Tomasz Å»ok

List of Publications by Year
in descending order

39 papers	**1,086** citations	623734 **14** h-index	454955 **30** g-index
41 all docs	**41** docs citations	**41** times ranked	**1156** citing authors

#	Article	IF	Citations
1	*RNA-Puzzles* Round II: assessment of RNA structure prediction programs applied to three large RNA structures. Rna, 2015, 21, 1066-1084.	3.5	161
2	RNA-Puzzles Round III: 3D RNA structure prediction of five riboswitches and one ribozyme. Rna, 2017, 23, 655-672.	3.5	158
3	New functionality of RNAComposer: application to shape the axis of miR160 precursor structure. Acta Biochimica Polonica, 2017, 63, 737-744.	0.5	112
4	RNA-Puzzles Round IV: 3D structure predictions of four ribozymes and two aptamers. Rna, 2020, 26, 982-995.	3.5	100
5	RNApdbee 2.0: multifunctional tool for RNA structure annotation. Nucleic Acids Research, 2018, 46, W30-W35.	14.5	81
6	RNApdbee—a webserver to derive secondary structures from pdb files of knotted and unknotted RNAs. Nucleic Acids Research, 2014, 42, W368-W372.	14.5	61
7	INDIGO-DataCloud: a Platform to Facilitate Seamless Access to E-Infrastructures. Journal of Grid Computing, 2018, 16, 381-408.	3.9	58
8	The European Integrated Tokamak Modelling (ITM) effort: achievements and first physics results. Nuclear Fusion, 2014, 54, 043018.	3.5	45
9	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
10	MCQ4Structures to compute similarity of molecule structures. Central European Journal of Operations Research, 2014, 22, 457-473.	1.8	33
11	New in silico approach to assessing RNA secondary structures with non-canonical base pairs. BMC Bioinformatics, 2015, 16, 276.	2.6	31
12	New algorithms to represent complex pseudoknotted RNA structures in dot-bracket notation. Bioinformatics, 2018, 34, 1304-1312.	4.1	29
13	Topology-based classification of tetrads and quadruplex structures. Bioinformatics, 2020, 36, 1129-1134.	4.1	20
14	ONQUADRO: a database of experimentally determined quadruplex structures. Nucleic Acids Research, 2022, 50, D253-D258.	14.5	17
15	LCS-TA to identify similar fragments in RNA 3D structures. BMC Bioinformatics, 2017, 18, 456.	2.6	15
16	Approaches to Distributed Execution of Scientific Workflows in Kepler. Fundamenta Informaticae, 2013, 128, 281-302.	0.4	13
17	Entanglements of structure elements revealed in RNA 3D models. Nucleic Acids Research, 2021, 49, 9625-9632.	14.5	13
18	RNAfitme: a webserver for modeling nucleobase and nucleoside residue conformation in fixed-backbone RNA structures. BMC Bioinformatics, 2018, 19, 304.	2.6	12

#	Article	IF	Citations
19	RNAthor â€" fast, accurate normalization, visualization and statistical analysis of RNA probing data resolved by capillary electrophoresis. PLoS ONE, 2020, 15, e0239287.	2.5	12
20	RNAvista: a webserver to assess RNA secondary structures with non-canonical base pairs. Bioinformatics, 2019, 35, 152-155.	4.1	11
21	ElTetrado: a tool for identification and classification of tetrads and quadruplexes. BMC Bioinformatics, 2020, 21, 40.	2.6	11
22	RNAloops: a database of RNA multiloops. Bioinformatics, 2022, 38, 4200-4205.	4.1	8
23	Distributed and cloud-based multi-model analytics experiments on large volumes of climate change data in the earth system grid federation eco-system. , 2016, , .		7
24	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
25	RNAspider: a webserver to analyze entanglements in RNA 3D structures. Nucleic Acids Research, 2022, 50, W663-W669.	14.5	6
26	Tools, Methods and Services Enhancing the Usage of the Kepler-based Scientific Workflow Framework. Procedia Computer Science, 2014, 29, 1733-1744.	2.0	5
27	Running simultaneous Kepler sessions for the parallelization of parametric scans and optimization studies applied to complex workflows. Journal of Computational Science, 2017, 20, 103-111.	2.9	3
28	High level tools for fusion simulations workflows in distributed computing environment. , 2012, , .		2
29	Application Scenarios Using Serpens Suite for Kepler Scientific Workflow System. Procedia Computer Science, 2012, 9, 1604-1613.	2.0	2
30	BioCommons: a robust java library for RNA structural bioinformatics. Bioinformatics, 2021, 37, 2766-2767.	4.1	2
31	Workflows orchestration in distributed computing infrastructures. , 2012, , .		1
32	Progress in the transferability of fusion workflows across HPC systems. Plasma Physics and Controlled Fusion, 2021, 63, 084004.	2.1	1
33	User-Friendly Frameworks for Accessing Computational Resources. Lecture Notes in Computer Science, 2012, , 191-204.	1.3	1
34	DrawTetrado to create layer diagrams of G4 structures. Bioinformatics, 2022, 38, 3835-3836.	4.1	1
35	Flexible Approach to Astronomical Data Reduction Workflows in Kepler. Procedia Computer Science, 2014, 29, 1756-1761.	2.0	0
36	Best Practices in Debugging Kepler Workflows. Procedia Computer Science, 2016, 80, 2332-2337.	2.0	0

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37	Running Simultaneous Kepler Sessions for the Parallelization of Parametric Scans and Optimization Studies Applied to Complex Workflows. Procedia Computer Science, 2016, 80, 690-699.	2.0	0
38	Kepler-Based Workflow Environment for Astronomy. Lecture Notes in Computer Science, 2014, , 278-292.	1.3	0
39	Morality, protection, security and gain: lessons from a minimalistic, economically inspired multi-agent model. Foundations of Computing and Decision Sciences, 2020, 45, 17-33.	1.2	0