

# Michelle M Meyer

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/964171/publications.pdf>

Version: 2024-02-01

44

papers

1,579

citations

304743

22

h-index

330143

37

g-index

47

all docs

47

docs citations

47

times ranked

1673

citing authors

#	ARTICLE	IF	CITATIONS
1	2021 Zuckerkandl Prize. <i>Journal of Molecular Evolution</i> , 2022, 90, 1-1.	1.8	0
2	Revisiting the Relationships Between Genomic G+C Content, RNA Secondary Structures, and Optimal Growth Temperature. <i>Journal of Molecular Evolution</i> , 2021, 89, 165-171.	1.8	13
3	Debating tRNA Origins. <i>Journal of Molecular Evolution</i> , 2020, 88, 227-227.	1.8	1
4	Emerging Frontiers in the Study of Molecular Evolution. <i>Journal of Molecular Evolution</i> , 2020, 88, 211-226.	1.8	8
5	Comparative Metatranscriptomics of Periodontitis Supports a Common Polymicrobial Shift in Metabolic Function and Identifies Novel Putative Disease-Associated ncRNAs. <i>Frontiers in Microbiology</i> , 2020, 11, 482.	3.5	16
6	‘‘Siblings or doppelgängers?’’ Deciphering the evolution of structured cis-regulatory RNAs beyond homology. <i>Biochemical Society Transactions</i> , 2020, 48, 1941-1951.	3.4	3
7	Regulatory context drives conservation of glycine riboswitch aptamers. <i>PLoS Computational Biology</i> , 2019, 15, e1007564.	3.2	6
8	Regulatory context drives conservation of glycine riboswitch aptamers. , 2019, 15, e1007564.		0
9	Regulatory context drives conservation of glycine riboswitch aptamers. , 2019, 15, e1007564.		0
10	Regulatory context drives conservation of glycine riboswitch aptamers. , 2019, 15, e1007564.		0
11	Regulatory context drives conservation of glycine riboswitch aptamers. , 2019, 15, e1007564.		0
12	rRNA Mimicry in RNA Regulation of Gene Expression. <i>Microbiology Spectrum</i> , 2018, 6, .	3.0	17
13	The Transcriptional landscape of <i>Streptococcus pneumoniae</i> TIGR4 reveals a complex operon architecture and abundant riboregulation critical for growth and virulence. <i>PLoS Pathogens</i> , 2018, 14, e1007461.	4.7	37
14	rRNA Mimicry in RNA Regulation of Gene Expression. , 2018, , 101-116.		0
15	Fitness advantages conferred by the L20-interacting RNA< i>cis</i>-regulator of ribosomal protein synthesis in< i>Bacillus subtilis</i>. <i>Rna</i> , 2018, 24, 1133-1143.	3.5	9
16	The role of <sc>mRNA</sc> structure in bacterial translational regulation. <i>Wiley Interdisciplinary Reviews RNA</i> , 2017, 8, e1370.	6.4	33
17	< i>In Vivo</i> Behavior of the Tandem Glycine Riboswitch in < i>Bacillus subtilis</i>. <i>MBio</i> , 2017, 8, .	4.1	36
18	Recognizing RNA structural motifs in HT-SELEX data for ribosomal protein S15. <i>BMC Bioinformatics</i> , 2017, 18, 298.	2.6	9

