

List of Publications by Year in
Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

81 papers	2,177 citations	22 h-index	45 g-index
102 ext. papers	3,075 ext. citations	7.9 avg, IF	5.09 L-index

#	Paper	IF	Citations
81	m5C-Atlas: a comprehensive database for decoding and annotating the 5-methylcytosine (m5C) epitranscriptome.. <i>Nucleic Acids Research</i> , 2022 , 50, D196-D203	20.1	3
80	Hepatitis B Viral Protein HBx and the Molecular Mechanisms Modulating the Hallmarks of Hepatocellular Carcinoma: A Comprehensive Review.. <i>Cells</i> , 2022 , 11,	7.9	3
79	m6AmPred: Identifying RNA N6, 2FO-dimethyladenosine (mA) sites based on sequence-derived information. <i>Methods</i> , 2021 ,	4.6	4
78	Dynamics of m6A RNA Methylome on the Hallmarks of Hepatocellular Carcinoma. <i>Frontiers in Cell and Developmental Biology</i> , 2021 , 9, 642443	5.7	3
77	Funm6AViewer: a web server and R package for functional analysis of context-specific m6A RNA methylation. <i>Bioinformatics</i> , 2021 ,	7.2	2
76	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,	13.4	10
75	Attention-based multi-label neural networks for integrated prediction and interpretation of twelve widely occurring RNA modifications. <i>Nature Communications</i> , 2021 , 12, 4011	17.4	10
74	Weakly supervised learning of RNA modifications from low-resolution epitranscriptome data. <i>Bioinformatics</i> , 2021 , 37, i222-i230	7.2	5
73	RMDisease: a database of genetic variants that affect RNA modifications, with implications for epitranscriptome pathogenesis. <i>Nucleic Acids Research</i> , 2021 , 49, D1396-D1404	20.1	31
72	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	7.2	2
71	m6A-Atlas: a comprehensive knowledgebase for unraveling the N6-methyladenosine (m6A) epitranscriptome. <i>Nucleic Acids Research</i> , 2021 , 49, D134-D143	20.1	52
70	WHISTLE: A Functionally Annotated High-Accuracy Map of Human mA Epitranscriptome. <i>Methods in Molecular Biology</i> , 2021 , 2284, 519-529	1.4	3
69	Recent advances in functional annotation and prediction of the epitranscriptome. <i>Computational and Structural Biotechnology Journal</i> , 2021 , 19, 3015-3026	6.8	2
68	MeT-DB V2.0: Elucidating Context-Specific Functions of N6-Methyl-Adenosine Methyltranscriptome. <i>Methods in Molecular Biology</i> , 2021 , 2284, 507-518	1.4	
67	FBCwPlaid: A Functional Bi-clustering Analysis of Epi-transcriptome Profiling Data via a Weighted Plaid Model. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021 , PP,	3	3
66	m5UPred: A Web Server for the Prediction of RNA 5-Methyluridine Sites from Sequences. <i>Molecular Therapy - Nucleic Acids</i> , 2020 , 22, 742-747	10.7	8
65	LITHOPHONE: Improving lncRNA Methylation Site Prediction Using an Ensemble Predictor. <i>Frontiers in Genetics</i> , 2020 , 11, 545	4.5	8

