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	ONQUADRO: a database of experimentally determined quadruplex structures. Nucleic Acids Research, 2022, 50, D253-D258.	14.5	17
2	RNAspider: a webserver to analyze entanglements in RNA 3D structures. Nucleic Acids Research, 2022, 50, W663-W669.	14.5	6
3	DrawTetrado to create layer diagrams of G4 structures. Bioinformatics, 2022, 38, 3835-3836.	4.1	1
4	RNAloops: a database of RNA multiloops. Bioinformatics, 2022, 38, 4200-4205.	4.1	8
5	BioCommons: a robust java library for RNA structural bioinformatics. Bioinformatics, 2021, 37, 2766-2767.	4.1	2
6	Progress in the transferability of fusion workflows across HPC systems. Plasma Physics and Controlled Fusion, 2021, 63, 084004.	2.1	1
7	Entanglements of structure elements revealed in RNA 3D models. Nucleic Acids Research, 2021, 49, 9625-9632.	14.5	13
8	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
9	Topology-based classification of tetrads and quadruplex structures. Bioinformatics, 2020, 36, 1129-1134.	4.1	20
10	RNA-Puzzles Round IV: 3D structure predictions of four ribozymes and two aptamers. Rna, 2020, 26, 982-995.	3.5	100
11	ElTetrado: a tool for identification and classification of tetrads and quadruplexes. BMC Bioinformatics, 2020, 21, 40.	2.6	11
12	RNAthor – fast, accurate normalization, visualization and statistical analysis of RNA probing data resolved by capillary electrophoresis. PLoS ONE, 2020, 15, e0239287.	2.5	12
13	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
14	RNAvista: a webserver to assess RNA secondary structures with non-canonical base pairs. Bioinformatics, 2019, 35, 152-155.	4.1	11
15	New algorithms to represent complex pseudoknotted RNA structures in dot-bracket notation. Bioinformatics, 2018, 34, 1304-1312.	4.1	29
16	RNApdbee 2.0: multifunctional tool for RNA structure annotation. Nucleic Acids Research, 2018, 46, W30-W35.	14.5	81
17	INDIGO-DataCloud: a Platform to Facilitate Seamless Access to E-Infrastructures. Journal of Grid Computing, 2018, 16, 381-408.	3.9	58
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	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
20	RNA-Puzzles Round III: 3D RNA structure prediction of five riboswitches and one ribozyme. Rna, 2017, 23, 655-672.	3.5	158
21	New functionality of RNAComposer: application to shape the axis of miR160 precursor structure. Acta Biochimica Polonica, 2017, 63, 737-744.	0.5	112
22	LCS-TA to identify similar fragments in RNA 3D structures. BMC Bioinformatics, 2017, 18, 456.	2.6	15
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	Best Practices in Debugging Kepler Workflows. Procedia Computer Science, 2016, 80, 2332-2337.	2.0	0
25	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
26	New in silico approach to assessing RNA secondary structures with non-canonical base pairs. BMC Bioinformatics, 2015, 16, 276.	2.6	31
27	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
28	<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
29	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
30	MCQ4Structures to compute similarity of molecule structures. Central European Journal of Operations Research, 2014, 22, 457-473.	1.8	33
31	The European Integrated Tokamak Modelling (ITM) effort: achievements and first physics results. Nuclear Fusion, 2014, 54, 043018.	3.5	45
32	Tools, Methods and Services Enhancing the Usage of the Kepler-based Scientific Workflow Framework. Procedia Computer Science, 2014, 29, 1733-1744.	2.0	5
33	Flexible Approach to Astronomical Data Reduction Workflows in Kepler. Procedia Computer Science, 2014, 29, 1756-1761.	2.0	0
34	Kepler-Based Workflow Environment for Astronomy. Lecture Notes in Computer Science, 2014, , 278-292.	1.3	0
35	Approaches to Distributed Execution of Scientific Workflows in Kepler. Fundamenta Informaticae, 2013, 128, 281-302.	0.4	13
36	Workflows orchestration in distributed computing infrastructures. , 2012, , .		1

#	Article	IF	Citations
37	High level tools for fusion simulations workflows in distributed computing environment. , 2012, , .		2
38	Application Scenarios Using Serpens Suite for Kepler Scientific Workflow System. Procedia Computer Science, 2012, 9, 1604-1613.	2.0	2
39	User-Friendly Frameworks for Accessing Computational Resources. Lecture Notes in Computer Science, 2012, , 191-204.	1.3	1