

# Paul P Gardner

## List of Publications by Year in descending order

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Version: 2024-02-01

78  
papers

7,773  
citations

109321

35  
h-index

71685

76  
g-index

94  
all docs

94  
docs citations

94  
times ranked

13001  
citing authors

#	ARTICLE	IF	CITATIONS
1	Sustained software development, not number of citations or journal choice, is indicative of accurate bioinformatic software. <i>Genome Biology</i> , 2022, 23, 56.	8.8	8
2	TISIGNER.com: web services for improving recombinant protein production. <i>Nucleic Acids Research</i> , 2021, 49, W654-W661.	14.5	15
3	Evolution of virulence in a novel family of transmissible mega-plasmids. <i>Environmental Microbiology</i> , 2021, 23, 5289-5304.	3.8	5
4	On the optimistic performance evaluation of newly introduced bioinformatic methods. <i>Genome Biology</i> , 2021, 22, 152.	8.8	20
5	SorTn-seq: a high-throughput functional genomics approach to discovering regulators of bacterial gene expression. <i>Nature Protocols</i> , 2021, 16, 4382-4418.	12.0	7
6	The Rcs stress response inversely controls surface and CRISPR-Cas adaptive immunity to discriminate plasmids and phages. <i>Nature Microbiology</i> , 2021, 6, 162-172.	13.3	32
7	Analysis of 11,430 recombinant protein production experiments reveals that protein yield is tunable by synonymous codon changes of translation initiation sites. <i>PLoS Computational Biology</i> , 2021, 17, e1009461.	3.2	9
8	A jumbo phage that forms a nucleus-like structure evades CRISPR-Cas DNA targeting but is vulnerable to type III RNA-based immunity. <i>Nature Microbiology</i> , 2020, 5, 48-55.	13.3	123
9	The tuatara genome reveals ancient features of amniote evolution. <i>Nature</i> , 2020, 584, 403-409.	27.8	105
10	Solubility-Weighted Index: fast and accurate prediction of protein solubility. <i>Bioinformatics</i> , 2020, 36, 4691-4698.	4.1	40
11	ncVarDB: a manually curated database for pathogenic non-coding variants and benign controls. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	3.0	8
12	Essential guidelines for computational method benchmarking. <i>Genome Biology</i> , 2019, 20, 125.	8.8	114
13	Transcriptional noise and exaptation as sources for bacterial sRNAs. <i>Biochemical Society Transactions</i> , 2019, 47, 527-539.	3.4	38
14	Convergent regulatory evolution and loss of flight in paleognathous birds. <i>Science</i> , 2019, 364, 74-78.	12.6	189
15	Genomic correlates of extraintestinal infection are linked with changes in cell morphology in <i>Campylobacter jejuni</i> . <i>Microbial Genomics</i> , 2019, 5, .	2.0	6
16	Identifying accurate metagenome and amplicon software via a meta-analysis of sequence to taxonomy benchmarking studies. <i>PeerJ</i> , 2019, 7, e6160.	2.0	34
17	Towards robust and repeatable sampling methods in scDNA-based studies. <i>Molecular Ecology Resources</i> , 2018, 18, 940-952.	4.8	137
18	An Evaluation of Function of Multicopy Noncoding RNAs in Mammals Using ENCODE/FANTOM Data and Comparative Genomics. <i>Molecular Biology and Evolution</i> , 2018, 35, 1451-1462.	8.9	5

