

# Zasha Weinberg

## List of Publications by Year in descending order

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Version: 2024-02-01

67  
papers

7,233  
citations

81900  
39  
h-index

114465  
63  
g-index

70  
all docs

70  
docs citations

70  
times ranked

5964  
citing authors

#	ARTICLE	IF	CITATIONS
1	Application of RtcB ligase to monitor self-cleaving ribozyme activity by RNA-seq. <i>Biological Chemistry</i> , 2022, .	2.5	2
2	Spacer prioritization in CRISPR-Cas9 immunity is enabled by the leader RNA. <i>Nature Microbiology</i> , 2022, 7, 530-541.	13.3	9
3	RNAcentral 2021: secondary structure integration, improved sequence search and new member databases. <i>Nucleic Acids Research</i> , 2021, 49, D212-D220.	14.5	160
4	Rfam 14: expanded coverage of metagenomic, viral and microRNA families. <i>Nucleic Acids Research</i> , 2021, 49, D192-D200.	14.5	475
5	Beyond Plug and Pray: Context Sensitivity and <i>in silico</i> Design of Artificial Neomycin Riboswitches. <i>RNA Biology</i> , 2021, 18, 457-467.	3.1	6
6	Widespread bacterial utilization of guanidine as nitrogen source. <i>Molecular Microbiology</i> , 2021, 116, 200-210.	2.5	14
7	Biochemical analysis of cleavage and ligation activities of the pistol ribozyme from <i>Paenibacillus polymyxa</i> . <i>RNA Biology</i> , 2021, 18, 1-9.	3.1	9
8	Identification of over 200-fold more hairpin ribozymes than previously known in diverse circular RNAs. <i>Nucleic Acids Research</i> , 2021, 49, 6375-6388.	14.5	16
9	Satellite-Like W-Elements: Repetitive, Transcribed, and Putative Mobile Genetic Factors with Potential Roles for Biology and Evolution of <i>Schistosoma mansoni</i> . <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	8
10	cyPhyRNA-seq: a genome-scale RNA-seq method to detect active self-cleaving ribozymes by capturing RNAs with 2',3'-cyclic phosphates and 5'-hydroxyl ends. <i>RNA Biology</i> , 2021, 18, 818-831.	3.1	5
11	Natural circularly permuted group II introns in bacteria produce RNA circles. <i>iScience</i> , 2021, 24, 103431.	4.1	7
12	Discovery and characterization of a fourth class of guanidine riboswitches. <i>Nucleic Acids Research</i> , 2020, 48, 12889-12899.	14.5	23
13	A rare bacterial RNA motif is implicated in the regulation of the <i>purF</i> gene whose encoded enzyme synthesizes phosphoribosylamine. <i>Rna</i> , 2020, 26, 1838-1846.	3.5	5
14	Discovery of 20 novel ribosomal leader candidates in bacteria and archaea. <i>BMC Microbiology</i> , 2020, 20, 130.	3.3	10
15	A Plant Pathogen Type III Effector Protein Subverts Translational Regulation to Boost Host Polyamine Levels. <i>Cell Host and Microbe</i> , 2019, 26, 638-649.e5.	11.0	68
16	Novel ribozymes: discovery, catalytic mechanisms, and the quest to understand biological function. <i>Nucleic Acids Research</i> , 2019, 47, 9480-9494.	14.5	54
17	A streamlined protocol for the detection of mRNA-sRNA interactions using AMT-crosslinking <i>in vitro</i> . <i>BioTechniques</i> , 2019, 67, 178-183.	1.8	4
18	The structure of the SAM/SAH-binding riboswitch. <i>Nucleic Acids Research</i> , 2019, 47, 2654-2665.	14.5	33

