Piotr Lukasiak

List of Publications by Year
in descending order

20 papers	857 citations	1039406 9 h-index	887659 17 g-index
20 all docs	20 docs citations	20 times ranked	1243 citing authors

#	Article	IF	Citations
1	Automated 3D structure composition for large RNAs. Nucleic Acids Research, 2012, 40, e112-e112.	6.5	564
2	RNApdbee—a webserver to derive secondary structures from pdb files of knotted and unknotted RNAs. Nucleic Acids Research, 2014, 42, W368-W372.	6.5	61
3	RNA-Puzzles toolkit: a computational resource of RNA 3D structure benchmark datasets, structure manipulation, and evaluation tools. Nucleic Acids Research, 2020, 48, 576-588.	6.5	44
4	Automated 3D RNA Structure Prediction Using the RNAComposer Method for Riboswitches1. Methods in Enzymology, 2015, 553, 3-34.	0.4	34
5	RNAssess—a web server for quality assessment of RNA 3D structures. Nucleic Acids Research, 2015, 43, W502-W506.	6.5	24
6	Application of tabu search strategy for finding low energy structure of protein. Artificial Intelligence in Medicine, 2005, 35, 135-145.	3.8	23
7	RNAlyzer—novel approach for quality analysis of RNA structural models. Nucleic Acids Research, 2013, 41, 5978-5990.	6.5	22
8	SphereGrinder - reference structure-based tool for quality assessment of protein structural models. , 2015, , .		17
9	Some operations research methods for analyzing protein sequences and structures. Annals of Operations Research, 2010, 175, 9-35.	2.6	12
10	Modeling of the catalytic core of Arabidopsis thaliana Dicer-like 4 protein and its complex with double-stranded RNA. Computational Biology and Chemistry, 2017, 66, 44-56.	1.1	12
11	Web and Grid Technologies in Bioinformatics, Computational and Systems Biology: A Review. Current Bioinformatics, 2008, 3, 10-31.	0.7	11
12	Predicting secondary structures of proteins. IEEE Engineering in Medicine and Biology Magazine, 2005, 24, 88-94.	1.1	8
13	Building the library of RNA 3D nucleotide conformations using the clustering approach. International Journal of Applied Mathematics and Computer Science, 2015, 25, 689-700.	1.5	6
14	Virxicon: a lexicon of viral sequences. Bioinformatics, 2021, 36, 5507-5513.	1.8	6
15	GeVaDSs – decision support system for novel Genetic Vaccine development process. BMC Bioinformatics, 2012, 13, 91.	1.2	4
16	Structural alignment of protein descriptors – a combinatorial model. BMC Bioinformatics, 2016, 17, 383.	1.2	4
17	The Influence of Rice Protein, Hemp Protein and Transglutaminase Addition on the Quality of Instant Fried Noodles. Applied Sciences (Switzerland), 2021, 11, 9070.	1.3	4
18	DomGen-Graph based method for protein domain delineation. RAIRO - Operations Research, 2016, 50, 363-374.	1.0	1

#	Article	IF	Citations
19	Recent Advances in Operations Research in Computational Biology, Bioinformatics and Medicine. RAIRO - Operations Research, 2016, 50, 327-330.	1.0	0
20	The correctness of large scale analysis of genomic data. Foundations of Computing and Decision Sciences, 2021, 46, 423-436.	0.5	0