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	OUP accepted manuscript. Briefings in Bioinformatics, 2022, , .	6.5	11
2	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
3	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
4	iCarPS: a computational tool for identifying protein carbonylation sites by novel encoded features. Bioinformatics, 2021, 37, 171-177.	4.1	59
5	iPTT(2â€‰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
6	Comprehensive analysis of TCR repertoire in COVID-19 using single cell sequencing. Genomics, 2021, 113, 456-462.	2.9	47
7	Identification of potential vaccine targets for COVIDâ€19 by combining singleâ€cell and bulk TCR sequencing. Clinical and Translational Medicine, 2021, 11, e430.	4.0	12
8	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
9	Alternative splicing associated with cancer stemness in kidney renal clear cell carcinoma. BMC Cancer, 2021, 21, 703.	2.6	15
10	A pan-cancer analysis of alternative splicing of splicing factors in 6904 patients. Oncogene, 2021, 40, 5441-5450.	5.9	12
11	Single-cell transcriptome and TCR profiling reveal activated and expanded T cell populations in Parkinsonâ€™s disease. Cell Discovery, 2021, 7, 52.	6.7	51
12	Comprehensive analysis of partial methylation domains in colorectal cancer based on single-cell methylation profiles. Briefings in Bioinformatics, 2021, 22, .	6.5	7
13	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
14	DLpTCR: an ensemble deep learning framework for predicting immunogenic peptide recognized by T cell receptor. Briefings in Bioinformatics, 2021, 22, .	6.5	43
15	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
16	Identification of D Modification Sites by Integrating Heterogeneous Features in Saccharomyces cerevisiae. Molecules, 2019, 24, 380.	3.8	15
17	iRNAD: a computational tool for identifying D modification sites in RNA sequence. Bioinformatics, 2019, 35, 4922-4929.	4.1	75
18	Identifying Acetylation Protein by Fusing Its PseAAC and Functional Domain Annotation. Frontiers in Bioengineering and Biotechnology, 2019, 7, 311.	4.1	10

#	Article	IF	Citations
19	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
20	Comprehensive Analysis of Copy Number Variations in Kidney Cancer by Single-Cell Exome Sequencing. Frontiers in Genetics, 2019, 10, 1379.	2.3	9
21	iAI-DSAE: A Computational Method for Adenosine to Inosine Editing Site Prediction. Letters in Organic Chemistry, 2019, 16, 347-355.	0.5	1
22	iKcr-PseEns: Identify lysine crotonylation sites in histone proteins with pseudo components and ensemble classifier. Genomics, 2018, 110, 239-246.	2.9	127
23	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
24	iSS-PC: Identifying Splicing Sites via Physical-Chemical Properties Using Deep Sparse Auto-Encoder. Scientific Reports, 2017, 7, 8222.	3.3	21
25	iRNAm5C-PseDNC: identifying RNA 5-methylcytosine sites by incorporating physical-chemical properties into pseudo dinucleotide composition. Oncotarget, 2017, 8, 41178-41188.	1.8	191
26	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
27	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
28	iHyd-PseCp: Identify hydroxyproline and hydroxylysine in proteins by incorporating sequence-coupled effects into general PseAAC. Oncotarget, 2016, 7, 44310-44321.	1.8	150
29	iPTM-mLys: identifying multiple lysine PTM sites and their different types. Bioinformatics, 2016, 32, 3116-3123.	4.1	236
30	iPhos-PseEn: Identifying phosphorylation sites in proteins by fusing different pseudo components into an ensemble classifier. Oncotarget, 2016, 7, 51270-51283.	1.8	142