

# Jia Meng

## List of Publications by Year in descending order

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Version: 2024-02-01

100  
papers

3,651  
citations

186265

28  
h-index

149698

56  
g-index

102  
all docs

102  
docs citations

102  
times ranked

4157  
citing authors

#	ARTICLE	IF	CITATIONS
1	Tet1 Is Critical for Neuronal Activity-Regulated Gene Expression and Memory Extinction. <i>Neuron</i> , 2013, 79, 1109-1122.	8.1	393
2	Epigenetic Priming of Memory Updating during Reconsolidation to Attenuate Remote Fear Memories. <i>Cell</i> , 2014, 156, 261-276.	28.9	318
3	A protocol for RNA methylation differential analysis with MeRIP-Seq data and exomePeak R/Bioconductor package. <i>Methods</i> , 2014, 69, 274-281.	3.8	253
4	m6A-Atlas: a comprehensive knowledgebase for unraveling the <i>N</i> <sup>6</sup> -methyladenosine (m6A) epitranscriptome. <i>Nucleic Acids Research</i> , 2021, 49, D134-D143.	14.5	185
5	WHISTLE: a high-accuracy map of the human <i>N</i> <sup>6</sup> -methyladenosine (m6A) epitranscriptome predicted using a machine learning approach. <i>Nucleic Acids Research</i> , 2019, 47, e41-e41.	14.5	177
6	Exome-based analysis for RNA epigenome sequencing data. <i>Bioinformatics</i> , 2013, 29, 1565-1567.	4.1	139
7	Viral and cellular <i>N</i> <sup>6</sup> -methyladenosine and <i>N</i> <sup>6,2</sup> - <i>O</i> -dimethyladenosine epitranscriptomes in the KSHV life cycle. <i>Nature Microbiology</i> , 2018, 3, 108-120.	13.3	137
8	MeT-DB V2.0: elucidating context-specific functions of <i>N</i> <sup>6</sup> -methyl-adenosine methyltranscriptome. <i>Nucleic Acids Research</i> , 2018, 46, D281-D287.	14.5	115
9	Direct and efficient cellular transformation of primary rat mesenchymal precursor cells by KSHV. <i>Journal of Clinical Investigation</i> , 2012, 122, 1076-1081.	8.2	98
10	Guitar: An R/Bioconductor Package for Gene Annotation Guided Transcriptomic Analysis of RNA-Related Genomic Features. <i>BioMed Research International</i> , 2016, 2016, 1-8.	1.9	95
11	lncRScan-SVM: A Tool for Predicting Long Non-Coding RNAs Using Support Vector Machine. <i>PLoS ONE</i> , 2015, 10, e0139654.	2.5	92
12	Histone deacetylase 3 associates with MeCP2 to regulate FOXO and social behavior. <i>Nature Neuroscience</i> , 2016, 19, 1497-1505.	14.8	88
13	Early remodeling of the neocortex upon episodic memory encoding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 11852-11857.	7.1	86
14	m7GHub: deciphering the location, regulation and pathogenesis of internal mRNA <i>N</i> <sup>7</sup> -methylguanosine (m7G) sites in human. <i>Bioinformatics</i> , 2020, 36, 3528-3536.	4.1	85
15	A novel algorithm for calling mRNA m <sup>6</sup> A peaks by modeling biological variances in MeRIP-seq data. <i>Bioinformatics</i> , 2016, 32, i378-i385.	4.1	81
16	MeTDiff: A Novel Differential RNA Methylation Analysis for MeRIP-Seq Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 526-534.	3.0	79
17	RNA methylation and diseases: experimental results, databases, Web servers and computational models. <i>Briefings in Bioinformatics</i> , 2019, 20, 896-917.	6.5	74
18	RMDisease: a database of genetic variants that affect RNA modifications, with implications for epitranscriptome pathogenesis. <i>Nucleic Acids Research</i> , 2021, 49, D1396-D1404.	14.5	65

