

Gang Xu

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9738607/publications.pdf>

Version: 2024-02-01

18
papers

429
citations

933447

10
h-index

940533

16
g-index

22
all docs

22
docs citations

22
times ranked

622
citing authors

#	ARTICLE	IF	CITATIONS
1	POSTAR2: deciphering the post-transcriptional regulatory logics. <i>Nucleic Acids Research</i> , 2019, 47, D203-D211.	14.5	145
2	OPUS-TASS: a protein backbone torsion angles and secondary structure predictor based on ensemble neural networks. <i>Bioinformatics</i> , 2020, 36, 5021-5026.	4.1	42
3	The acclimation of <i>Chlorella</i> to high-level nitrite for potential application in biological NOx removal from industrial flue gases. <i>Journal of Plant Physiology</i> , 2016, 195, 73-79.	3.5	33
4	Automatic deep learning-based colorectal adenoma detection system and its similarities with pathologists. <i>BMJ Open</i> , 2020, 10, e036423.	1.9	32
5	<i>Arabidopsis</i> ALA1 and ALA2 Mediate RNAi-Based Antiviral Immunity. <i>Frontiers in Plant Science</i> , 2017, 8, 422.	3.6	27
6	OPUS-DOSP: A Distance- and Orientation-Dependent All-Atom Potential Derived from Side-Chain Packing. <i>Journal of Molecular Biology</i> , 2017, 429, 3113-3120.	4.2	26
7	OPUS-Rota3: Improving Protein Side-Chain Modeling by Deep Neural Networks and Ensemble Methods. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 6691-6697.	5.4	21
8	<i>Arabidopsis</i> ENOR3 regulates RNAi-mediated antiviral defense. <i>Journal of Genetics and Genomics</i> , 2018, 45, 33-40.	3.9	20
9	OPUS-Rota2: An Improved Fast and Accurate Side-Chain Modeling Method. <i>Journal of Chemical Theory and Computation</i> , 2019, 15, 5154-5160.	5.3	18
10	OPUS-CCSF: A Contact-based scoring function for ranking protein structural models. <i>Protein Science</i> , 2018, 27, 286-292.	7.6	16
11	OPUS-Rota4: a gradient-based protein side-chain modeling framework assisted by deep learning-based predictors. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	12
12	RiboMiner: a toolset for mining multi-dimensional features of the translome with ribosome profiling data. <i>BMC Bioinformatics</i> , 2020, 21, 340.	2.6	10
13	CCG: an integrative resource of cancer protein-coding genes and long noncoding RNAs. <i>Discovery Medicine</i> , 2016, 22, 351-359.	0.5	7
14	OPUS-SSSF: A side-chain-inclusive scoring function for ranking protein structural models. <i>Protein Science</i> , 2019, 28, 1157-1162.	7.6	5
15	OPUS-X: an open-source toolkit for protein torsion angles, secondary structure, solvent accessibility, contact map predictions and 3D folding. <i>Bioinformatics</i> , 2021, 38, 108-114.	4.1	5
16	OUP accepted manuscript. <i>Briefings in Bioinformatics</i> , 2022, , .	6.5	3
17	Identification of the targets of HbEIN3/EILs in genomic wide in <i>Hevea brasiliensis</i> . <i>Bioscience, Biotechnology and Biochemistry</i> , 2019, 83, 1270-1283.	1.3	1
18	Expression of Concern to: OPUS-Rota4: a gradient-based protein side-chain modeling framework assisted by deep learning-based predictors. <i>Briefings in Bioinformatics</i> , 2022, , .	6.5	1