Zhao-Chun Xu

List of Publications by Year
in descending order

30 papers	1,421 citations	516710 16 h-index	454955 30 g-index
30 all docs	30 docs citations	30 times ranked	987 citing authors

#	Article	IF	Citations
1	iPTM-mLys: identifying multiple lysine PTM sites and their different types. Bioinformatics, 2016, 32, 3116-3123.	4.1	236
2	iRNAm5C-PseDNC: identifying RNA 5-methylcytosine sites by incorporating physical-chemical properties into pseudo dinucleotide composition. Oncotarget, 2017, 8, 41178-41188.	1.8	191
3	iHyd-PseCp: Identify hydroxyproline and hydroxylysine in proteins by incorporating sequence-coupled effects into general PseAAC. Oncotarget, 2016, 7, 44310-44321.	1.8	150
4	iPhos-PseEn: Identifying phosphorylation sites in proteins by fusing different pseudo components into an ensemble classifier. Oncotarget, 2016, 7, 51270-51283.	1.8	142
5	iKcr-PseEns: Identify lysine crotonylation sites in histone proteins with pseudo components and ensemble classifier. Genomics, 2018, 110, 239-246.	2.9	127
6	iRNAD: a computational tool for identifying D modification sites in RNA sequence. Bioinformatics, 2019, 35, 4922-4929.	4.1	75
7	iPSW(2L)-PseKNC: A two-layer predictor for identifying promoters and their strength by hybrid features via pseudo K-tuple nucleotide composition. Genomics, 2019, 111, 1785-1793.	2.9	60
8	iCarPS: a computational tool for identifying protein carbonylation sites by novel encoded features. Bioinformatics, 2021, 37, 171-177.	4.1	59
9	Single-cell transcriptome and TCR profiling reveal activated and expanded T cell populations in Parkinson's disease. Cell Discovery, 2021, 7, 52.	6.7	51
10	Comprehensive analysis of TCR repertoire in COVID-19 using single cell sequencing. Genomics, 2021, 113, 456-462.	2.9	47
11	DLpTCR: an ensemble deep learning framework for predicting immunogenic peptide recognized by T cell receptor. Briefings in Bioinformatics, 2021, 22, .	6.5	43
12	Single cell RNA and immune repertoire profiling of COVID-19 patients reveal novel neutralizing antibody. Protein and Cell, 2021, 12, 751-755.	11.0	32
13	Global characterization of B cell receptor repertoire in COVID-19 patients by single-cell V(D)J sequencing. Briefings in Bioinformatics, 2021, 22, .	6.5	28
14	iPromoter-5mC: A Novel Fusion Decision Predictor for the Identification of 5-Methylcytosine Sites in Genome-Wide DNA Promoters. Frontiers in Cell and Developmental Biology, 2020, 8, 614.	3.7	27
15	iSS-PC: Identifying Splicing Sites via Physical-Chemical Properties Using Deep Sparse Auto-Encoder. Scientific Reports, 2017, 7, 8222.	3.3	21
16	N439K Variant in Spike Protein Alter the Infection Efficiency and Antigenicity of SARS-CoV-2 Based on Molecular Dynamics Simulation. Frontiers in Cell and Developmental Biology, 2021, 9, 697035.	3.7	19
17	Identification of D Modification Sites by Integrating Heterogeneous Features in Saccharomyces cerevisiae. Molecules, 2019, 24, 380.	3.8	15
18	Alternative splicing associated with cancer stemness in kidney renal clear cell carcinoma. BMC Cancer, 2021, 21, 703.	2.6	15

#	Article	IF	Citations
19	Identification of potential vaccine targets for COVID‑19 by combining single‑cell and bulk TCR sequencing. Clinical and Translational Medicine, 2021, 11, e430.	4.0	12
20	A pan-cancer analysis of alternative splicing of splicing factors in 6904 patients. Oncogene, 2021, 40, 5441-5450.	5.9	12
21	iDHSs-PseTNC: Identifying DNase I Hypersensitive Sites with Pseuo Trinucleotide Component by Deep Sparse Auto-encoder. Letters in Organic Chemistry, 2017, 14, .	0.5	12
22	OUP accepted manuscript. Briefings in Bioinformatics, 2022, , .	6.5	11
23	Identifying Acetylation Protein by Fusing Its PseAAC and Functional Domain Annotation. Frontiers in Bioengineering and Biotechnology, 2019, 7, 311.	4.1	10
24	Comprehensive Analysis of Copy Number Variations in Kidney Cancer by Single-Cell Exome Sequencing. Frontiers in Genetics, 2019, 10, 1379.	2.3	9
25	Comprehensive analysis of partial methylation domains in colorectal cancer based on single-cell methylation profiles. Briefings in Bioinformatics, 2021, 22, .	6.5	7
26	PAI-SAE: Predicting Adenosine To Inosine Editing Sites Based On Hybrid Features By Using Spare Auto-Encoder. IOP Conference Series: Earth and Environmental Science, 2018, 170, 052018.	0.3	3
27	iPTT(2‑L)-CNN: A Two-Layer Predictor for Identifying Promoters and Their Types in Plant Genomes by Convolutional Neural Network. Computational and Mathematical Methods in Medicine, 2021, 2021, 1-9.	1.3	3
28	MutCov: A pipeline for evaluating the effect of mutations in spike protein on infectivity and antigenicity of SARS-CoV-2. Computers in Biology and Medicine, 2022, 145, 105509.	7.0	2
29	iRSpotH-TNCPseAAC: Identifying Recombination Spots in Human by Using Pseudo Trinucleotide Composition With an Ensemble of Support Vector Machine Classifiers. Letters in Organic Chemistry, 2017, 14, .	0.5	1
30	iAI-DSAE: A Computational Method for Adenosine to Inosine Editing Site Prediction. Letters in Organic Chemistry, 2019, 16, 347-355.	0.5	1