64	m7GHub: deciphering the location, regulation and pathogenesis of internal mRNA N7-methylguanosine (m7G) sites in human. <i>Bioinformatics</i> , 2020 , 36, 3528-3536	7.2	31
63	PIANO: A Web Server for Pseudouridine-Site (U) Identification and Functional Annotation. <i>Frontiers in Genetics</i> , 2020 , 11, 88	4.5	18
62	WITMSG: Large-scale Prediction of Human Intronic mA RNA Methylation Sites from Sequence and Genomic Features. <i>Current Genomics</i> , 2020 , 21, 67-76	2.6	12
61	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	3.6	4
60	Bioinformatics approaches for deciphering the epitranscriptome: Recent progress and emerging topics. <i>Computational and Structural Biotechnology Journal</i> , 2020 , 18, 1587-1604	6.8	18
59	PSI-MOUSE: Predicting Mouse Pseudouridine Sites From Sequence and Genome-Derived Features. <i>Evolutionary Bioinformatics</i> , 2020 , 16, 1176934320925752	1.9	8
58	ISGM1A: Integration of Sequence Features and Genomic Features to Improve the Prediction of Human m1A RNA Methylation Sites. <i>IEEE Access</i> , 2020 , 8, 81971-81977	3.5	4
57	Prediction of RNA Methylation Status From Gene Expression Data Using Classification and Regression Methods. <i>Evolutionary Bioinformatics</i> , 2020 , 16, 1176934320915707	1.9	2
56	mA Reader: Epitranscriptome Target Prediction and Functional Characterization of -Methyladenosine (mA) Readers. <i>Frontiers in Cell and Developmental Biology</i> , 2020 , 8, 741	5.7	8
55	Autophagy Induced by Simian Retrovirus Infection Controls Viral Replication and Apoptosis of Jurkat T Lymphocytes. <i>Viruses</i> , 2020 , 12,	6.2	1
54	Predict Epitranscriptome Targets and Regulatory Functions of -Methyladenosine (mA) Writers and Erasers. <i>Evolutionary Bioinformatics</i> , 2019 , 15, 1176934319871290	1.9	13
53	DRUM: Inference of Disease-Associated mA RNA Methylation Sites From a Multi-Layer Heterogeneous Network. <i>Frontiers in Genetics</i> , 2019 , 10, 266	4.5	18
52	m6Acomet: large-scale functional prediction of individual mA RNA methylation sites from an RNA co-methylation network. <i>BMC Bioinformatics</i> , 2019 , 20, 223	3.6	17
51	FunDMDeep-m6A: identification and prioritization of functional differential m6A methylation genes. <i>Bioinformatics</i> , 2019 , 35, i90-i98	7.2	16
50	WHISTLE: a high-accuracy map of the human N6-methyladenosine (m6A) epitranscriptome predicted using a machine learning approach. <i>Nucleic Acids Research</i> , 2019 , 47, e41	20.1	106
49	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	5	25
48	RNA methylation and diseases: experimental results, databases, Web servers and computational models. <i>Briefings in Bioinformatics</i> , 2019 , 20, 896-917	13.4	44
47	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	45

46	MeT-DB V2.0: elucidating context-specific functions of N6-methyl-adenosine methyltranscriptome. <i>Nucleic Acids Research</i> , 2018 , 46, D281-D287	20.1	73
45	trumpet: transcriptome-guided quality assessment of mA-seq data. <i>BMC Bioinformatics</i> , 2018 , 19, 260	3.6	7
44	Topological Characterization of Human and Mouse mC Epitranscriptome Revealed by Bisulfite Sequencing. <i>International Journal of Genomics</i> , 2018 , 2018, 1351964	2.5	11
43	Functional examination of novel kisspeptin phosphinic peptides. <i>PLoS ONE</i> , 2018 , 13, e0195089	3.7	2
42	Enhancing Epitranscriptome Module Detection from mA-Seq Data Using Threshold-Based Measurement Weighting Strategy. <i>BioMed Research International</i> , 2018 , 2018, 2075173	3	6
41	Clustering Count-based RNA Methylation Data Using a Nonparametric Generative Model. <i>Current Bioinformatics</i> , 2018 , 14, 11-23	4.7	10
40	Viral and cellular N-methyladenosine and N,2FO-dimethyladenosine epitranscriptomes in the KSHV life cycle. <i>Nature Microbiology</i> , 2018 , 3, 108-120	26.6	83
39	Cancer Progression Prediction Using Gene Interaction Regularized Elastic Net. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017 , 14, 145-154	3	17
38	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	3.6	25
37	Novel numerical and computational techniques for remote sensor based monitoring of freshwater quality 2016 ,		1
36	Histone deacetylase 3 associates with MeCP2 to regulate FOXO and social behavior. <i>Nature Neuroscience</i> , 2016 , 19, 1497-1505	25.5	65
35	Cortical neurons gradually attain a post-mitotic state. <i>Cell Research</i> , 2016 , 26, 1033-47	24.7	10
34	A novel algorithm for calling mRNA m6A peaks by modeling biological variances in MeRIP-seq data. <i>Bioinformatics</i> , 2016 , 32, i378-i385	7.2	48
33	DRME: Count-based differential RNA methylation analysis at small sample size scenario. <i>Analytical Biochemistry</i> , 2016 , 499, 15-23	3.1	12
32	Guitar: An R/Bioconductor Package for Gene Annotation Guided Transcriptomic Analysis of RNA-Related Genomic Features. <i>BioMed Research International</i> , 2016 , 2016, 8367534	3	48
31	m6A-Driver: Identifying Context-Specific mRNA m6A Methylation-Driven Gene Interaction Networks. <i>PLoS Computational Biology</i> , 2016 , 12, e1005287	5	25
30	A hierarchical model for clustering m(6)A methylation peaks in MeRIP-seq data. <i>BMC Genomics</i> , 2016 , 17 Suppl 7, 520	4.5	12
29	MeT-DB: a database of transcriptome methylation in mammalian cells. <i>Nucleic Acids Research</i> , 2015 , 43, D197-203	20.1	43

