

# Hui Yang

## List of Publications by Citations

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23  
papers

1,580  
citations

15  
h-index

23  
g-index

23  
ext. papers

1,886  
ext. citations

6.4  
avg, IF

5.33  
L-index

#	Paper	IF	Citations
23	iRNA-PseColl: Identifying the Occurrence Sites of Different RNA Modifications by Incorporating Collective Effects of Nucleotides into PseKNC. <i>Molecular Therapy - Nucleic Acids</i> , <b>2017</b> , 7, 155-163	10.7	228
22	iDNA4mC: identifying DNA N4-methylcytosine sites based on nucleotide chemical properties. <i>Bioinformatics</i> , <b>2017</b> , 33, 3518-3523	7.2	198
21	iRNA-AI: identifying the adenosine to inosine editing sites in RNA sequences. <i>Oncotarget</i> , <b>2017</b> , 8, 4208-4217	3.5	191
20	iDNA6mA-PseKNC: Identifying DNA N-methyladenosine sites by incorporating nucleotide physicochemical properties into PseKNC. <i>Genomics</i> , <b>2019</b> , 111, 96-102	4.3	190
19	iRNA-3typeA: Identifying Three Types of Modification at RNA's Adenosine Sites. <i>Molecular Therapy - Nucleic Acids</i> , <b>2018</b> , 11, 468-474	10.7	135
18	iRSpot-Pse6NC: Identifying recombination spots in by incorporating hexamer composition into general PseKNC. <i>International Journal of Biological Sciences</i> , <b>2018</b> , 14, 883-891	11.2	130
17	iRNA-2OM: A Sequence-Based Predictor for Identifying 2aO-Methylation Sites in Homo sapiens. <i>Journal of Computational Biology</i> , <b>2018</b> , 25, 1266-1277	1.7	103
16	A comparison and assessment of computational method for identifying recombination hotspots in <i>Saccharomyces cerevisiae</i> . <i>Briefings in Bioinformatics</i> , <b>2020</b> , 21, 1568-1580	13.4	60
15	A computational platform to identify origins of replication sites in eukaryotes. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22, 1940-1950	13.4	56
14	iRNAD: a computational tool for identifying D modification sites in RNA sequence. <i>Bioinformatics</i> , <b>2019</b> , 35, 4922-4929	7.2	53
13	iDNA-MS: An Integrated Computational Tool for Detecting DNA Modification Sites in Multiple Genomes. <i>IScience</i> , <b>2020</b> , 23, 100991	6.1	51
12	Pro54DB: a database for experimentally verified sigma-54 promoters. <i>Bioinformatics</i> , <b>2017</b> , 33, 467-469	7.2	47
11	Recent Advances in Conotoxin Classification by Using Machine Learning Methods. <i>Molecules</i> , <b>2017</b> , 22,	4.8	40
10	iCarPS: a computational tool for identifying protein carbonylation sites by novel encoded features. <i>Bioinformatics</i> , <b>2021</b> , 37, 171-177	7.2	28
9	Predicting Preference of Transcription Factors for Methylated DNA Using Sequence Information. <i>Molecular Therapy - Nucleic Acids</i> , <b>2020</b> , 22, 1043-1050	10.7	16
8	Prediction of N7-methylguanosine sites in human RNA based on optimal sequence features. <i>Genomics</i> , <b>2020</b> , 112, 4342-4347	4.3	15
7	PPD: A Manually Curated Database for Experimentally Verified Prokaryotic Promoters. <i>Journal of Molecular Biology</i> , <b>2021</b> , 433, 166860	6.5	14

6	Identification of D Modification Sites by Integrating Heterogeneous Features in. <i>Molecules</i> , <b>2019</b> , 24,	4.8	9
5	Screening of Prospective Plant Compounds as H1R and CL1R Inhibitors and Its Antiallergic Efficacy through Molecular Docking Approach. <i>Computational and Mathematical Methods in Medicine</i> , <b>2021</b> , 2021, 1-9	2.8	8
4	Advances in mapping the epigenetic modifications of 5-methylcytosine (5mC), N6-methyladenine (6mA), and N4-methylcytosine (4mC). <i>Biotechnology and Bioengineering</i> , <b>2021</b> , 118, 4204-4216	4.9	4
3	Identification of Potential Inhibitors against SARS-Cov-2 using Computational Drug Repurposing Study. <i>Current Bioinformatics</i> , <b>2021</b> , 16,	4.7	2
2	Risk prediction of diabetes and pre-diabetes based on physical examination data.. <i>Mathematical Biosciences and Engineering</i> , <b>2022</b> , 19, 3597-3608	2.1	1
1	A Brief Survey for MicroRNA Precursor Identification Using Machine Learning Methods. <i>Current Genomics</i> , <b>2020</b> , 21, 11-25	2.6	1