

Marta Szachniuk

List of Publications by Year in descending order

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Version: 2024-02-01

51
papers

2,056
citations

489802

18
h-index

299063

42
g-index

53
all docs

53
docs citations

53
times ranked

2295
citing authors

#	ARTICLE	IF	CITATIONS
1	A new molecular mechanism of RNA circularization and the microRNA sponge formation. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 3038-3045.	2.0	6
2	ONQUADRO: a database of experimentally determined quadruplex structures. <i>Nucleic Acids Research</i> , 2022, 50, D253-D258.	6.5	17
3	Evaluation of the stereochemical quality of predicted RNA 3D models in the RNA-Puzzles submissions. <i>Rna</i> , 2022, 28, 250-262.	1.6	12
4	RNAspider: a webserver to analyze entanglements in RNA 3D structures. <i>Nucleic Acids Research</i> , 2022, 50, W663-W669.	6.5	6
5	DrawTetrado to create layer diagrams of G4 structures. <i>Bioinformatics</i> , 2022, 38, 3835-3836.	1.8	1
6	RNA solo: a repository of cleaned PDB-derived RNA 3D structures. <i>Bioinformatics</i> , 2022, 38, 3668-3670.	1.8	13
7	RNA loops: a database of RNA multiloops. <i>Bioinformatics</i> , 2022, 38, 4200-4205.	1.8	8
8	How bioinformatics resources work with G4 RNAs. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	12
9	Entanglements of structure elements revealed in RNA 3D models. <i>Nucleic Acids Research</i> , 2021, 49, 9625-9632.	6.5	13
10	Virxicon: a lexicon of viral sequences. <i>Bioinformatics</i> , 2021, 36, 5507-5513.	1.8	6
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.	6.5	44
12	Topology-based classification of tetrads and quadruplex structures. <i>Bioinformatics</i> , 2020, 36, 1129-1134.	1.8	20
13	In Vitro and in Silico Analysis of miR-125a with rs12976445 Polymorphism in Breast Cancer Patients. <i>Applied Sciences (Switzerland)</i> , 2020, 10, 7275.	1.3	2
14	RNA-Puzzles Round IV: 3D structure predictions of four ribozymes and two aptamers. <i>Rna</i> , 2020, 26, 982-995.	1.6	100
15	ETetrado: a tool for identification and classification of tetrads and quadruplexes. <i>BMC Bioinformatics</i> , 2020, 21, 40.	1.2	11
16	RNAthor – fast, accurate normalization, visualization and statistical analysis of RNA probing data resolved by capillary electrophoresis. <i>PLoS ONE</i> , 2020, 15, e0239287.	1.1	12
17	Title is missing!. , 2020, 15, e0239287.		0
18	Title is missing!. , 2020, 15, e0239287.		0

#	ARTICLE	IF	CITATIONS
19	Title is missing!. , 2020, 15, e0239287.		0
20	Title is missing!. , 2020, 15, e0239287.		0
21	Title is missing!. , 2020, 15, e0239287.		0
22	Title is missing!. , 2020, 15, e0239287.		0
23	RNAvista: a webserver to assess RNA secondary structures with non-canonical base pairs. <i>Bioinformatics</i> , 2019, 35, 152-155.	1.8	11
24	RNApolis: Computational Platform for RNA Structure Analysis. <i>Foundations of Computing and Decision Sciences</i> , 2019, 44, 241-257.	0.5	13
25	New algorithms to represent complex pseudoknotted RNA structures in dot-bracket notation. <i>Bioinformatics</i> , 2018, 34, 1304-1312.	1.8	29
26	RNApdbee 2.0: multifunctional tool for RNA structure annotation. <i>Nucleic Acids Research</i> , 2018, 46, W30-W35.	6.5	81
27	RNAfitme: a webserver for modeling nucleobase and nucleoside residue conformation in fixed-backbone RNA structures. <i>BMC Bioinformatics</i> , 2018, 19, 304.	1.2	12
28	Discovering Structural Motifs in miRNA Precursors from the Viridiplantae Kingdom. <i>Molecules</i> , 2018, 23, 1367.	1.7	9
29	RNA-Puzzles Round III: 3D RNA structure prediction of five riboswitches and one ribozyme. <i>Rna</i> , 2017, 23, 655-672.	1.6	158
30	New functionality of RNAComposer: application to shape the axis of miR160 precursor structure. <i>Acta Biochimica Polonica</i> , 2017, 63, 737-744.	0.3	112
31	LCS-TA to identify similar fragments in RNA 3D structures. <i>BMC Bioinformatics</i> , 2017, 18, 456.	1.2	15
32	Recent Advances in Operations Research in Computational Biology, Bioinformatics and Medicine. <i>RAIRO - Operations Research</i> , 2016, 50, 327-330.	1.0	0
33	Automated RNA 3D Structure Prediction with RNAComposer. <i>Methods in Molecular Biology</i> , 2016, 1490, 199-215.	0.4	118
34	New in silico approach to assessing RNA secondary structures with non-canonical base pairs. <i>BMC Bioinformatics</i> , 2015, 16, 276.	1.2	31
35	RNAAssess—a web server for quality assessment of RNA 3D structures. <i>Nucleic Acids Research</i> , 2015, 43, W502-W506.	6.5	24
36	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

#	ARTICLE	IF	CITATIONS
37	<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.	1.6	161
38	Optimal pathway reconstruction on 3D NMR maps. <i>Discrete Applied Mathematics</i> , 2015, 182, 134-149.	0.5	7
39	Sorting signal targeting mRNA into hepatic extracellular vesicles. <i>RNA Biology</i> , 2014, 11, 836-844.	1.5	42
40	The Orderly Colored Longest Path Problem – a survey of applications and new algorithms. <i>RAIRO - Operations Research</i> , 2014, 48, 25-51.	1.0	15
41	RNApdbee – 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
42	MCQ4Structures to compute similarity of molecule structures. <i>Central European Journal of Operations Research</i> , 2014, 22, 457-473.	1.1	33
43	MLP accompanied beam search for the resonance assignment problem. <i>Journal of Heuristics</i> , 2013, 19, 443-464.	1.1	6
44	RNAlyzer – novel approach for quality analysis of RNA structural models. <i>Nucleic Acids Research</i> , 2013, 41, 5978-5990.	6.5	22
45	Turning data into folds using RNAComposer. , 2013, , .		0
46	Automated 3D structure composition for large RNAs. <i>Nucleic Acids Research</i> , 2012, 40, e112-e112.	6.5	564
47	Poseidon: An information retrieval and extraction system for metagenomic marine science. <i>Ecological Informatics</i> , 2012, 12, 10-15.	2.3	7
48	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.	1.2	130
49	An assignment walk through 3D NMR spectrum. , 2009, , .		8
50	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.	6.5	78
51	RNA tertiary structure determination: NOE pathways construction by tabu search. <i>Bioinformatics</i> , 2005, 21, 2356-2361.	1.8	18