# Jia Meng

List of Publications by Year
in descending order

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|---|---|---|---|
| 100<br>papers | 3,651<br>citations | 186265<br>28<br>h-index | 149698<br>56<br>g-index |
| 102<br>all docs | 102<br>docs citations | 102<br>times ranked | 4157<br>citing authors |

| # | Article | IF | Citations |
|---|---------|----|-----------|
| 1 | FBCwPlaid: A Functional Biclustering Analysis of Epi-Transcriptome Profiling Data Via a Weighted Plaid Model. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 1640-1650. | 3.0 | 7 |
| 2 | m5C-Atlas: a comprehensive database for decoding and annotating the 5-methylcytosine (m5C) epitranscriptome. Nucleic Acids Research, 2022, 50, D196-D203. | 14.5 | 53 |
| 3 | Hepatitis B Viral Protein HBx and the Molecular Mechanisms Modulating the Hallmarks of Hepatocellular Carcinoma: A Comprehensive Review. Cells, 2022, 11, 741. | 4.1 | 24 |
| 4 | RMDisease: a database of genetic variants that affect RNA modifications, with implications for epitranscriptome pathogenesis. Nucleic Acids Research, 2021, 49, D1396-D1404. | 14.5 | 65 |
| 5 | MetaTX: deciphering the distribution of mRNA-related features in the presence of isoform ambiguity, with applications in epitranscriptome analysis. Bioinformatics, 2021, 37, 1285-1291. | 4.1 | 10 |
| 6 | m6A-Atlas: a comprehensive knowledgebase for unraveling the *N*6-methyladenosine (m6A) epitranscriptome. Nucleic Acids Research, 2021, 49, D134-D143. | 14.5 | 185 |
| 7 | WHISTLE: A Functionally Annotated High-Accuracy Map of Human m6A Epitranscriptome. Methods in Molecular Biology, 2021, 2284, 519-529. | 0.9 | 9 |
| 8 | Recent advances in functional annotation and prediction of the epitranscriptome. Computational and Structural Biotechnology Journal, 2021, 19, 3015-3026. | 4.1 | 13 |
| 9 | MeT-DB V2.0: Elucidating Context-Specific Functions of N6-Methyl-Adenosine Methyltranscriptome. Methods in Molecular Biology, 2021, 2284, 507-518. | 0.9 | 2 |
| 10 | Dynamics of m6A RNA Methylome on the Hallmarks of Hepatocellular Carcinoma. Frontiers in Cell and Developmental Biology, 2021, 9, 642443. | 3.7 | 13 |
| 11 | Funm6AViewer: a web server and R package for functional analysis of context-specific m6A RNA methylation. Bioinformatics, 2021, 37, 4277-4279. | 4.1 | 4 |
| 12 | ConsRM: collection and large-scale prediction of the evolutionarily conserved RNA methylation sites, with implications for the functional epitranscriptome. Briefings in Bioinformatics, 2021, 22, . | 6.5 | 34 |
| 13 | Attention-based multi-label neural networks for integrated prediction and interpretation of twelve widely occurring RNA modifications. Nature Communications, 2021, 12, 4011. | 12.8 | 61 |
| 14 | Prediction of m6A Reader Substrate Sites Using Deep Convolutional and Recurrent Neural Network. , 2021, , . |  | 0 |
| 15 | Weakly supervised learning of RNA modifications from low-resolution epitranscriptome data. Bioinformatics, 2021, 37, i222-i230. | 4.1 | 24 |
| 16 | A Meta-analysis: Evaluating the Effect of METTL3/METTL14 on m6A Level Based on Knockdown Samples. , 2021, , . |  | 0 |
| 17 | m6AmPred: Identifying RNA N6, 2â€²-O-dimethyladenosine (m6Am) sites based on sequence-derived information. Methods, 2021, , . | 3.8 | 15 |
| 18 | REW-ISA: unveiling local functional blocks in epi-transcriptome profiling data via an RNA expression-weighted iterative signature algorithm. BMC Bioinformatics, 2020, 21, 447. | 2.6 | 5 |

