Michael T Wolfinger

List of Publications by Year
in descending order

79 papers	17,366 citations	136885 32 h-index	82499 72 g-index
101 all docs	101 docs citations	101 times ranked	32356 citing authors

#	ARTICLE	IF	CITATIONS
1	Generic Context-Aware Group Contributions. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 429-442.	1.9	1
2	Investigating Japanese encephalitis virus long-range terminal region interactions. Biophysical Journal, 2022, 121, 206a.	0.2	0
3	Investigating flaviviral genomic cyclization. Biophysical Journal, 2022, 121, 311a.	0.2	0
4	Insights into the secondary and tertiary structure of the Bovine Viral Diarrhea Virus Internal Ribosome Entry Site. RNA Biology, 2022, 19, 496-506.	1.5	3
5	Biophysical characterisation of human LincRNA-p21 sense and antisense Alu inverted repeats. Nucleic Acids Research, 2022, 50, 5881-5898.	6.5	8
6	Evolutionary traits of Tick-borne encephalitis virus: Pervasive non-coding RNA structure conservation and molecular epidemiology. Virus Evolution, 2022, 8, .	2.2	10
7	Theoretical studies on RNA recognition by Musashi 1 RNA-binding protein. Scientific Reports, 2022, 12, .	1.6	5
8	Dynamic Molecular Epidemiology Reveals Lineage-Associated Single-Nucleotide Variants That Alter RNA Structure in Chikungunya Virus. Genes, 2021, 12, 239.	1.0	7
9	RNAxplorer: harnessing the power of guiding potentials to sample RNA landscapes. Bioinformatics, 2021, 37, 2126-2133.	1.8	3
10	An African tick flavivirus forming an independent clade exhibits unique exoribonuclease-resistant RNA structures in the genomic 3â€²-untranslated region. Scientific Reports, 2021, 11, 4883.	1.6	4
11	Gene Expression Profiling of Pseudomonas aeruginosa Upon Exposure to Colistin and Tobramycin. Frontiers in Microbiology, 2021, 12, 626715.	1.5	16
12	Functional RNA Structures in the 3â€² UTR of Mosquito-Borne Flaviviruses. , 2021, , 65-100.		4
13	Discoveries of Exoribonuclease-Resistant Structures of Insect-Specific Flaviviruses Isolated in Zambia. Viruses, 2020, 12, 1017.	1.5	11
14	Genomic epidemiology of superspreading events in Austria reveals mutational dynamics and transmission properties of SARS-CoV-2. Science Translational Medicine, 2020, 12, .	5.8	203
15	Distinctive Regulation of Carbapenem Susceptibility in Pseudomonas aeruginosa by Hfq. Frontiers in Microbiology, 2020, 11, 1001.	1.5	16
16	Bi-alignments as Models of Incongruent Evolution of RNA Sequence and Secondary Structure. Lecture Notes in Computer Science, 2020, , 159-170.	1.0	2
17	The role of Arbovirus genome untranslated regions on neurotropism. International Journal of Infectious Diseases, 2019, 79, 142.	1.5	0
18	Updated Phylogeny of Chikungunya Virus Suggests Lineage-Specific RNA Architecture. Viruses, 2019, 11, 798.	1.5	32