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19	MeT-DB: a database of transcriptome methylation in mammalian cells. <i>Nucleic Acids Research</i> , 2015, 43, D197-D203.	14.5	63
20	Attention-based multi-label neural networks for integrated prediction and interpretation of twelve widely occurring RNA modifications. <i>Nature Communications</i> , 2021, 12, 4011.	12.8	61
21	m5C-Atlas: a comprehensive database for decoding and annotating the 5-methylcytosine (m5C) epitranscriptome. <i>Nucleic Acids Research</i> , 2022, 50, D196-D203.	14.5	53
22	Global analysis of N6-methyladenosine functions and its disease association using deep learning and network-based methods. <i>PLoS Computational Biology</i> , 2019, 15, e1006663.	3.2	41
23	QNB: differential RNA methylation analysis for count-based small-sample sequencing data with a quad-negative binomial model. <i>BMC Bioinformatics</i> , 2017, 18, 387.	2.6	40
24	m6A-Driver: Identifying Context-Specific mRNA m6A Methylation-Driven Gene Interaction Networks. <i>PLoS Computational Biology</i> , 2016, 12, e1005287.	3.2	38
25	Bioinformatics approaches for deciphering the epitranscriptome: Recent progress and emerging topics. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1587-1604.	4.1	38
26	FunDMDeep-m6A: identification and prioritization of functional differential m6A methylation genes. <i>Bioinformatics</i> , 2019, 35, i90-i98.	4.1	34
27	ConsRM: collection and large-scale prediction of the evolutionarily conserved RNA methylation sites, with implications for the functional epitranscriptome. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	34
28	DRUM: Inference of Disease-Associated m6A RNA Methylation Sites From a Multi-Layer Heterogeneous Network. <i>Frontiers in Genetics</i> , 2019, 10, 266.	2.3	32
29	m6Acomet: large-scale functional prediction of individual m6A RNA methylation sites from an RNA co-methylation network. <i>BMC Bioinformatics</i> , 2019, 20, 223.	2.6	32
30	m6A Reader: Epitranscriptome Target Prediction and Functional Characterization of N6-Methyladenosine (m6A) Readers. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 741.	3.7	31
31	PIANO: A Web Server for Pseudouridine-Site ( $\hat{\pi}$ ) Identification and Functional Annotation. <i>Frontiers in Genetics</i> , 2020, 11, 88.	2.3	30
32	m5UPred: A Web Server for the Prediction of RNA 5-Methyluridine Sites from Sequences. <i>Molecular Therapy - Nucleic Acids</i> , 2020, 22, 742-747.	5.1	28
33	A Deep Learning method for classification of images RSVP events with EEG data. , 2013, , .		26
34	Decomposition of RNA methylome reveals co-methylation patterns induced by latent enzymatic regulators of the epitranscriptome. <i>Molecular BioSystems</i> , 2015, 11, 262-274.	2.9	26
35	Cancer Progression Prediction Using Gene Interaction Regularized Elastic Net. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017, 14, 145-154.	3.0	25
36	Cortical neurons gradually attain a post-mitotic state. <i>Cell Research</i> , 2016, 26, 1033-1047.	12.0	24