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| 19 | Bioinformatics approaches for deciphering the epitranscriptome: Recent progress and emerging topics. Computational and Structural Biotechnology Journal, 2020, 18, 1587-1604. | 4.1 | 38 |
| 20 | PSI-MOUSE: Predicting Mouse Pseudouridine Sites From Sequence and Genome-Derived Features. Evolutionary Bioinformatics, 2020, 16, 117693432092575. | 1.2 | 12 |
| 21 | ISGm1A: Integration of Sequence Features and Genomic Features to Improve the Prediction of Human m$_1$A RNA Methylation Sites. IEEE Access, 2020, 8, 81971-81977. | 4.2 | 11 |
| 22 | Prediction of RNA Methylation Status From Gene Expression Data Using Classification and Regression Methods. Evolutionary Bioinformatics, 2020, 16, 117693432091570. | 1.2 | 3 |
| 23 | m6A Reader: Epitranscriptome Target Prediction and Functional Characterization of N6-Methyladenosine (m6A) Readers. Frontiers in Cell and Developmental Biology, 2020, 8, 741. | 3.7 | 31 |
| 24 | m5UPred: A Web Server for the Prediction of RNA 5-Methyluridine Sites from Sequences. Molecular Therapy - Nucleic Acids, 2020, 22, 742-747. | 5.1 | 28 |
| 25 | LITHOPHONE: Improving lncRNA Methylation Site Prediction Using an Ensemble Predictor. Frontiers in Genetics, 2020, 11, 545. | 2.3 | 16 |
| 26 | m7GHub: deciphering the location, regulation and pathogenesis of internal mRNA N7-methylguanosine (m7G) sites in human. Bioinformatics, 2020, 36, 3528-3536. | 4.1 | 85 |
| 27 | PIANO: A Web Server for Pseudouridine-Site (Î¨) Identification and Functional Annotation. Frontiers in Genetics, 2020, 11, 88. | 2.3 | 30 |
| 28 | Autophagy Induced by Simian Retrovirus Infection Controls Viral Replication and Apoptosis of Jurkat T Lymphocytes. Viruses, 2020, 12, 381. | 3.3 | 4 |
| 29 | WITMSG: Large-scale Prediction of Human Intronic m6A RNA Methylation Sites from Sequence and Genomic Features. Current Genomics, 2020, 21, 67-76. | 1.6 | 21 |
| 30 | An Improved Algorithm for Estimating the Distribution of RNA-related Genomic Features. , 2020, , . |  | 0 |
| 31 | Gibbs Sampling Based Banoian Biclustering of Gene Expression Data. , 2020, , . |  | 0 |
| 32 | FunDMDeep-m6A: identification and prioritization of functional differential m6A methylation genes. Bioinformatics, 2019, 35, i90-i98. | 4.1 | 34 |
| 33 | Predict Epitranscriptome Targets and Regulatory Functions of N6-Methyladenosine (m6A) Writers and Erasers. Evolutionary Bioinformatics, 2019, 15, 117693431987129. | 1.2 | 19 |
| 34 | DRUM: Inference of Disease-Associated m6A RNA Methylation Sites From a Multi-Layer Heterogeneous Network. Frontiers in Genetics, 2019, 10, 266. | 2.3 | 32 |
| 35 | m6Acomet: large-scale functional prediction of individual m6A RNA methylation sites from an RNA co-methylation network. BMC Bioinformatics, 2019, 20, 223. | 2.6 | 32 |
| 36 | WHISTLE: a high-accuracy map of the human N6-methyladenosine (m6A) epitranscriptome predicted using a machine learning approach. Nucleic Acids Research, 2019, 47, e41-e41. | 14.5 | 177 |