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19	Musashi binding elements in Zika and related Flavivirus 3′UTRs: A comparative study in silico. Scientific Reports, 2019, 9, 6911.	1.6	16
20	Functional RNA Structures in the 3′UTR of Tick-Borne, Insect-Specific and No-Known-Vector Flaviviruses. Viruses, 2019, 11, 298.	1.5	43
21	Control of Cognate Sense mRNA Translation by cis-Natural Antisense RNAs. Plant Physiology, 2019, 180, 305-322.	2.3	41
22	Indications for a moonlighting function of translation factor aIF5A in the crenarchaeum Sulfolobus solfataricus. RNA Biology, 2019, 16, 675-685.	1.5	11
23	RNA modifications in structure prediction – Status quo and future challenges. Methods, 2019, 156, 32-39.	1.9	31
24	Interplay between the catabolite repression control protein Crc, Hfq and RNA in Hfq-dependent translational regulation in Pseudomonas aeruginosa. Nucleic Acids Research, 2018, 46, 1470-1485.	6.5	85
25	Efficient computation of co-transcriptional RNA-ligand interaction dynamics. Methods, 2018, 143, 70-76.	1.9	13
26	Harnessing Metabolic Regulation to Increase Hfq-Dependent Antibiotic Susceptibility in Pseudomonas aeruginosa. Frontiers in Microbiology, 2018, 9, 2709.	1.5	27
27	In silico design of ligand triggered RNA switches. Methods, 2018, 143, 90-101.	1.9	14
28	TERribly Difficult: Searching for Telomerase RNAs in Saccharomycetes. Genes, 2018, 9, 372.	1.0	12
29	RNA Structure Elements Conserved between Mouse and 59 Other Vertebrates. Genes, 2018, 9, 392.	1.0	16
30	NMR Structural Profiling of Transcriptional Intermediates Reveals Riboswitch Regulation by Metastable RNA Conformations. Journal of the American Chemical Society, 2017, 139, 2647-2656.	6.6	43
31	The SmAP1/2 proteins of the crenarchaeon Sulfolobus solfataricus interact with the exosome and stimulate A-rich tailing of transcripts. Nucleic Acids Research, 2017, 45, 7938-7949.	6.5	24
32	RNAblueprint: flexible multiple target nucleic acid sequence design. Bioinformatics, 2017, 33, 2850-2858.	1.8	17
33	RNA structure prediction: from 2D to 3D. Emerging Topics in Life Sciences, 2017, 1, 275-285.	1.1	13
34	The Anaerobically Induced sRNA PaiI Affects Denitrification in Pseudomonas aeruginosa PA14. Frontiers in Microbiology, 2017, 8, 2312.	1.5	14
35	SHAPE directed RNA folding. Bioinformatics, 2016, 32, 145-147.	1.8	91
36	RNASeq Based Transcriptional Profiling of Pseudomonas aeruginosa PA14 after Short- and Long-Term Anoxic Cultivation in Synthetic Cystic Fibrosis Sputum Medium. PLoS ONE, 2016, 11, e0147811.	1.1	42

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37	Cross-regulation by CrcZ RNA controls anoxic biofilm formation in Pseudomonas aeruginosa. Scientific Reports, 2016, 6, 39621.	1.6	45
38	Differential transcriptional responses to Ebola and Marburg virus infection in bat and human cells. Scientific Reports, 2016, 6, 34589.	1.6	47
39	Predicting RNA secondary structures from sequence and probing data. Methods, 2016, 103, 86-98.	1.9	110
40	Transcriptome-wide effects of inverted SINEs on gene expression and their impact on RNA polymerase II activity. Genome Biology, 2016, 17, 220.	3.8	20
41	Tristetraprolin binding site atlas in the macrophage transcriptome reveals a switch for inflammationÂresolution. Molecular Systems Biology, 2016, 12, 868.	3.2	74
42	AREsite2: an enhanced database for the comprehensive investigation of AU/GU/U-rich elements. Nucleic Acids Research, 2016, 44, D90-D95.	6.5	77
43	The MazF-regulon: a toolbox for the post-transcriptional stress response in<i>Escherichia coli</i>. Nucleic Acids Research, 2016, 44, 6660-6675.	6.5	45
44	Computational Design of a Circular RNA with Prionlike Behavior. Artificial Life, 2016, 22, 172-184.	1.0	3
45	Thermodynamic and Kinetic Folding of Riboswitches. Methods in Enzymology, 2015, 553, 193-213.	0.4	19
46	Enhanced transcriptome maps from multiple mouse tissues reveal evolutionary constraint in gene expression. Nature Communications, 2015, 6, 5903.	5.8	73
47	General and MicroRNA-Mediated mRNA Degradation Occurs on Ribosome Complexes in <i>Drosophila</i> Cells. Molecular and Cellular Biology, 2015, 35, 2309-2320.	1.1	41
48	ViennaNGS: A toolbox for building efficient next- generation sequencing analysis pipelines. F1000Research, 2015, 4, 50.	0.8	31
49	ViennaNGS: A toolbox for building efficient next- generation sequencing analysis pipelines. F1000Research, 2015, 4, 50.	0.8	33
50	Memory-efficient RNA energy landscape exploration. Bioinformatics, 2014, 30, 2584-2591.	1.8	10
51	A comparative encyclopedia of DNA elements in the mouse genome. Nature, 2014, 515, 355-364.	13.7	1,444
52	Comparative analysis of the transcriptome across distant species. Nature, 2014, 512, 445-448.	13.7	289
53	A multi-split mapping algorithm for circular RNA, splicing, trans-splicing and fusion detection. Genome Biology, 2014, 15, R34.	13.9	242
54	TSSAR: TSS annotation regime for dRNA-seq data. BMC Bioinformatics, 2014, 15, 89.	1.2	73

