

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 [NIF](#) .

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.