JÃ©rÃ´me WaldispÃ¼hl

List of Publications by Year
in descending order

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

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

#	Article	IF	Citations
1	Phylo: A Citizen Science Approach for Improving Multiple Sequence Alignment. PLoS ONE, 2012, 7, e31362.	2.5	166
2	A method for probing the mutational landscape of amyloid structure. Bioinformatics, 2011, 27, i34-i42.	4.1	58
3	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
4	<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
5	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
6	Efficient Algorithms for Probing the RNA Mutation Landscape. PLoS Computational Biology, 2008, 4, e1000124.	3.2	38
7	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
8	Computational Assembly of Polymorphic Amyloid Fibrils Reveals Stable Aggregates. Biophysical Journal, 2013, 104, 683-693.	0.5	36
9	Design of RNAs: comparing programs for inverse RNA folding. Briefings in Bioinformatics, 2018, 19, bbw120.	6.5	35
10	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
11	A global sampling approach to designing and reengineering RNA secondary structures. Nucleic Acids Research, 2012, 40, 10041-10052.	14.5	32
12	Augmented base pairing networks encode RNA-small molecule binding preferences. Nucleic Acids Research, 2020, 48, 7690-7699.	14.5	30
13	Modeling ensembles of transmembrane Î²â€barrel proteins. Proteins: Structure, Function and Bioinformatics, 2008, 71, 1097-1112.	2.6	26
14	Open-Phylo: a customizable crowd-computing platform for multiple sequence alignment. Genome Biology, 2013, 14, R116.	9.6	20
15	Leveling up citizen science. Nature Biotechnology, 2020, 38, 1124-1126.	17.5	20
16	Ten simple rules to create a serious game, illustrated with examples from structural biology. PLoS Computational Biology, 2018, 14, e1005955.	3.2	20
17	RNAmutants: a web server to explore the mutational landscape of RNA secondary structures. Nucleic Acids Research, 2009, 37, W281-W286.	14.5	19
18	RNA-MoIP: prediction of RNA secondary structure and local 3D motifs from sequence data. Nucleic Acids Research, 2017, 45, W440-W444.	14.5	17

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19	Predicting Positions of Bridging Water Molecules in Nucleic Acidâ€“Ligand Complexes. Journal of Chemical Information and Modeling, 2019, 59, 2941-2951.	5.4	14
20	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
21	SPARCS: a web server to analyze (un)structured regions in coding RNA sequences. Nucleic Acids Research, 2013, 41, W480-W485.	14.5	13
22	Storage, visualization, and navigation of 3D genomics data. Methods, 2018, 142, 74-80.	3.8	13
23	Automated, customizable and efficient identification of 3D base pair modules with BayesPairing. Nucleic Acids Research, 2019, 47, 3321-3332.	14.5	11
24	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
25	<tt>incaRNAfbinv</tt>: a web server for the fragment-based design of RNA sequences. Nucleic Acids Research, 2016, 44, W308-W314.	14.5	10
26	corRna: a web server for predicting multiple-point deleterious mutations in structural RNAs. Nucleic Acids Research, 2011, 39, W160-W166.	14.5	8
27	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
28	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
29	Efficient Traversal of Beta-Sheet Protein Folding Pathways Using Ensemble Models. Journal of Computational Biology, 2011, 18, 1635-1647.	1.6	6
30	On the emergence of structural complexity in RNA replicators. Rna, 2019, 25, 1579-1591.	3.5	6
31	Finding recurrent RNA structural networks with fast maximal common subgraphs of edge-colored graphs. PLoS Computational Biology, 2021, 17, e1008990.	3.2	6
32	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
33	Combining structure probing data on RNA mutants with evolutionary information reveals RNA-binding interfaces. Nucleic Acids Research, 2016, 44, e104-e104.	14.5	5
34	Modeling and Predicting RNA Three-Dimensional Structures. Methods in Molecular Biology, 2015, 1269, 101-121.	0.9	5
35	CROWDSOURCING RNA STRUCTURAL ALIGNMENTS WITH AN ONLINE COMPUTER GAME. , 2014, , .		5
36	Collaborative Solving in a Human Computing Game Using a Market, Skills and Challenges. , 2016, , .		5

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37	<scp>Verna</scp>l: a tool for mining fuzzy network motifs in RNA. Bioinformatics, 2022, 38, 970-976.	4.1	5
38	Crowdsourcing RNA structural alignments with an online computer game. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2015, , 330-41.	0.7	5
39	Probing the binding affinity of amyloids to reduce toxicity of oligomers in diabetes. Bioinformatics, 2015, 31, 2294-2302.	4.1	4
40	Modeling and Predicting RNA Three-Dimensional Structures. Methods in Molecular Biology, 2021, 2284, 17-42.	0.9	4
41	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
42	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
43	Computational Intractability Generates the Topology of Biological Networks. , 2017, , .		2
44	<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
45	RNAglib: a python package for RNA 2.5 D graphs. Bioinformatics, 2022, 38, 1458-1459.	4.1	2
46	Human-supervised clustering of multidimensional data using crowdsourcing. Royal Society Open Science, 2022, 9, .	2.4	2
47	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
48	Computational re-engineering of Amylin sequence with reduced amyloidogenic potential. BMC Structural Biology, 2015, 15, 7.	2.3	1
49	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
50	Simultaneous Alignment and Folding of Protein Sequences. Journal of Computational Biology, 2014, 21, 477-491.	1.6	0
51	Reconstruction of ancestral RNA sequences under multiple structural constraints. BMC Genomics, 2016, 17, 862.	2.8	0
52	On Stable States in a Topologically Driven Protein Folding Model. Journal of Computational Biology, 2017, 24, 851-862.	1.6	0
53	A Nested 2-Level Cross-Validation Ensemble Learning Pipeline Suggests a Negative Pressure Against Crosstalk snoRNA-mRNA Interactions in Saccharomyces Cerevisiae. Lecture Notes in Computer Science, 2018, , 177-193.	1.3	0
54	Mortal Kombat: modeling amyloid fibrils and health implications. FASEB Journal, 2013, 27, 996.16.	0.5	0

#	Article	IF	Citations
55	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