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55	On the Complexity of Reconstructing Chemical Reaction Networks. Mathematics in Computer Science, 2013, 7, 275-292.	0.2	2
56	2D Meets 4G: G-Quadruplexes in RNA Secondary Structure Prediction. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 832-844.	1.9	37
57	Computational design of RNAs with complex energy landscapes. Biopolymers, 2013, 99, n/a-n/a.	1.2	27
58	GENCODE: The reference human genome annotation for The ENCODE Project. Genome Research, 2012, 22, 1760-1774.	2.4	4,217
59	Landscape of transcription in human cells. Nature, 2012, 489, 101-108.	13.7	4,484
60	ViennaRNA Package 2.0. Algorithms for Molecular Biology, 2011, 6, 26.	0.3	3,719
61	In Silico Evolution of Early Metabolism. Artificial Life, 2011, 17, 87-108.	1.0	10
62	BarMap: RNA folding on dynamic energy landscapes. Rna, 2010, 16, 1308-1316.	1.6	53
63	Beyond energy minimization: approaches to the kinetic folding of RNA. Monatshefte Für Chemie, 2008, 139, 447-457.	0.9	49
64	Folding Kinetics of Large RNAs. Journal of Molecular Biology, 2008, 379, 160-173.	2.0	77
65	Visualization of Barrier Tree Sequences Revisited. Mathematics and Visualization, 2008, , 275-290.	0.4	1
66	A minimal and self-consistent in silico cell model based on macromolecular interactions. Philosophical Transactions of the Royal Society B: Biological Sciences, 2007, 362, 1831-1839.	1.8	7
67	Saddles and Barrier in Landscapes of Generalized Search Operators. Lecture Notes in Computer Science, 2007, , 194-212.	1.0	10
68	Partition function and base pairing probabilities of RNA heterodimers. Algorithms for Molecular Biology, 2006, 1, 3.	0.3	239
69	Visualization of Barrier Tree Sequences. IEEE Transactions on Visualization and Computer Graphics, 2006, 12, 781-788.	2.9	13
70	Evolution of MicroRNAs. , 2006, 342, 335-350.		32
71	Exploring the lower part of discrete polymer model energy landscapes. Europhysics Letters, 2006, 74, 726-732.	0.7	19
72	Efficient computation of RNA folding dynamics. Journal of Physics A, 2004, 37, 4731-4741.	1.6	99

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73	Barrier Trees on Poset-Valued Landscapes. Genetic Programming and Evolvable Machines, 2003, 4, 7-20.	1.5	19
74	Barrier Trees of Degenerate Landscapes. Zeitschrift Fur Physikalische Chemie, 2002, 216, .	1.4	130
75	Design of multistable RNA molecules. Rna, 2001, 7, 254-265.	1.6	138
76	RNA folding at elementary step resolution. Rna, 2000, 6, 325-338.	1.6	266
77	Automatic detection of conserved RNA structure elements in complete RNA virus genomes. Nucleic Acids Research, 1998, 26, 3825-3836.	6.5	115
78	Visualization of Lattice-Based Protein Folding Simulations. , 0, , .		2
79	Rewiring of Gene Expression in Pseudomonas aeruginosa During Diauxic Growth Reveals an Indirect Regulation of the MexGHI-OpmD Efflux Pump by Hfq. Frontiers in Microbiology, 0, 13, .	1.5	5