

# Michael T Wolfinger

## List of Publications by Year in descending order

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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	Landscape of transcription in human cells. <i>Nature</i> , 2012, 489, 101-108.	13.7	4,484
2	GENCODE: The reference human genome annotation for The ENCODE Project. <i>Genome Research</i> , 2012, 22, 1760-1774.	2.4	4,217
3	ViennaRNA Package 2.0. <i>Algorithms for Molecular Biology</i> , 2011, 6, 26.	0.3	3,719
4	A comparative encyclopedia of DNA elements in the mouse genome. <i>Nature</i> , 2014, 515, 355-364.	13.7	1,444
5	Comparative analysis of the transcriptome across distant species. <i>Nature</i> , 2014, 512, 445-448.	13.7	289
6	RNA folding at elementary step resolution. <i>Rna</i> , 2000, 6, 325-338.	1.6	266
7	A multi-split mapping algorithm for circular RNA, splicing, trans-splicing and fusion detection. <i>Genome Biology</i> , 2014, 15, R34.	13.9	242
8	Partition function and base pairing probabilities of RNA heterodimers. <i>Algorithms for Molecular Biology</i> , 2006, 1, 3.	0.3	239
9	Genomic epidemiology of superspreading events in Austria reveals mutational dynamics and transmission properties of SARS-CoV-2. <i>Science Translational Medicine</i> , 2020, 12, .	5.8	203
10	Design of multistable RNA molecules. <i>Rna</i> , 2001, 7, 254-265.	1.6	138
11	Barrier Trees of Degenerate Landscapes. <i>Zeitschrift Fur Physikalische Chemie</i> , 2002, 216, .	1.4	130
12	Automatic detection of conserved RNA structure elements in complete RNA virus genomes. <i>Nucleic Acids Research</i> , 1998, 26, 3825-3836.	6.5	115
13	Predicting RNA secondary structures from sequence and probing data. <i>Methods</i> , 2016, 103, 86-98.	1.9	110
14	Efficient computation of RNA folding dynamics. <i>Journal of Physics A</i> , 2004, 37, 4731-4741.	1.6	99
15	SHAPE directed RNA folding. <i>Bioinformatics</i> , 2016, 32, 145-147.	1.8	91
16	Interplay between the catabolite repression control protein Crc, Hfq and RNA in Hfq-dependent translational regulation in <i>Pseudomonas aeruginosa</i> . <i>Nucleic Acids Research</i> , 2018, 46, 1470-1485.	6.5	85
17	Folding Kinetics of Large RNAs. <i>Journal of Molecular Biology</i> , 2008, 379, 160-173.	2.0	77
18	AREsite2: an enhanced database for the comprehensive investigation of AU/GU/U-rich elements. <i>Nucleic Acids Research</i> , 2016, 44, D90-D95.	6.5	77

