Jérôme Waldispühl

List of Publications by Year
in descending order

55	913	516710	501196
papers	citations	16	28
		h-index	g-index

64	64	64	1035
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	<scp>Verna</scp>l: a tool for mining fuzzy network motifs in RNA. Bioinformatics, 2022, 38, 970-976.	4.1	5
2	RNAglib: a python package for RNA 2.5 D graphs. Bioinformatics, 2022, 38, 1458-1459.	4.1	2
3	Human-supervised clustering of multidimensional data using crowdsourcing. Royal Society Open Science, 2022, 9, .	2.4	2
4	Adaptive Instructional System for Complex Equipment Trainings in the Post-covid Era: Breaking the Ice of Time-Consuming Tasks. Lecture Notes in Computer Science, 2022, , 207-225.	1.3	0
5	Modeling and Predicting RNA Three-Dimensional Structures. Methods in Molecular Biology, 2021, 2284, 17-42.	0.9	4
6	Finding recurrent RNA structural networks with fast maximal common subgraphs of edge-colored graphs. PLoS Computational Biology, 2021, 17, e1008990.	3.2	6
7	Fast and flexible coarse-grained prediction of protein folding routes using ensemble modeling and evolutionary sequence variation. Bioinformatics, 2020, 36, 1420-1428.	4.1	3
8	Leveling up citizen science. Nature Biotechnology, 2020, 38, 1124-1126.	17.5	20
9	Augmented base pairing networks encode RNA-small molecule binding preferences. Nucleic Acids Research, 2020, 48, 7690-7699.	14.5	30
10	A Nested 2-Level Cross-Validation Ensemble Learning Pipeline Suggests a Negative Pressure Against Crosstalk snoRNA-mRNA Interactions in Saccharomyces cerevisiae. Journal of Computational Biology, 2020, 27, 390-402.	1.6	1
11	<tt>incaRNAfbinv 2.0</tt>: a webserver and software with motif control for fragment-based design of RNAs. Bioinformatics, 2020, 36, 2920-2922.	4.1	2
12	Stochastic Sampling of Structural Contexts Improves the Scalability and Accuracy of RNA 3D Module Identification. Lecture Notes in Computer Science, 2020, , 186-201.	1.3	4
13	<tt>OptiMol</tt>: Optimization of Binding Affinities in Chemical Space for Drug Discovery. Journal of Chemical Information and Modeling, 2020, 60, 5658-5666.	5.4	44
14	Predicting Positions of Bridging Water Molecules in Nucleic Acid–Ligand Complexes. Journal of Chemical Information and Modeling, 2019, 59, 2941-2951.	5.4	14
15	Automated, customizable and efficient identification of 3D base pair modules with BayesPairing. Nucleic Acids Research, 2019, 47, 3321-3332.	14.5	11
16	Challenges and current status of computational methods for docking small molecules to nucleic acids. European Journal of Medicinal Chemistry, 2019, 168, 414-425.	5.5	48
17	On the emergence of structural complexity in RNA replicators. Rna, 2019, 25, 1579-1591.	3.5	6
18	Design of RNAs: comparing programs for inverse RNA folding. Briefings in Bioinformatics, 2018, 19, bbw120.	6.5	35

