Marcin Magnus

List of Publications by Year
in descending order

17 papers	996 citations	759233 12 h-index	940533 16 g-index
22 all docs	22 docs citations	22 times ranked	1346 citing authors

#	Article	IF	Citations
1	rna-tools.online: a Swiss army knife for RNA 3D structure modeling workflow. Nucleic Acids Research, 2022, 50, W657-W662.	14.5	4
2	RNA-Puzzles toolkit: a computational resource of RNA 3D structure benchmark datasets, structure manipulation, and evaluation tools. Nucleic Acids Research, 2020, 48, 576-588.	14.5	44
3	RNA-Puzzles Round IV: 3D structure predictions of four ribozymes and two aptamers. Rna, 2020, 26, 982-995.	3.5	100
4	Rearrangements within the U6 snRNA Core during the Transition between the Two Catalytic Steps of Splicing. Molecular Cell, 2019, 75, 538-548.e3.	9.7	17
5	RNA 3D structure prediction guided by independent folding of homologous sequences. BMC Bioinformatics, 2019, 20, 512.	2.6	21
6	RNA-Puzzles Round III: 3D RNA structure prediction of five riboswitches and one ribozyme. Rna, 2017, 23, 655-672.	3.5	158
7	RNArchitecture: a database and a classification system of RNA families, with a focus on structural information. Nucleic Acids Research, 2017, 46, D202-D205.	14.5	31
8	SimRNAweb: a web server for RNA 3D structure modeling with optional restraints. Nucleic Acids Research, 2016, 44, W315-W319.	14.5	112
9	Modeling of Protein–RNA Complex Structures Using Computational Docking Methods. Methods in Molecular Biology, 2016, 1414, 353-372.	0.9	9
10	RNA 3D Structure Modeling by Combination of Template-Based Method ModeRNA, Template-Free Folding with SimRNA, and Refinement with QRNAS. Methods in Molecular Biology, 2016, 1490, 217-235.	0.9	13
11	NPDock: a web server for protein–nucleic acid docking. Nucleic Acids Research, 2015, 43, W425-W430.	14.5	180
12	<i>RNA-Puzzles</i> Round II: assessment of RNA structure prediction programs applied to three large RNA structures. Rna, 2015, 21, 1066-1084.	3.5	161
13	Computational modeling of RNA 3D structures, with the aid of experimental restraints. RNA Biology, 2014, 11, 522-536.	3.1	39
14	Computational modeling of protein–RNA complex structures. Methods, 2014, 65, 310-319.	3.8	27
15	Structural bioinformatics of the human spliceosomal proteome. Nucleic Acids Research, 2012, 40, 7046-7065.	14.5	40
16	MetaLocGramN: A meta-predictor of protein subcellular localization for Gram-negative bacteria. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2012, 1824, 1425-1433.	2.3	26
17	Structures of MicroRNA Precursors. , 2008, , 1-16.		8