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37	Weakly supervised learning of RNA modifications from low-resolution epitranscriptome data. <i>Bioinformatics</i> , 2021, 37, i222-i230.	4.1	24
38	Hepatitis B Viral Protein HBx and the Molecular Mechanisms Modulating the Hallmarks of Hepatocellular Carcinoma: A Comprehensive Review. <i>Cells</i> , 2022, 11, 741.	4.1	24
39	WITMSG: Large-scale Prediction of Human Intronic m6A RNA Methylation Sites from Sequence and Genomic Features. <i>Current Genomics</i> , 2020, 21, 67-76.	1.6	21
40	Predict Epitranscriptome Targets and Regulatory Functions of N6-Methyladenosine (m6A) Writers and Erasers. <i>Evolutionary Bioinformatics</i> , 2019, 15, 117693431987129.	1.2	19
41	Enrichment constrained time-dependent clustering analysis for finding meaningful temporal transcription modules. <i>Bioinformatics</i> , 2009, 25, 1521-1527.	4.1	18
42	DRME: Count-based differential RNA methylation analysis at small sample size scenario. <i>Analytical Biochemistry</i> , 2016, 499, 15-23.	2.4	18
43	Characterization and Robust Classification of EEG Signal from Image RSVP Events with Independent Time-Frequency Features. <i>PLoS ONE</i> , 2012, 7, e44464.	2.5	17
44	A hierarchical model for clustering m6A methylation peaks in MeRIP-seq data. <i>BMC Genomics</i> , 2016, 17, 520.	2.8	17
45	Topological Characterization of Human and Mouse m <sup>5</sup> C Epitranscriptome Revealed by Bisulfite Sequencing. <i>International Journal of Genomics</i> , 2018, 2018, 1-19.	1.6	17
46	LITHOPHONE: Improving lncRNA Methylation Site Prediction Using an Ensemble Predictor. <i>Frontiers in Genetics</i> , 2020, 11, 545.	2.3	16
47	HEPeak: an HMM-based exome peak-finding package for RNA epigenome sequencing data. <i>BMC Genomics</i> , 2015, 16, S2.	2.8	15
48	m6AmPred: Identifying RNA N6, 2-O-dimethyladenosine (m6Am) sites based on sequence-derived information. <i>Methods</i> , 2021, , .	3.8	15
49	Recent advances in functional annotation and prediction of the epitranscriptome. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 3015-3026.	4.1	13
50	Dynamics of m6A RNA Methylome on the Hallmarks of Hepatocellular Carcinoma. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 642443.	3.7	13
51	Clustering Count-based RNA Methylation Data Using a Nonparametric Generative Model. <i>Current Bioinformatics</i> , 2018, 14, 11-23.	1.5	13
52	A nonparametric Bayesian approach for clustering bisulfate-based DNA methylation profiles. <i>BMC Genomics</i> , 2012, 13, S20.	2.8	12
53	PSI-MOUSE: Predicting Mouse Pseudouridine Sites From Sequence and Genome-Derived Features. <i>Evolutionary Bioinformatics</i> , 2020, 16, 117693432092575.	1.2	12
54	Spatially Enhanced Differential RNA Methylation Analysis from Affinity-Based Sequencing Data with Hidden Markov Model. <i>BioMed Research International</i> , 2015, 2015, 1-12.	1.9	11

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55	ISGm1A: Integration of Sequence Features and Genomic Features to Improve the Prediction of Human m <sup>1</sup> A RNA Methylation Sites. <i>IEEE Access</i> , 2020, 8, 81971-81977.	4.2	11
56	trumpet: transcriptome-guided quality assessment of m6A-seq data. <i>BMC Bioinformatics</i> , 2018, 19, 260.	2.6	10
57	Enhancing Epitranscriptome Module Detection from m6A-Seq Data Using Threshold-Based Measurement Weighting Strategy. <i>BioMed Research International</i> , 2018, 2018, 1-15.	1.9	10
58	MetaTX: deciphering the distribution of mRNA-related features in the presence of isoform ambiguity, with applications in epitranscriptome analysis. <i>Bioinformatics</i> , 2021, 37, 1285-1291.	4.1	10
59	WHISTLE: A Functionally Annotated High-Accuracy Map of Human m6A Epitranscriptome. <i>Methods in Molecular Biology</i> , 2021, 2284, 519-529.	0.9	9
60	A bag-of-words model for task-load prediction from EEG in complex environments. , 2013, , .		8
61	Bayesian non-negative factor analysis for reconstructing transcription factor mediated regulatory networks. <i>Proteome Science</i> , 2011, 9, S9.	1.7	7
62	Uncover cooperative gene regulations by microRNAs and transcription factors in glioblastoma using a nonnegative hybrid factor model. , 2011, , .		7
63	Understanding MicroRNA Regulation: A computational perspective. <i>IEEE Signal Processing Magazine</i> , 2012, 29, 77-88.	5.6	7
64	FBCwPlaid: A Functional Biclustering Analysis of Epi-Transcriptome Profiling Data Via a Weighted Plaid Model. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 1640-1650.	3.0	7
65	Uncovering Transcriptional Regulatory Networks by Sparse Bayesian Factor Model. <i>Eurasip Journal on Advances in Signal Processing</i> , 2010, 2010, .	1.7	6
66	Unveiling the dynamics in RNA epigenetic regulations. , 2013, , .		6
67	REW-ISA: unveiling local functional blocks in epi-transcriptome profiling data via an RNA expression-weighted iterative signature algorithm. <i>BMC Bioinformatics</i> , 2020, 21, 447.	2.6	5
68	Autophagy Induced by Simian Retrovirus Infection Controls Viral Replication and Apoptosis of Jurkat T Lymphocytes. <i>Viruses</i> , 2020, 12, 381.	3.3	4
69	Funm6AViewer: a web server and R package for functional analysis of context-specific m6A RNA methylation. <i>Bioinformatics</i> , 2021, 37, 4277-4279.	4.1	4
70	Classification of Imperfectly Time-Locked Image RSVP Events with EEG Device. <i>Neuroinformatics</i> , 2014, 12, 261-275.	2.8	3
71	Functional examination of novel kisspeptin phosphinic peptides. <i>PLoS ONE</i> , 2018, 13, e0195089.	2.5	3
72	Prediction of RNA Methylation Status From Gene Expression Data Using Classification and Regression Methods. <i>Evolutionary Bioinformatics</i> , 2020, 16, 117693432091570.	1.2	3