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|---|---------|-----|-----------|
| 37 | Detection of m6A RNA Methylation in Nanopore Sequencing Data Using Support Vector Machine. , 2019, , . | | 0 |
| 38 | Global analysis of N6-methyladenosine functions and its disease association using deep learning and network-based methods. PLoS Computational Biology, 2019, 15, e1006663. | 3.2 | 41 |
| 39 | RNA methylation and diseases: experimental results, databases, Web servers and computational models. Briefings in Bioinformatics, 2019, 20, 896-917. | 6.5 | 74 |
| 40 | MeTDiff: A Novel Differential RNA Methylation Analysis for MeRIP-Seq Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 526-534. | 3.0 | 79 |
| 41 | MeT-DB V2.0: elucidating context-specific functions of N6-methyl-adenosine methyltranscriptome. Nucleic Acids Research, 2018, 46, D281-D287. | 14.5 | 115 |
| 42 | Viral and cellular N6-methyladenosine and N6,2â€²-O-dimethyladenosine epitranscriptomes in the KSHV life cycle. Nature Microbiology, 2018, 3, 108-120. | 13.3 | 137 |
| 43 | A Machine Learning Approach for Uncovering N6-methyladenosine-Disease Association. , 2018, , . | | 0 |
| 44 | trumpet: transcriptome-guided quality assessment of m6A-seq data. BMC Bioinformatics, 2018, 19, 260. | 2.6 | 10 |
| 45 | Topological Characterization of Human and Mouse m$^5$C Epitranscriptome Revealed by Bisulfite Sequencing. International Journal of Genomics, 2018, 2018, 1-19. | 1.6 | 17 |
| 46 | Functional examination of novel kisspeptin phosphinic peptides. PLoS ONE, 2018, 13, e0195089. | 2.5 | 3 |
| 47 | Enhancing Epitranscriptome Module Detection from m6A-Seq Data Using Threshold-Based Measurement Weighting Strategy. BioMed Research International, 2018, 2018, 1-15. | 1.9 | 10 |
| 48 | Clustering Count-based RNA Methylation Data Using a Nonparametric Generative Model. Current Bioinformatics, 2018, 14, 11-23. | 1.5 | 13 |
| 49 | Cancer Progression Prediction Using Gene Interaction Regularized Elastic Net. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 145-154. | 3.0 | 25 |
| 50 | QNB: differential RNA methylation analysis for count-based small-sample sequencing data with a quad-negative binomial model. BMC Bioinformatics, 2017, 18, 387. | 2.6 | 40 |
| 51 | Guitar: An R/Bioconductor Package for Gene Annotation Guided Transcriptomic Analysis of RNA-Related Genomic Features. BioMed Research International, 2016, 2016, 1-8. | 1.9 | 95 |
| 52 | m6A-Driver: Identifying Context-Specific mRNA m6A Methylation-Driven Gene Interaction Networks. PLoS Computational Biology, 2016, 12, e1005287. | 3.2 | 38 |
| 53 | A hierarchical model for clustering m6A methylation peaks in MeRIP-seq data. BMC Genomics, 2016, 17, 520. | 2.8 | 17 |
| 54 | Novel numerical and computational techniques for remote sensor based monitoring of freshwater quality. , 2016, , . | | 1 |

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| 55 | Histone deacetylase 3 associates with MeCP2 to regulate FOXO and social behavior. Nature Neuroscience, 2016, 19, 1497-1505. | 14.8 | 88 |
| 56 | Cortical neurons gradually attain a post-mitotic state. Cell Research, 2016, 26, 1033-1047. | 12.0 | 24 |
| 57 | A novel algorithm for calling mRNA m 6 A peaks by modeling biological variances in MeRIP-seq data. Bioinformatics, 2016, 32, i378-i385. | 4.1 | 81 |
| 58 | DRME: Count-based differential RNA methylation analysis at small sample size scenario. Analytical Biochemistry, 2016, 499, 15-23. | 2.4 | 18 |
| 59 | HEPeak: an HMM-based exome peak-finding package for RNA epigenome sequencing data. BMC Genomics, 2015, 16, S2. | 2.8 | 15 |
| 60 | lncRScan-SVM: A Tool for Predicting Long Non-Coding RNAs Using Support Vector Machine. PLoS ONE, 2015, 10, e0139654. | 2.5 | 92 |
| 61 | Spatially Enhanced Differential RNA Methylation Analysis from Affinity-Based Sequencing Data with Hidden Markov Model. BioMed Research International, 2015, 2015, 1-12. | 1.9 | 11 |
| 62 | Sketching the distribution of transcriptomic features on RNA transcripts with Travis coordinates. , 2015, , . | | 0 |
| 63 | MeT-DB: a database of transcriptome methylation in mammalian cells. Nucleic Acids Research, 2015, 43, D197-D203. | 14.5 | 63 |
| 64 | Modeling of replicates variances for detecting RNA methylation site in MERIP-SEQ data. , 2015, , . | | 0 |
| 65 | Decomposition of RNA methylome reveals co-methylation patterns induced by latent enzymatic regulators of the epitranscriptome. Molecular BioSystems, 2015, 11, 262-274. | 2.9 | 26 |
| 66 | Detecting differentially methylated mRNA from MeRIP-Seq with likelihood ratio test. , 2014, , . | | 2 |
| 67 | Epigenetic Priming of Memory Updating during Reconsolidation to Attenuate Remote Fear Memories. Cell, 2014, 156, 261-276. | 28.9 | 318 |
| 68 | A protocol for RNA methylation differential analysis with MeRIP-Seq data and exomePeak R/Bioconductor package. Methods, 2014, 69, 274-281. | 3.8 | 253 |
| 69 | Early remodeling of the neocortex upon episodic memory encoding. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 11852-11857. | 7.1 | 86 |
| 70 | Classification of Imperfectly Time-Locked Image RSVP Events with EEG Device. Neuroinformatics, 2014, 12, 261-275. | 2.8 | 3 |
| 71 | Differential analysis of RNA methylome with improved spatial resolution. , 2014, , . | | 0 |
| 72 | Tet1 Is Critical for Neuronal Activity-Regulated Gene Expression and Memory Extinction. Neuron, 2013, 79, 1109-1122. | 8.1 | 393 |

