

Piotr Lukasiak

List of Publications by Year in descending order

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20
papers

857
citations

1039406

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887659

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20
all docs

20
docs citations

20
times ranked

1243
citing authors

#	ARTICLE	IF	CITATIONS
1	The Influence of Rice Protein, Hemp Protein and Transglutaminase Addition on the Quality of Instant Fried Noodles. <i>Applied Sciences (Switzerland)</i> , 2021, 11, 9070.	1.3	4
2	Virxicon: a lexicon of viral sequences. <i>Bioinformatics</i> , 2021, 36, 5507-5513.	1.8	6
3	The correctness of large scale analysis of genomic data. <i>Foundations of Computing and Decision Sciences</i> , 2021, 46, 423-436.	0.5	0
4	RNA-Puzzles toolkit: a computational resource of RNA 3D structure benchmark datasets, structure manipulation, and evaluation tools. <i>Nucleic Acids Research</i> , 2020, 48, 576-588.	6.5	44
5	Modeling of the catalytic core of <i>Arabidopsis thaliana</i> Dicer-like 4 protein and its complex with double-stranded RNA. <i>Computational Biology and Chemistry</i> , 2017, 66, 44-56.	1.1	12
6	Recent Advances in Operations Research in Computational Biology, Bioinformatics and Medicine. <i>RAIRO - Operations Research</i> , 2016, 50, 327-330.	1.0	0
7	Structural alignment of protein descriptors – a combinatorial model. <i>BMC Bioinformatics</i> , 2016, 17, 383.	1.2	4
8	DomGen-Graph based method for protein domain delineation. <i>RAIRO - Operations Research</i> , 2016, 50, 363-374.	1.0	1
9	RNAAssess – a web server for quality assessment of RNA 3D structures. <i>Nucleic Acids Research</i> , 2015, 43, W502-W506.	6.5	24
10	SphereGrinder - reference structure-based tool for quality assessment of protein structural models. , 2015, , .		17
11	Building the library of RNA 3D nucleotide conformations using the clustering approach. <i>International Journal of Applied Mathematics and Computer Science</i> , 2015, 25, 689-700.	1.5	6
12	Automated 3D RNA Structure Prediction Using the RNAComposer Method for Riboswitches1. <i>Methods in Enzymology</i> , 2015, 553, 3-34.	0.4	34
13	RNApdb – a webserver to derive secondary structures from pdb files of knotted and unknotted RNAs. <i>Nucleic Acids Research</i> , 2014, 42, W368-W372.	6.5	61
14	RNAlyzer – novel approach for quality analysis of RNA structural models. <i>Nucleic Acids Research</i> , 2013, 41, 5978-5990.	6.5	22
15	Automated 3D structure composition for large RNAs. <i>Nucleic Acids Research</i> , 2012, 40, e112-e112.	6.5	564
16	GeVaDSs – decision support system for novel Genetic Vaccine development process. <i>BMC Bioinformatics</i> , 2012, 13, 91.	1.2	4
17	Some operations research methods for analyzing protein sequences and structures. <i>Annals of Operations Research</i> , 2010, 175, 9-35.	2.6	12
18	Web and Grid Technologies in Bioinformatics, Computational and Systems Biology: A Review. <i>Current Bioinformatics</i> , 2008, 3, 10-31.	0.7	11

#	ARTICLE	IF	CITATIONS
19	Application of tabu search strategy for finding low energy structure of protein. Artificial Intelligence in Medicine, 2005, 35, 135-145.	3.8	23
20	Predicting secondary structures of proteins. IEEE Engineering in Medicine and Biology Magazine, 2005, 24, 88-94.	1.1	8