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73	Robust inference of the context specific structure and temporal dynamics of gene regulatory network. BMC Genomics, 2010, 11, S11.	2.8	2
74	Uncovering transcriptional regulatory networks by sparse Bayesian factor model. , 2010, , .		2
75	Clustering DNA methylation expressions using nonparametric beta mixture model. , 2011, , .		2
76	Detecting differentially methylated mRNA from MeRIP-Seq with likelihood ratio test. , 2014, , .		2
77	MeT-DB V2.0: Elucidating Context-Specific Functions of N6-Methyl-Adenosine Methyltranscriptome. Methods in Molecular Biology, 2021, 2284, 507-518.	0.9	2
78	Biclustering of Time Series Microarray Data. Methods in Molecular Biology, 2012, 802, 87-100.	0.9	2
79	Exploiting correlated discriminant features in time frequency and space for characterization and robust classification of image RSVP events with EEG data. , 2012, , .		1
80	UNCOVER CONTEXT-SPECIFIC GENE REGULATION BY TRANSCRIPTION FACTORS AND microRNAs USING BAYESIAN SPARSE NONNEGATIVE FACTOR REGRESSION. Journal of Biological Systems, 2012, 20, 377-402.	1.4	1
81	Classification of EEG recordings without perfectly time-locked events. , 2012, , .		1
82	Novel numerical and computational techniques for remote sensor based monitoring of freshwater quality. , 2016, , .		1
83	An iterative time windowed signature algorithm for time-dependent transcription module discovery. , 2008, 2008, 1-4.		0
84	An Iterated Conditional Modes solution for sparse Bayesian factor modeling of transcriptional regulatory networks. , 2010, , .		0
85	An iterated conditional mode solution for Bayesian factor modeling of transcriptional regulatory networks. , 2010, , .		0
86	Bayesian non-negative factor analysis for reconstructing transcriptional regulatory network. , 2011, , .		0
87	Uncover transcription factor mediated gene regulations using Bayesian nonnegative factor models. , 2011, , .		0
88	Basis-expansion factor models for uncovering transcription factor regulatory network. , 2012, , .		0
89	Differential analysis of rna methylation sequencing data. , 2013, , .		0
90	Integration of gene expression, genome wide DNA methylation, and gene networks for clinical outcome prediction in ovarian cancer. , 2013, , .		0

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91	An HMM-based Exome Peak-finding package for RNA epigenome sequencing data. , 2013, , .		0
92	Differential analysis of RNA methylome with improved spatial resolution. , 2014, , .		0
93	Sketching the distribution of transcriptomic features on RNA transcripts with Travis coordinates. , 2015, , .		0
94	Modeling of replicates variances for detecting RNA methylation site in MERIP-SEQ data. , 2015, , .		0
95	A Machine Learning Approach for Uncovering N6-methyladenosine-Disease Association. , 2018, , .		0
96	Detection of m6A RNA Methylation in Nanopore Sequencing Data Using Support Vector Machine. , 2019, , .		0
97	Prediction of m6A Reader Substrate Sites Using Deep Convolutional and Recurrent Neural Network. , 2021, , .		0
98	A Meta-analysis: Evaluating the Effect of METTL3/METTL14 on m6A Level Based on Knockdown Samples. , 2021, , .		0
99	An Improved Algorithm for Estimating the Distribution of RNA-related Genomic Features. , 2020, , .		0
100	Gibbs Sampling Based Banoian Biclustering of Gene Expression Data. , 2020, , .		0