Hui Yang

List of Publications by Year in Descending Order

23	1,580	15	23
papers	citations	h-index	g-index
23	1,886	6.4	5.33
ext. papers	ext. citations	avg, IF	L-index

#	Paper	IF	Citations
23	Risk prediction of diabetes and pre-diabetes based on physical examination data.. *Mathematical Biosciences and Engineering*, **2022**, 19, 3597-3608	2.1	1
22	PPD: A Manually Curated Database for Experimentally Verified Prokaryotic Promoters. *Journal of Molecular Biology*, **2021**, 433, 166860	6.5	14
21	Identification of Potential Inhibitors against SARS-Cov-2 using Computational Drug Repurposing Study. *Current Bioinformatics*, **2021**, 16,	4.7	2
20	A computational platform to identify origins of replication sites in eukaryotes. *Briefings in Bioinformatics*, **2021**, 22, 1940-1950	13.4	56
19	iCarPS: a computational tool for identifying protein carbonylation sites by novel encoded features. *Bioinformatics*, **2021**, 37, 171-177	7.2	28
18	Screening of Prospective Plant Compounds as H1R and CL1R Inhibitors and Its Antiallergic Efficacy through Molecular Docking Approach. *Computational and Mathematical Methods in Medicine*, **2021**, 2021, 1-9	2.8	8
17	Advances in mapping the epigenetic modifications of 5-methylcytosine (5mC), N6-methyladenine (6mA), and N4-methylcytosine (4mC). *Biotechnology and Bioengineering*, **2021**, 118, 4204-4216	4.9	4
16	iDNA-MS: An Integrated Computational Tool for Detecting DNA Modification Sites in Multiple Genomes. *IScience*, **2020**, 23, 100991	6.1	51
15	A Brief Survey for MicroRNA Precursor Identification Using Machine Learning Methods. *Current Genomics*, **2020**, 21, 11-25	2.6	1
14	Predicting Preference of Transcription Factors for Methylated DNA Using Sequence Information. *Molecular Therapy - Nucleic Acids*, **2020**, 22, 1043-1050	10.7	16
13	Prediction of N7-methylguanosine sites in human RNA based on optimal sequence features. *Genomics*, **2020**, 112, 4342-4347	4.3	15
12	A comparison and assessment of computational method for identifying recombination hotspots in Saccharomyces cerevisiae. *Briefings in Bioinformatics*, **2020**, 21, 1568-1580	13.4	60
11	Identification of D Modification Sites by Integrating Heterogeneous Features in. *Molecules*, **2019**, 24,	4.8	9
10	iRNAD: a computational tool for identifying D modification sites in RNA sequence. *Bioinformatics*, **2019**, 35, 4922-4929	7.2	53
9	iDNA6mA-PseKNC: Identifying DNA N-methyladenosine sites by incorporating nucleotide physicochemical properties into PseKNC. *Genomics*, **2019**, 111, 96-102	4.3	190
8	iRSpot-Pse6NC: Identifying recombination spots in by incorporating hexamer composition into general PseKNC. *International Journal of Biological Sciences*, **2018**, 14, 883-891	11.2	130
7	iRNA-2OM: A Sequence-Based Predictor for Identifying 2ʹO-Methylation Sites in Homo sapiens. *Journal of Computational Biology*, **2018**, 25, 1266-1277	1.7	103

LIST OF PUBLICATIONS

6	iRNA-3typeA: Identifying Three Types of Modification at RNA's Adenosine Sites. *Molecular Therapy - Nucleic Acids*, **2018**, 11, 468-474	10.7	135
5	iRNA-PseColl: Identifying the Occurrence Sites of Different RNA Modifications by Incorporating Collective Effects of Nucleotides into PseKNC. *Molecular Therapy - Nucleic Acids*, **2017**, 7, 155-163	10.7	228
4	iRNA-AI: identifying the adenosine to inosine editing sites in RNA sequences. *Oncotarget*, **2017**, 8, 4208-4217	5.3	191
3	iDNA4mC: identifying DNA N4-methylcytosine sites based on nucleotide chemical properties. *Bioinformatics*, **2017**, 33, 3518-3523	7.2	198
2	Recent Advances in Conotoxin Classification by Using Machine Learning Methods. *Molecules*, **2017**, 22,	4.8	40
1	Pro54DB: a database for experimentally verified sigma-54 promoters. *Bioinformatics*, **2017**, 33, 467-469	7.2	47