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| 73 | Differential analysis of rna methylation sequencing data. , 2013, , . | | 0 |
| 74 | Integration of gene expression, genome wide DNA methylation, and gene networks for clinical outcome prediction in ovarian cancer. , 2013, , . | | 0 |
| 75 | An HMM-based Exome Peak-finding package for RNA epigenome sequencing data. , 2013, , . | | 0 |
| 76 | A Deep Learning method for classification of images RSVP events with EEG data. , 2013, , . | | 26 |
| 77 | Unveiling the dynamics in RNA epigenetic regulations. , 2013, , . | | 6 |
| 78 | Exome-based analysis for RNA epigenome sequencing data. Bioinformatics, 2013, 29, 1565-1567. | 4.1 | 139 |
| 79 | A bag-of-words model for task-load prediction from EEG in complex environments. , 2013, , . | | 8 |
| 80 | Basis-expansion factor models for uncovering transcription factor regulatory network. , 2012, , . | | 0 |
| 81 | Exploiting correlated discriminant features in time frequency and space for characterization and robust classification of image RSVP events with EEG data. , 2012, , . | | 1 |
| 82 | 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 |
| 83 | Classification of EEG recordings without perfectly time-locked events. , 2012, , . | | 1 |
| 84 | Understanding MicroRNA Regulation: A computational perspective. IEEE Signal Processing Magazine, 2012, 29, 77-88. | 5.6 | 7 |
| 85 | Characterization and Robust Classification of EEG Signal from Image RSVP Events with Independent Time-Frequency Features. PLoS ONE, 2012, 7, e44464. | 2.5 | 17 |
| 86 | A nonparametric Bayesian approach for clustering bisulfate-based DNA methylation profiles. BMC Genomics, 2012, 13, S20. | 2.8 | 12 |
| 87 | Biclustering of Time Series Microarray Data. Methods in Molecular Biology, 2012, 802, 87-100. | 0.9 | 2 |
| 88 | Direct and efficient cellular transformation of primary rat mesenchymal precursor cells by KSHV. Journal of Clinical Investigation, 2012, 122, 1076-1081. | 8.2 | 98 |
| 89 | Bayesian non-negative factor analysis for reconstructing transcriptional regulatory network. , 2011, , . | | 0 |
| 90 | Clustering DNA methylation expressions using nonparametric beta mixture model. , 2011, , . | | 2 |

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| 91 | Uncover transcription factor mediated gene regulations using Bayesian nonnegative factor models. , 2011, , . | | 0 |
| 92 | Bayesian non-negative factor analysis for reconstructing transcription factor mediated regulatory networks. Proteome Science, 2011, 9, S9. | 1.7 | 7 |
| 93 | Uncover cooperative gene regulations by microRNAs and transcription factors in glioblastoma using a nonnegative hybrid factor model. , 2011, , . | | 7 |
| 94 | Uncovering Transcriptional Regulatory Networks by Sparse Bayesian Factor Model. Eurasip Journal on Advances in Signal Processing, 2010, 2010, . | 1.7 | 6 |
| 95 | Robust inference of the context specific structure and temporal dynamics of gene regulatory network. BMC Genomics, 2010, 11, S11. | 2.8 | 2 |
| 96 | Uncovering transcriptional regulatory networks by sparse Bayesian factor model. , 2010, , . | | 2 |
| 97 | An Iterated Conditional Modes solution for sparse Bayesian factor modeling of transcriptional regulatory networks. , 2010, , . | | 0 |
| 98 | An iterated conditional mode solution for Bayesian factor modeling of transcriptional regulatory networks. , 2010, , . | | 0 |
| 99 | Enrichment constrained time-dependent clustering analysis for finding meaningful temporal transcription modules. Bioinformatics, 2009, 25, 1521-1527. | 4.1 | 18 |
| 100 | An iterative time windowed signature algorith for time-dependent transcription module discovery. , 2008, 2008, 1-4. | | 0 |