

Marta Szachniuk

List of Publications by Year in descending order

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Version: 2024-02-01

51
papers

2,056
citations

430874

18
h-index

265206

42
g-index

53
all docs

53
docs citations

53
times ranked

2052
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	<i>RNA-Puzzles</i> Round II: assessment of RNA structure prediction programs applied to three large RNA structures. <i>Rna</i> , 2015, 21, 1066-1084.	3.5	161
3	RNA-Puzzles Round III: 3D RNA structure prediction of five riboswitches and one ribozyme. <i>Rna</i> , 2017, 23, 655-672.	3.5	158
4	RNA FRABASE 2.0: an advanced web-accessible database with the capacity to search the three-dimensional fragments within RNA structures. <i>BMC Bioinformatics</i> , 2010, 11, 231.	2.6	130
5	Automated RNA 3D Structure Prediction with RNAComposer. <i>Methods in Molecular Biology</i> , 2016, 1490, 199-215.	0.9	118
6	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
7	RNA-Puzzles Round IV: 3D structure predictions of four ribozymes and two aptamers. <i>Rna</i> , 2020, 26, 982-995.	3.5	100
8	RNApdbee 2.0: multifunctional tool for RNA structure annotation. <i>Nucleic Acids Research</i> , 2018, 46, W30-W35.	14.5	81
9	RNA FRABASE version 1.0: an engine with a database to search for the three-dimensional fragments within RNA structures. <i>Nucleic Acids Research</i> , 2008, 36, D386-D391.	14.5	78
10	RNApdbeeâ€”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
11	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
12	Sorting signal targeting mRNA into hepatic extracellular vesicles. <i>RNA Biology</i> , 2014, 11, 836-844.	3.1	42
13	MCQ4Structures to compute similarity of molecule structures. <i>Central European Journal of Operations Research</i> , 2014, 22, 457-473.	1.8	33
14	New in silico approach to assessing RNA secondary structures with non-canonical base pairs. <i>BMC Bioinformatics</i> , 2015, 16, 276.	2.6	31
15	New algorithms to represent complex pseudoknotted RNA structures in dot-bracket notation. <i>Bioinformatics</i> , 2018, 34, 1304-1312.	4.1	29
16	RNAAssessâ€”a web server for quality assessment of RNA 3D structures. <i>Nucleic Acids Research</i> , 2015, 43, W502-W506.	14.5	24
17	RNAlyzerâ€”novel approach for quality analysis of RNA structural models. <i>Nucleic Acids Research</i> , 2013, 41, 5978-5990.	14.5	22
18	Topology-based classification of tetrads and quadruplex structures. <i>Bioinformatics</i> , 2020, 36, 1129-1134.	4.1	20

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19	RNA tertiary structure determination: NOE pathways construction by tabu search. <i>Bioinformatics</i> , 2005, 21, 2356-2361.	4.1	18
20	ONQUADRO: a database of experimentally determined quadruplex structures. <i>Nucleic Acids Research</i> , 2022, 50, D253-D258.	14.5	17
21	The Orderly Colored Longest Path Problem – a survey of applications and new algorithms. <i>RAIRO - Operations Research</i> , 2014, 48, 25-51.	1.8	15
22	LCS-TA to identify similar fragments in RNA 3D structures. <i>BMC Bioinformatics</i> , 2017, 18, 456.	2.6	15
23	Entanglements of structure elements revealed in RNA 3D models. <i>Nucleic Acids Research</i> , 2021, 49, 9625-9632.	14.5	13
24	RNApolis: Computational Platform for RNA Structure Analysis. <i>Foundations of Computing and Decision Sciences</i> , 2019, 44, 241-257.	1.2	13
25	RNAsolo: a repository of cleaned PDB-derived RNA 3D structures. <i>Bioinformatics</i> , 2022, 38, 3668-3670.	4.1	13
26	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
27	How bioinformatics resources work with G4 RNAs. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	12
28	RNAthor – fast, accurate normalization, visualization and statistical analysis of RNA probing data resolved by capillary electrophoresis. <i>PLoS ONE</i> , 2020, 15, e0239287.	2.5	12
29	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
30	RNAvista: a webserver to assess RNA secondary structures with non-canonical base pairs. <i>Bioinformatics</i> , 2019, 35, 152-155.	4.1	11
31	EITetrado: a tool for identification and classification of tetrads and quadruplexes. <i>BMC Bioinformatics</i> , 2020, 21, 40.	2.6	11
32	Discovering Structural Motifs in miRNA Precursors from the Viridiplantae Kingdom. <i>Molecules</i> , 2018, 23, 1367.	3.8	9
33	An assignment walk through 3D NMR spectrum. , 2009, , .		8
34	RNAloops: a database of RNA multiloops. <i>Bioinformatics</i> , 2022, 38, 4200-4205.	4.1	8
35	Poseidon: An information retrieval and extraction system for metagenomic marine science. <i>Ecological Informatics</i> , 2012, 12, 10-15.	5.2	7
36	Optimal pathway reconstruction on 3D NMR maps. <i>Discrete Applied Mathematics</i> , 2015, 182, 134-149.	0.9	7

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37	MLP accompanied beam search for the resonance assignment problem. Journal of Heuristics, 2013, 19, 443-464.	1.4	6
38	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
39	A new molecular mechanism of RNA circularization and the microRNA sponge formation. Journal of Biomolecular Structure and Dynamics, 2022, 40, 3038-3045.	3.5	6
40	Virxicon: a lexicon of viral sequences. Bioinformatics, 2021, 36, 5507-5513.	4.1	6
41	RNAspider: a webserver to analyze entanglements in RNA 3D structures. Nucleic Acids Research, 2022, 50, W663-W669.	14.5	6
42	In Vitro and in Silico Analysis of miR-125a with rs12976445 Polymorphism in Breast Cancer Patients. Applied Sciences (Switzerland), 2020, 10, 7275.	2.5	2
43	DrawTetrado to create layer diagrams of G4 structures. Bioinformatics, 2022, 38, 3835-3836.	4.1	1
44	Turning data into folds using RNAComposer. , 2013, , .		0
45	Recent Advances in Operations Research in Computational Biology, Bioinformatics and Medicine. RAIRO - Operations Research, 2016, 50, 327-330.	1.8	0
46	Title is missing!. , 2020, 15, e0239287.		0
47	Title is missing!. , 2020, 15, e0239287.		0
48	Title is missing!. , 2020, 15, e0239287.		0
49	Title is missing!. , 2020, 15, e0239287.		0
50	Title is missing!. , 2020, 15, e0239287.		0
51	Title is missing!. , 2020, 15, e0239287.		0