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List of Publications by Year in descending order

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

#	Article	IF	CITATIONS
1	NPDock: a web server for protein–nucleic acid docking. Nucleic Acids Research, 2015, 43, W425-W430.	14.5	180
2	<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
3	RNA-Puzzles Round III: 3D RNA structure prediction of five riboswitches and one ribozyme. Rna, 2017, 23, 655-672.	3.5	158
4	SimRNAweb: a web server for RNA 3D structure modeling with optional restraints. Nucleic Acids Research, 2016, 44, W315-W319.	14.5	112
5	RNA-Puzzles Round IV: 3D structure predictions of four ribozymes and two aptamers. Rna, 2020, 26, 982-995.	3.5	100
6	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
7	Structural bioinformatics of the human spliceosomal proteome. Nucleic Acids Research, 2012, 40, 7046-7065.	14.5	40
8	Computational modeling of RNA 3D structures, with the aid of experimental restraints. RNA Biology, 2014, 11, 522-536.	3.1	39
9	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
10	Computational modeling of protein–RNA complex structures. Methods, 2014, 65, 310-319.	3.8	27
11	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
12	RNA 3D structure prediction guided by independent folding of homologous sequences. BMC Bioinformatics, 2019, 20, 512.	2.6	21
13	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
14	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
15	Modeling of Protein–RNA Complex Structures Using Computational Docking Methods. Methods in Molecular Biology, 2016, 1414, 353-372.	0.9	9
16	Structures of MicroRNA Precursors. , 2008, , 1-16.		8
17	rna-tools.online: a Swiss army knife for RNA 3D structure modeling workflow. Nucleic Acids Research, 2022, 50, W657-W662.	14.5	4