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19	Mining for recurrent long-range interactions in RNA structures reveals embedded hierarchies in network families. Nucleic Acids Research, 2018, 46, 3841-3851.	14.5	35
20	Storage, visualization, and navigation of 3D genomics data. Methods, 2018, 142, 74-80.	3.8	13
21	A Nested 2-Level Cross-Validation Ensemble Learning Pipeline Suggests a Negative Pressure Against Crosstalk snoRNA-mRNA Interactions in Saccharomyces Cerevisae. Lecture Notes in Computer Science, 2018, , 177-193.	1.3	0
22	Ten simple rules to create a serious game, illustrated with examples from structural biology. PLoS Computational Biology, 2018, 14, e1005955.	3.2	20
23	On Stable States in a Topologically Driven Protein Folding Model. Journal of Computational Biology, 2017, 24, 851-862.	1.6	0
24	RNA-MoIP: prediction of RNA secondary structure and local 3D motifs from sequence data. Nucleic Acids Research, 2017, 45, W440-W444.	14.5	17
25	Computational Intractability Generates the Topology of Biological Networks. , 2017, , .		2
26	Investigating Mutations to Reduce Huntingtin Aggregation by Increasing Htt-N-Terminal Stability and Weakening Interactions with PolyQ Domain. Computational and Mathematical Methods in Medicine, 2016, 2016, 1-12.	1.3	5
27	Reconstruction of ancestral RNA sequences under multiple structural constraints. BMC Genomics, 2016, 17, 862.	2.8	0
28	Combining structure probing data on RNA mutants with evolutionary information reveals RNA-binding interfaces. Nucleic Acids Research, 2016, 44, e104-e104.	14.5	5
29	<tt>incaRNAfbinv</tt>: a web server for the fragment-based design of RNA sequences. Nucleic Acids Research, 2016, 44, W308-W314.	14.5	10
30	Collaborative Solving in a Human Computing Game Using a Market, Skills and Challenges. , 2016, , .		5
31	Computational re-engineering of Amylin sequence with reduced amyloidogenic potential. BMC Structural Biology, 2015, 15, 7.	2.3	1
32	A low-latency, big database system and browser for storage, querying and visualization of 3D genomic data. Nucleic Acids Research, 2015, 43, e103-e103.	14.5	8
33	Probing the binding affinity of amyloids to reduce toxicity of oligomers in diabetes. Bioinformatics, 2015, 31, 2294-2302.	4.1	4
34	Complete characterization of the mutation landscape reveals the effect on amylin stability and amyloidogenicity. Proteins: Structure, Function and Bioinformatics, 2015, 83, 1014-1026.	2.6	10
35	Modeling and Predicting RNA Three-Dimensional Structures. Methods in Molecular Biology, 2015, 1269, 101-121.	0.9	5
36	Crowdsourcing RNA structural alignments with an online computer game. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2015, , 330-41.	0.7	5

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37	Exploration of the Dynamic Properties of Protein Complexes Predicted from Spatially Constrained Protein-Protein Interaction Networks. PLoS Computational Biology, 2014, 10, e1003654.	3.2	7
38	Simultaneous Alignment and Folding of Protein Sequences. Journal of Computational Biology, 2014, 21, 477-491.	1.6	0
39	CROWDSOURCING RNA STRUCTURAL ALIGNMENTS WITH AN ONLINE COMPUTER GAME. , 2014, , .		5
40	Computational Assembly of Polymorphic Amyloid Fibrils Reveals Stable Aggregates. Biophysical Journal, 2013, 104, 683-693.	0.5	36
41	Using Structural and Evolutionary Information to Detect and Correct Pyrosequencing Errors in Noncoding RNAs. Journal of Computational Biology, 2013, 20, 905-919.	1.6	1
42	A weighted sampling algorithm for the design of RNA sequences with targeted secondary structure and nucleotide distribution. Bioinformatics, 2013, 29, i308-i315.	4.1	38
43	SPARCS: a web server to analyze (un)structured regions in coding RNA sequences. Nucleic Acids Research, 2013, 41, W480-W485.	14.5	13
44	Open-Phylo: a customizable crowd-computing platform for multiple sequence alignment. Genome Biology, 2013, 14, R116.	9.6	20
45	Mortal Kombat: modeling amyloid fibrils and health implications. FASEB Journal, 2013, 27, 996.16.	0.5	0
46	Towards 3D structure prediction of large RNA molecules: an integer programming framework to insert local 3D motifs in RNA secondary structure. Bioinformatics, 2012, 28, i207-i214.	4.1	41
47	A global sampling approach to designing and reengineering RNA secondary structures. Nucleic Acids Research, 2012, 40, 10041-10052.	14.5	32
48	Phylo: A Citizen Science Approach for Improving Multiple Sequence Alignment. PLoS ONE, 2012, 7, e31362.	2.5	166
49	An Unbiased Adaptive Sampling Algorithm for the Exploration of RNA Mutational Landscapes Under Evolutionary Pressure. Journal of Computational Biology, 2011, 18, 1465-1479.	1.6	13
50	A method for probing the mutational landscape of amyloid structure. Bioinformatics, 2011, 27, i34-i42.	4.1	58
51	Efficient Traversal of Beta-Sheet Protein Folding Pathways Using Ensemble Models. Journal of Computational Biology, 2011, 18, 1635-1647.	1.6	6
52	corRna: a web server for predicting multiple-point deleterious mutations in structural RNAs. Nucleic Acids Research, 2011, 39, W160-W166.	14.5	8
53	RNAmutants: a web server to explore the mutational landscape of RNA secondary structures. Nucleic Acids Research, 2009, 37, W281-W286.	14.5	19
54	Modeling ensembles of transmembrane β-barrel proteins. Proteins: Structure, Function and Bioinformatics, 2008, 71, 1097-1112.	2.6	26

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55	Efficient Algorithms for Probing the RNA Mutation Landscape. PLoS Computational Biology, 2008, 4, e1000124.	3.2	38