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19	Tristetraprolin binding site atlas in the macrophage transcriptome reveals a switch for inflammation resolution. <i>Molecular Systems Biology</i> , 2016, 12, 868.	3.2	74
20	TSSAR: TSS annotation regime for dRNA-seq data. <i>BMC Bioinformatics</i> , 2014, 15, 89.	1.2	73
21	Enhanced transcriptome maps from multiple mouse tissues reveal evolutionary constraint in gene expression. <i>Nature Communications</i> , 2015, 6, 5903.	5.8	73
22	BarMap: RNA folding on dynamic energy landscapes. <i>Rna</i> , 2010, 16, 1308-1316.	1.6	53
23	Beyond energy minimization: approaches to the kinetic folding of RNA. <i>Monatshefte für Chemie</i> , 2008, 139, 447-457.	0.9	49
24	Differential transcriptional responses to Ebola and Marburg virus infection in bat and human cells. <i>Scientific Reports</i> , 2016, 6, 34589.	1.6	47
25	Cross-regulation by CrcZ RNA controls anoxic biofilm formation in <i>Pseudomonas aeruginosa</i> . <i>Scientific Reports</i> , 2016, 6, 39621.	1.6	45
26	The MazF-regulon: a toolbox for the post-transcriptional stress response in <i>Escherichia coli</i> . <i>Nucleic Acids Research</i> , 2016, 44, 6660-6675.	6.5	45
27	NMR Structural Profiling of Transcriptional Intermediates Reveals Riboswitch Regulation by Metastable RNA Conformations. <i>Journal of the American Chemical Society</i> , 2017, 139, 2647-2656.	6.6	43
28	Functional RNA Structures in the 3' UTR of Tick-Borne, Insect-Specific and No-Known-Vector Flaviviruses. <i>Viruses</i> , 2019, 11, 298.	1.5	43
29	RNASeq Based Transcriptional Profiling of <i>Pseudomonas aeruginosa</i> PA14 after Short- and Long-Term Anoxic Cultivation in Synthetic Cystic Fibrosis Sputum Medium. <i>PLoS ONE</i> , 2016, 11, e0147811.	1.1	42
30	General and MicroRNA-Mediated mRNA Degradation Occurs on Ribosome Complexes in <i>Drosophila</i> Cells. <i>Molecular and Cellular Biology</i> , 2015, 35, 2309-2320.	1.1	41
31	Control of Cognate Sense mRNA Translation by cis-Natural Antisense RNAs. <i>Plant Physiology</i> , 2019, 180, 305-322.	2.3	41
32	2D Meets 4G: G-Quadruplexes in RNA Secondary Structure Prediction. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 832-844.	1.9	37
33	ViennaNGS: A toolbox for building efficient next-generation sequencing analysis pipelines. <i>F1000Research</i> , 2015, 4, 50.	0.8	33
34	Evolution of MicroRNAs. <i>Nature Reviews Genetics</i> , 2006, 7, 335-350.		32
35	Updated Phylogeny of Chikungunya Virus Suggests Lineage-Specific RNA Architecture. <i>Viruses</i> , 2019, 11, 798.	1.5	32
36	RNA modifications in structure prediction – Status quo and future challenges. <i>Methods</i> , 2019, 156, 32-39.	1.9	31

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37	ViennaNGS: A toolbox for building efficient next-generation sequencing analysis pipelines. <i>F1000Research</i> , 2015, 4, 50.	0.8	31
38	Computational design of RNAs with complex energy landscapes. <i>Biopolymers</i> , 2013, 99, n/a-n/a.	1.2	27
39	Harnessing Metabolic Regulation to Increase Hfq-Dependent Antibiotic Susceptibility in <i>Pseudomonas aeruginosa</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 2709.	1.5	27
40	The SmAP1/2 proteins of the crenarchaeon <i>Sulfolobus solfataricus</i> interact with the exosome and stimulate A-rich tailing of transcripts. <i>Nucleic Acids Research</i> , 2017, 45, 7938-7949.	6.5	24
41	Transcriptome-wide effects of inverted SINEs on gene expression and their impact on RNA polymerase II activity. <i>Genome Biology</i> , 2016, 17, 220.	3.8	20
42	Barrier Trees on Poset-Valued Landscapes. <i>Genetic Programming and Evolvable Machines</i> , 2003, 4, 7-20.	1.5	19
43	Exploring the lower part of discrete polymer model energy landscapes. <i>Europhysics Letters</i> , 2006, 74, 726-732.	0.7	19
44	Thermodynamic and Kinetic Folding of Riboswitches. <i>Methods in Enzymology</i> , 2015, 553, 193-213.	0.4	19
45	RNAblueprint: flexible multiple target nucleic acid sequence design. <i>Bioinformatics</i> , 2017, 33, 2850-2858.	1.8	17
46	RNA Structure Elements Conserved between Mouse and 59 Other Vertebrates. <i>Genes</i> , 2018, 9, 392.	1.0	16
47	Musashi binding elements in Zika and related Flavivirus 3'UTRs: A comparative study in silico. <i>Scientific Reports</i> , 2019, 9, 6911.	1.6	16
48	Distinctive Regulation of Carbapenem Susceptibility in <i>Pseudomonas aeruginosa</i> by Hfq. <i>Frontiers in Microbiology</i> , 2020, 11, 1001.	1.5	16
49	Gene Expression Profiling of <i>Pseudomonas aeruginosa</i> Upon Exposure to Colistin and Tobramycin. <i>Frontiers in Microbiology</i> , 2021, 12, 626715.	1.5	16
50	The Anaerobically Induced sRNA Pail Affects Denitrification in <i>Pseudomonas aeruginosa</i> PA14. <i>Frontiers in Microbiology</i> , 2017, 8, 2312.	1.5	14
51	In silico design of ligand triggered RNA switches. <i>Methods</i> , 2018, 143, 90-101.	1.9	14
52	Visualization of Barrier Tree Sequences. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2006, 12, 781-788.	2.9	13
53	RNA structure prediction: from 2D to 3D. <i>Emerging Topics in Life Sciences</i> , 2017, 1, 275-285.	1.1	13
54	Efficient computation of co-transcriptional RNA-ligand interaction dynamics. <i>Methods</i> , 2018, 143, 70-76.	1.9	13

