

Maciej Antczak

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4942767/publications.pdf>

Version: 2024-02-01

24
papers

1,455
citations

687363

13
h-index

642732

23
g-index

26
all docs

26
docs citations

26
times ranked

1603
citing authors

#	ARTICLE	IF	CITATIONS
1	Automated 3D structure composition for large RNAs. <i>Nucleic Acids Research</i> , 2012, 40, e112-e112.	14.5	564
2	RNA-Puzzles Round III: 3D RNA structure prediction of five riboswitches and one ribozyme. <i>Rna</i> , 2017, 23, 655-672.	3.5	158
3	New functionality of RNAComposer: application to shape the axis of miR160 precursor structure. <i>Acta Biochimica Polonica</i> , 2017, 63, 737-744.	0.5	112
4	RNA-Puzzles Round IV: 3D structure predictions of four ribozymes and two aptamers. <i>Rna</i> , 2020, 26, 982-995.	3.5	100
5	A Survey on Online Judge Systems and Their Applications. <i>ACM Computing Surveys</i> , 2019, 51, 1-34.	23.0	99
6	RNApdbee 2.0: multifunctional tool for RNA structure annotation. <i>Nucleic Acids Research</i> , 2018, 46, W30-W35.	14.5	81
7	RNApdbee – a webserver to derive secondary structures from pdb files of knotted and unknotted RNAs. <i>Nucleic Acids Research</i> , 2014, 42, W368-W372.	14.5	61
8	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.	14.5	44
9	Automated 3D RNA Structure Prediction Using the RNAComposer Method for Riboswitches1. <i>Methods in Enzymology</i> , 2015, 553, 3-34.	1.0	34
10	New in silico approach to assessing RNA secondary structures with non-canonical base pairs. <i>BMC Bioinformatics</i> , 2015, 16, 276.	2.6	31
11	New algorithms to represent complex pseudoknotted RNA structures in dot-bracket notation. <i>Bioinformatics</i> , 2018, 34, 1304-1312.	4.1	29
12	RNAAssess – a web server for quality assessment of RNA 3D structures. <i>Nucleic Acids Research</i> , 2015, 43, W502-W506.	14.5	24
13	RNAlyzer – novel approach for quality analysis of RNA structural models. <i>Nucleic Acids Research</i> , 2013, 41, 5978-5990.	14.5	22
14	Entanglements of structure elements revealed in RNA 3D models. <i>Nucleic Acids Research</i> , 2021, 49, 9625-9632.	14.5	13
15	RNA solo: a repository of cleaned PDB-derived RNA 3D structures. <i>Bioinformatics</i> , 2022, 38, 3668-3670.	4.1	13
16	RNAfitme: a webserver for modeling nucleobase and nucleoside residue conformation in fixed-backbone RNA structures. <i>BMC Bioinformatics</i> , 2018, 19, 304.	2.6	12
17	Evaluation of the stereochemical quality of predicted RNA 3D models in the RNA-Puzzles submissions. <i>Rna</i> , 2022, 28, 250-262.	3.5	12
18	RNAvista: a webserver to assess RNA secondary structures with non-canonical base pairs. <i>Bioinformatics</i> , 2019, 35, 152-155.	4.1	11

#	ARTICLE	IF	CITATIONS
19	RNAloops: a database of RNA multiloops. <i>Bioinformatics</i> , 2022, 38, 4200-4205.	4.1	8
20	Optil.io: Cloud Based Platform For Solving Optimization Problems Using Crowdsourcing Approach. , 2016, , .		7
21	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
22	RNAspider: a webserver to analyze entanglements in RNA 3D structures. <i>Nucleic Acids Research</i> , 2022, 50, W663-W669.	14.5	6
23	Structural alignment of protein descriptors â€“ a combinatorial model. <i>BMC Bioinformatics</i> , 2016, 17, 383.	2.6	4
24	High-order statistical compressor for long-term storage of DNA sequencing data. <i>RAIRO - Operations Research</i> , 2016, 50, 351-361.	1.8	2