#	ARTICLE	IF	CITATIONS
19	RNA regulators responding to ribosomal protein S15 are frequent in sequence space. <i>Nucleic Acids Research</i> , 2016, 44, gkw754.	14.5	5
20	Co-evolution of Bacterial Ribosomal Protein S15 with Diverse mRNA Regulatory Structures. <i>PLoS Genetics</i> , 2015, 11, e1005720.	3.5	15
21	Sampled ensemble neutrality as a feature to classify potential structured RNAs. <i>BMC Genomics</i> , 2015, 16, 35.	2.8	3
22	An S6:S18 complex inhibits translation of <i>E. coli rpsF</i>. <i>Rna</i> , 2015, 21, 2039-2046.	3.5	19
23	The Impact of mRNA Structures Regulating Transcription Attenuation on Bacterial Fitness. <i>FASEB Journal</i> , 2015, 29, 711.14.	0.5	0
24	Complete RNA inverse folding: computational design of functional hammerhead ribozymes. <i>Nucleic Acids Research</i> , 2014, 42, 11752-11762.	14.5	29
25	Bacterial RNA motif in the 5â€² UTR of <i>rpsF</i> interacts with an S6:S18 complex. <i>Rna</i> , 2014, 20, 168-176.	3.5	27
26	Discovery and validation of novel and distinct RNA regulators for ribosomal protein S15 in diverse bacterial phyla. <i>BMC Genomics</i> , 2014, 15, 657.	2.8	21
27	Heterochromatin assembly and transcriptome repression by Set1 in coordination with a class II histone deacetylase. <i>ELife</i> , 2014, 3, e04506.	6.0	26
28	Scribl: an HTML5 Canvas-based graphics library for visualizing genomic data over the web. <i>Bioinformatics</i> , 2013, 29, 381-383.	4.1	23
29	RNA structures regulating ribosomal protein biosynthesis in bacilli. <i>RNA Biology</i> , 2013, 10, 1180-1184.	3.1	36
30	Most RNAs regulating ribosomal protein biosynthesis in <i>Escherichia coli</i> are narrowly distributed to Gammaproteobacteria. <i>Nucleic Acids Research</i> , 2013, 41, 3491-3503.	14.5	92
31	Challenges of ligand identification for riboswitch candidates. <i>RNA Biology</i> , 2011, 8, 5-10.	3.1	61
32	A variant riboswitch aptamer class for <i>S</i>-adenosylmethionine common in marine bacteria. <i>Rna</i> , 2009, 15, 2046-2056.	3.5	96
33	Identification of candidate structured RNAs in the marine organism 'Candidatus Pelagibacter ubique'. <i>BMC Genomics</i> , 2009, 10, 268.	2.8	56
34	Exceptional structured noncoding RNAs revealed by bacterial metagenome analysis. <i>Nature</i> , 2009, 462, 656-659.	27.8	102
35	Unique glycine-activated riboswitch linked to glycine-serine auxotrophy in SAR11. <i>Environmental Microbiology</i> , 2009, 11, 230-238.	3.8	90
36	Confirmation of a second natural preQ <sub>1</sub> aptamer class in Streptococcaceae bacteria. <i>Rna</i> , 2008, 14, 685-695.	3.5	102

#	ARTICLE		IF	CITATIONS
37	Structure-guided SCHEMA recombination of distantly related $\beta$ -lactamases. <i>Protein Engineering, Design and Selection</i> , 2006, 19, 563-570.		2.1	103
38	On the conservative nature of intragenic recombination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 5380-5385.		7.1	95
39	Library analysis of SCHEMA-guided protein recombination. <i>Protein Science</i> , 2003, 12, 1686-1693.		7.6	138
40	Directed Evolution Experiments Reveal Mutations at Cycloartenol Synthase Residue His477 that Dramatically Alter Catalysis. <i>Organic Letters</i> , 2002, 4, 4459-4462.		4.6	44
41	Directed Evolution To Generate Cycloartenol Synthase Mutants that Produce Lanosterol. <i>Organic Letters</i> , 2002, 4, 1395-1398.		4.6	65
42	Cloning and characterization of the <i>Dictyostelium discoideum</i> cycloartenol synthase cDNA. <i>Lipids</i> , 2000, 35, 249-255.		1.7	29
43	Steric Bulk at Cycloartenol Synthase Position 481 Influences Cyclization and Deprotonation. <i>Organic Letters</i> , 2000, 2, 2261-2263.		4.6	45
44	Arabidopsis thaliana LUP1 Converts Oxidosqualene to Multiple Triterpene Alcohols and a Triterpene Diol. <i>Organic Letters</i> , 2000, 2, 2257-2259.		4.6	69