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55	TERribly Difficult: Searching for Telomerase RNAs in Saccharomycetes. <i>Genes</i> , 2018, 9, 372.	1.0	12
56	Indications for a moonlighting function of translation factor alF5A in the crenarchaeum <i>Sulfolobus solfataricus</i> . <i>RNA Biology</i> , 2019, 16, 675-685.	1.5	11
57	Discoveries of Exoribonuclease-Resistant Structures of Insect-Specific Flaviviruses Isolated in Zambia. <i>Viruses</i> , 2020, 12, 1017.	1.5	11
58	In Silico Evolution of Early Metabolism. <i>Artificial Life</i> , 2011, 17, 87-108.	1.0	10
59	Memory-efficient RNA energy landscape exploration. <i>Bioinformatics</i> , 2014, 30, 2584-2591.	1.8	10
60	Saddles and Barrier in Landscapes of Generalized Search Operators. <i>Lecture Notes in Computer Science</i> , 2007, , 194-212.	1.0	10
61	Evolutionary traits of Tick-borne encephalitis virus: Pervasive non-coding RNA structure conservation and molecular epidemiology. <i>Virus Evolution</i> , 2022, 8, .	2.2	10
62	Biophysical characterisation of human LincRNA-p21 sense and antisense Alu inverted repeats. <i>Nucleic Acids Research</i> , 2022, 50, 5881-5898.	6.5	8
63	A minimal and self-consistent in silico cell model based on macromolecular interactions. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2007, 362, 1831-1839.	1.8	7
64	Dynamic Molecular Epidemiology Reveals Lineage-Associated Single-Nucleotide Variants That Alter RNA Structure in Chikungunya Virus. <i>Genes</i> , 2021, 12, 239.	1.0	7
65	Rewiring of Gene Expression in <i>Pseudomonas aeruginosa</i> During Diauxic Growth Reveals an Indirect Regulation of the MexGHI-OpmD Efflux Pump by Hfq. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	5
66	Theoretical studies on RNA recognition by Musashi 1 RNA-binding protein. <i>Scientific Reports</i> , 2022, 12, .	1.6	5
67	An African tick flavivirus forming an independent clade exhibits unique exoribonuclease-resistant RNA structures in the genomic 3' untranslated region. <i>Scientific Reports</i> , 2021, 11, 4883.	1.6	4
68	Functional RNA Structures in the 3' UTR of Mosquito-Borne Flaviviruses. , 2021, , 65-100.		4
69	Computational Design of a Circular RNA with Prionlike Behavior. <i>Artificial Life</i> , 2016, 22, 172-184.	1.0	3
70	RNAxplorer: harnessing the power of guiding potentials to sample RNA landscapes. <i>Bioinformatics</i> , 2021, 37, 2126-2133.	1.8	3
71	Insights into the secondary and tertiary structure of the Bovine Viral Diarrhea Virus Internal Ribosome Entry Site. <i>RNA Biology</i> , 2022, 19, 496-506.	1.5	3
72	Visualization of Lattice-Based Protein Folding Simulations. , 0, , .		2

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73	On the Complexity of Reconstructing Chemical Reaction Networks. Mathematics in Computer Science, 2013, 7, 275-292.	0.2	2
74	Bi-alignments as Models of Incongruent Evolution of RNA Sequence and Secondary Structure. Lecture Notes in Computer Science, 2020, , 159-170.	1.0	2
75	Generic Context-Aware Group Contributions. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 429-442.	1.9	1
76	Visualization of Barrier Tree Sequences Revisited. Mathematics and Visualization, 2008, , 275-290.	0.4	1
77	The role of Arbovirus genome untranslated regions on neurotropism. International Journal of Infectious Diseases, 2019, 79, 142.	1.5	0
78	Investigating Japanese encephalitis virus long-range terminal region interactions. Biophysical Journal, 2022, 121, 206a.	0.2	0
79	Investigating flaviviral genomic cyclization. Biophysical Journal, 2022, 121, 311a.	0.2	0