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19	SAM-VI RNAs selectively bind <i>S</i> -adenosylmethionine and exhibit similarities to SAM-III riboswitches. <i>RNA Biology</i> , 2018, 15, 371-378.	3.1	42
20	Bioinformatic analysis of riboswitch structures uncovers variant classes with altered ligand specificity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E2077-E2085.	7.1	75
21	Activation of the <i>glmS</i> Ribozyme Confers Bacterial Growth Inhibition. <i>ChemBioChem</i> , 2017, 18, 435-440.	2.6	24
22	Detection of 224 candidate structured RNAs by comparative analysis of specific subsets of intergenic regions. <i>Nucleic Acids Research</i> , 2017, 45, 10811-10823.	14.5	116
23	Numerous small hammerhead ribozyme variants associated with Penelope-like retrotransposons cleave RNA as dimers. <i>RNA Biology</i> , 2017, 14, 1499-1507.	3.1	17
24	Reporter Gene-Based Screening for TPP Riboswitch Activators. <i>Methods in Molecular Biology</i> , 2017, 1520, 227-235.	0.9	9
25	tRNA Modifications: Impact on Structure and Thermal Adaptation. <i>Biomolecules</i> , 2017, 7, 35.	4.0	241
26	Biochemical analysis of hatchet self-cleaving ribozymes. <i>Rna</i> , 2015, 21, 1845-1851.	3.5	36
27	Biochemical analysis of pistol self-cleaving ribozymes. <i>Rna</i> , 2015, 21, 1852-1858.	3.5	59
28	New classes of self-cleaving ribozymes revealed by comparative genomics analysis. <i>Nature Chemical Biology</i> , 2015, 11, 606-610.	8.0	174
29	Bacterial Riboswitches Cooperatively Bind Ni <sup>2+</sup> or Co <sup>2+</sup> Ions and Control Expression of Heavy Metal Transporters. <i>Molecular Cell</i> , 2015, 57, 1088-1098.	9.7	147
30	Control of bacterial exoelectrogenesis by c-AMP-GMP. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 5389-5394.	7.1	98
31	Novel TPP-riboswitch activators bypass metabolic enzyme dependency. <i>Frontiers in Chemistry</i> , 2014, 2, 53.	3.6	17
32	The promise of riboswitches as potential antibacterial drug targets. <i>International Journal of Medical Microbiology</i> , 2014, 304, 79-92.	3.6	65
33	A widespread self-cleaving ribozyme class is revealed by bioinformatics. <i>Nature Chemical Biology</i> , 2014, 10, 56-60.	8.0	217
34	Structural, Functional, and Taxonomic Diversity of Three PreQ1 Riboswitch Classes. <i>Chemistry and Biology</i> , 2014, 21, 880-889.	6.0	78
35	Screening Assays to Identify Artificial <i>glmS</i> Ribozyme Activators. <i>Methods in Molecular Biology</i> , 2014, 1103, 199-209.	0.9	2
36	Riboswitches in eubacteria sense the second messenger c-di-AMP. <i>Nature Chemical Biology</i> , 2013, 9, 834-839.	8.0	247

