.

Lhoumaud P, et al. (2014) Insulators recruit histone methyltransferase dMes4 to regulate chromatin of flanking genes. *The EMBO journal*, 33(14), 1599.

Kumari M, et al. (2014) Clinical Profile of Plasmodium vivax Malaria in Children and Study of Severity Parameters in relation to Mortality: A Tertiary Care Centre Perspective in Mumbai, India. *Malaria research and treatment*, 2014, 765657.

Stadelmayer B, et al. (2014) Integrator complex regulates NELF-mediated RNA polymerase II pause/release and processivity at coding genes. *Nature communications*, 5, 5531.

Yalcin A, et al. (2013) MeDIP coupled with a promoter tiling array as a platform to investigate global DNA methylation patterns in AML cells. *Leukemia research*, 37(1), 102.