28	Decomposition of RNA methylome reveals co-methylation patterns induced by latent enzymatic regulators of the epitranscriptome. <i>Molecular BioSystems</i> , 2015 , 11, 262-74		20
27	HEPeak: an HMM-based exome peak-finding package for RNA epigenome sequencing data. <i>BMC Genomics</i> , 2015 , 16 Suppl 4, S2	4.5	9
26	lncRScan-SVM: A Tool for Predicting Long Non-Coding RNAs Using Support Vector Machine. <i>PLoS ONE</i> , 2015 , 10, e0139654	3.7	61
25	Spatially Enhanced Differential RNA Methylation Analysis from Affinity-Based Sequencing Data with Hidden Markov Model. <i>BioMed Research International</i> , 2015 , 2015, 852070	3	7
24	Epigenetic priming of memory updating during reconsolidation to attenuate remote fear memories. <i>Cell</i> , 2014 , 156, 261-76	56.2	246
23	A protocol for RNA methylation differential analysis with MeRIP-Seq data and exomePeak R/Bioconductor package. <i>Methods</i> , 2014 , 69, 274-81	4.6	132
22	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, 11852-7	11.5	60
21	Classification of imperfectly time-locked image RSVP events with EEG device. <i>Neuroinformatics</i> , 2014 , 12, 261-75	3.2	3
20	Detecting differentially methylated mRNA from MeRIP-Seq with likelihood ratio test 2014 ,		2
19	Tet1 is critical for neuronal activity-regulated gene expression and memory extinction. <i>Neuron</i> , 2013 , 79, 1109-1122	13.9	337
18	A Deep Learning method for classification of images RSVP events with EEG data 2013 ,		21
17	Unveiling the dynamics in RNA epigenetic regulations 2013 ,		3
16	Exome-based analysis for RNA epigenome sequencing data. <i>Bioinformatics</i> , 2013 , 29, 1565-7	7.2	83
15	A bag-of-words model for task-load prediction from EEG in complex environments 2013 ,		7
14	Classification of EEG recordings without perfectly time-locked events 2012 ,		1
13	. <i>IEEE Signal Processing Magazine</i> , 2012 , 29, 77-88	9.4	6
12	Characterization and robust classification of EEG signal from image RSVP events with independent time-frequency features. <i>PLoS ONE</i> , 2012 , 7, e44464	3.7	15
11	A nonparametric Bayesian approach for clustering bisulfate-based DNA methylation profiles. <i>BMC Genomics</i> , 2012 , 13 Suppl 6, S20	4.5	7

10	UNCOVER CONTEXT-SPECIFIC GENE REGULATION BY TRANSCRIPTION FACTORS AND microRNAs USING BAYESIAN SPARSE NONNEGATIVE FACTOR REGRESSION. <i>Journal of Biological Systems</i> , 2012 , 20, 377-402	1.6	1
9	Direct and efficient cellular transformation of primary rat mesenchymal precursor cells by KSHV. <i>Journal of Clinical Investigation</i> , 2012 , 122, 1076-81	15.9	82
8	Biclustering of time series microarray data. <i>Methods in Molecular Biology</i> , 2012 , 802, 87-100	1.4	2
7	Bayesian non-negative factor analysis for reconstructing transcription factor mediated regulatory networks. <i>Proteome Science</i> , 2011 , 9 Suppl 1, S9	2.6	7
6	Clustering DNA methylation expressions using nonparametric beta mixture model 2011 ,		2
5	Uncover cooperative gene regulations by microRNAs and transcription factors in glioblastoma using a nonnegative hybrid factor model 2011 ,		6
4	Uncovering Transcriptional Regulatory Networks by Sparse Bayesian Factor Model. <i>Eurasip Journal on Advances in Signal Processing</i> , 2010 , 2010,	1.9	2
3	Robust inference of the context specific structure and temporal dynamics of gene regulatory network. <i>BMC Genomics</i> , 2010 , 11 Suppl 3, S11	4.5	1
2	Enrichment constrained time-dependent clustering analysis for finding meaningful temporal transcription modules. <i>Bioinformatics</i> , 2009 , 25, 1521-7	7.2	17
1	An Iterative Time Windowed Signature Algorithm for Time Dependent Transcription Module Discovery 2008 , 2008, 1-4		