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37	Small, Highly Active DNAs That Hydrolyze DNA. <i>Journal of the American Chemical Society</i> , 2013, 135, 9121-9129.	13.7	134
38	Fluoride resistance and transport by riboswitch-controlled CLC antiporters. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 15289-15294.	7.1	125
39	Widespread Genetic Switches and Toxicity Resistance Proteins for Fluoride. <i>Science</i> , 2012, 335, 233-235.	12.6	356
40	Carba-sugars Activate the glmS-Riboswitch of <i>Staphylococcus aureus</i> . <i>ACS Chemical Biology</i> , 2011, 6, 675-678.	3.4	66
41	Meeting report of the RNA Ontology Consortium January 8-9, 2011. <i>Standards in Genomic Sciences</i> , 2011, 4, 252-256.	1.5	1
42	RNA diagnostics: real-time RT-PCR strategies and promising novel target RNAs. <i>Wiley Interdisciplinary Reviews RNA</i> , 2011, 2, 32-41.	6.4	26
43	R2R - software to speed the depiction of aesthetic consensus RNA secondary structures. <i>BMC Bioinformatics</i> , 2011, 12, 3.	2.6	226
44	RNIE: genome-wide prediction of bacterial intrinsic terminators. <i>Nucleic Acids Research</i> , 2011, 39, 5845-5852.	14.5	71
45	Identification of Hammerhead Ribozymes in All Domains of Life Reveals Novel Structural Variations. <i>PLoS Computational Biology</i> , 2011, 7, e1002031.	3.2	124
46	An Aptamer Targeting the Apical Loop Domain Modulates pri-miRNA Processing. <i>Angewandte Chemie - International Edition</i> , 2010, 49, 4674-4677.	13.8	49
47	A Eubacterial Riboswitch Class That Senses the Coenzyme Tetrahydrofolate. <i>Chemistry and Biology</i> , 2010, 17, 681-685.	6.0	86
48	An Allosteric Self-Splicing Ribozyme Triggered by a Bacterial Second Messenger. <i>Science</i> , 2010, 329, 845-848.	12.6	309
49	Comparative genomics reveals 104 candidate structured RNAs from bacteria, archaea, and their metagenomes. <i>Genome Biology</i> , 2010, 11, R31.	9.6	348
50	Identification of candidate structured RNAs in the marine organism 'Candidatus Pelagibacter ubique'. <i>BMC Genomics</i> , 2009, 10, 268.	2.8	56
51	Exceptional structured noncoding RNAs revealed by bacterial metagenome analysis. <i>Nature</i> , 2009, 462, 656-659.	27.8	102
52	FINDING NON-CODING RNAs THROUGH GENOME-SCALE CLUSTERING. <i>Journal of Bioinformatics and Computational Biology</i> , 2009, 07, 373-388.	0.8	28
53	A widespread riboswitch candidate that controls bacterial genes involved in molybdenum cofactor and tungsten cofactor metabolism. <i>Molecular Microbiology</i> , 2008, 68, 918-932.	2.5	142
54	The aptamer core of SAM-IV riboswitches mimics the ligand-binding site of SAM-I riboswitches. <i>Rna</i> , 2008, 14, 822-828.	3.5	103

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55	The RNA WikiProject: Community annotation of RNA families. <i>Rna</i> , 2008, 14, 2462-2464.	3.5	66
56	A Computational Pipeline for High- Throughput Discovery of cis-Regulatory Noncoding RNA in Prokaryotes. <i>PLoS Computational Biology</i> , 2007, 3, e126.	3.2	77
57	Identification of 22 candidate structured RNAs in bacteria using the CMfinder comparative genomics pipeline. <i>Nucleic Acids Research</i> , 2007, 35, 4809-4819.	14.5	292
58	FINDING NON-CODING RNAs THROUGH GENOME-SCALE CLUSTERING. , 2007, , .		0
59	Macronuclear Genome Sequence of the Ciliate <i>Tetrahymena thermophila</i> , a Model Eukaryote. <i>PLoS Biology</i> , 2006, 4, e286.	5.6	657
60	CMfinder—a covariance model based RNA motif finding algorithm. <i>Bioinformatics</i> , 2006, 22, 445-452.	4.1	316
61	Sequence-based heuristics for faster annotation of non-coding RNA families. <i>Bioinformatics</i> , 2006, 22, 35-39.	4.1	98
62	6S RNA is a widespread regulator of eubacterial RNA polymerase that resembles an open promoter. <i>Rna</i> , 2005, 11, 774-784.	3.5	210
63	Exploiting conserved structure for faster annotation of non-coding RNAs without loss of accuracy. <i>Bioinformatics</i> , 2004, 20, i334-i341.	4.1	56
64	Faster genome annotation of non-coding RNA families without loss of accuracy. , 2004, , .		43
65	A Glycine-Dependent Riboswitch That Uses Cooperative Binding to Control Gene Expression. <i>Science</i> , 2004, 306, 275-279.	12.6	491
66	An approximate search engine for structural databases. , 2000, , .		1
67	An approximate search engine for structural databases. <i>SIGMOD Record</i> , 2000, 29, 584.	1.2	0