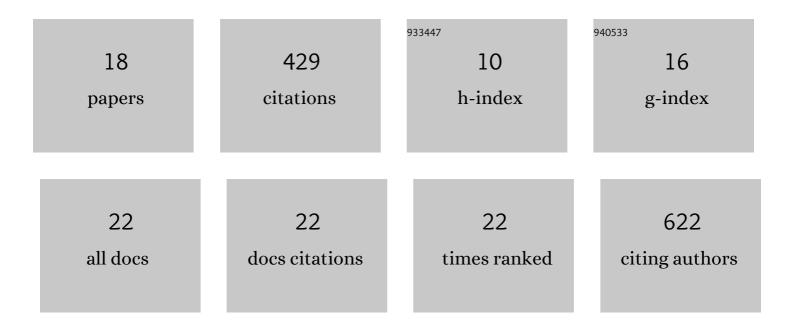


List of Publications by Year in descending order

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