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19	Machine learning identifies signatures of host adaptation in the bacterial pathogen <i>Salmonella enterica</i> . <i>PLoS Genetics</i> , 2018, 14, e1007333.	3.5	73
20	A comprehensive benchmark of RNA-RNA interaction prediction tools for all domains of life. <i>Bioinformatics</i> , 2017, 33, 988-996.	4.1	54
21	Why so narrow: Distribution of anti-sense regulated, type I toxin-antitoxin systems compared with type II and type III systems. <i>RNA Biology</i> , 2017, 14, 275-280.	3.1	27
22	Genomic, Transcriptomic, and Phenotypic Analyses of <i>Neisseria meningitidis</i> Isolates from Disease Patients and Their Household Contacts. <i>MSystems</i> , 2017, 2, .	3.8	3
23	Complete Genome Sequences of Two Geographically Distinct <i>Legionella micdadei</i> Clinical Isolates. <i>Genome Announcements</i> , 2017, 5, .	0.8	0
24	Analysis of the genome of the New Zealand giant collembolan ( <i>Holacanthella duospinosa</i> ) sheds light on hexapod evolution. <i>BMC Genomics</i> , 2017, 18, 795.	2.8	28
25	Transposon insertion libraries for the characterization of mutants from the kiwifruit pathogen <i>Pseudomonas syringae</i> pv. <i>actinidiae</i> . <i>PLoS ONE</i> , 2017, 12, e0172790.	2.5	26
26	A profile-based method for identifying functional divergence of orthologous genes in bacterial genomes. <i>Bioinformatics</i> , 2016, 32, 3566-3574.	4.1	25
27	Studying RNA Homology and Conservation with Infernal: From Single Sequences to RNA Families. <i>Current Protocols in Bioinformatics</i> , 2016, 54, 12.13.1-12.13.25.	25.8	21
28	An evaluation of the accuracy and speed of metagenome analysis tools. <i>Scientific Reports</i> , 2016, 6, 19233.	3.3	278
29	Avoidance of stochastic RNA interactions can be harnessed to control protein expression levels in bacteria and archaea. <i>ELife</i> , 2016, 5, .	6.0	25
30	Conservation and Losses of Non-Coding RNAs in Avian Genomes. <i>PLoS ONE</i> , 2015, 10, e0121797.	2.5	18
31	Annotating RNA motifs in sequences and alignments. <i>Nucleic Acids Research</i> , 2015, 43, 691-698.	14.5	21
32	Third Report on Chicken Genes and Chromosomes 2015. <i>Cytogenetic and Genome Research</i> , 2015, 145, 78-179.	1.1	97
33	Rfam 12.0: updates to the RNA families database. <i>Nucleic Acids Research</i> , 2015, 43, D130-D137.	14.5	1,000
34	Crowdsourcing RNA structural alignments with an online computer game. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2015, , 330-41.	0.7	5
35	Molecular characterization of a new member of the lariat capping twin-ribozyme introns. <i>Mobile DNA</i> , 2014, 5, 25.	3.6	14
36	Robust Identification of Noncoding RNA from Transcriptomes Requires Phylogenetically-Informed Sampling. <i>PLoS Computational Biology</i> , 2014, 10, e1003907.	3.2	49

#	ARTICLE	IF	CITATIONS
37	Comparative genomics reveals insights into avian genome evolution and adaptation. <i>Science</i> , 2014, 346, 1311-1320.	12.6	895
38	An Introduction to RNA Databases. <i>Methods in Molecular Biology</i> , 2014, 1097, 107-123.	0.9	7
39	CROWDSOURCING RNA STRUCTURAL ALIGNMENTS WITH AN ONLINE COMPUTER GAME. , 2014, , .		5
40	Letter from the Editor. <i>RNA Biology</i> , 2013, 10, 1-1.	3.1	47
41	Genome and Transcriptome Adaptation Accompanying Emergence of the Definitive Type 2 Host-Restricted <i>Salmonella enterica</i> Serovar Typhimurium Pathovar. <i>MBio</i> , 2013, 4, e00565-13.	4.1	57
42	Rfam 11.0: 10 years of RNA families. <i>Nucleic Acids Research</i> , 2013, 41, D226-D232.	14.5	745
43	A comparison of dense transposon insertion libraries in the <i>Salmonella</i> serovars Typhi and Typhimurium. <i>Nucleic Acids Research</i> , 2013, 41, 4549-4564.	14.5	108
44	Comparative Analysis of RNA Families Reveals Distinct Repertoires for Each Domain of Life. <i>PLoS Computational Biology</i> , 2012, 8, e1002752.	3.2	50
45	A VapBC Toxin-Antitoxin Module Is a Posttranscriptional Regulator of Metabolic Flux in <i>Mycobacteria</i> . <i>Journal of Bacteriology</i> , 2012, 194, 2189-2204.	2.2	75
46	Making your database available through Wikipedia: the pros and cons. <i>Nucleic Acids Research</i> , 2012, 40, D9-D12.	14.5	31
47	RNASTAR: An RNA STructural Alignment Repository that provides insight into the evolution of natural and artificial RNAs. <i>Rna</i> , 2012, 18, 1319-1327.	3.5	30
48	Three years of RNA Families. <i>RNA Biology</i> , 2012, 9, 2-3.	3.1	3
49	RNIE: genome-wide prediction of bacterial intrinsic terminators. <i>Nucleic Acids Research</i> , 2011, 39, 5845-5852.	14.5	71
50	Rfam: Wikipedia, clans and the "decimal" release. <i>Nucleic Acids Research</i> , 2011, 39, D141-D145.	14.5	355
51	RNAcentral: A vision for an international database of RNA sequences. <i>Rna</i> , 2011, 17, 1941-1946.	3.5	67
52	Two covariance models for iron-responsive elements. <i>RNA Biology</i> , 2011, 8, 792-801.	3.1	11
53	Quantitative RNA-seq analysis of the <i>Campylobacter jejuni</i> transcriptome. <i>Microbiology (United Kingdom)</i> 151: 1073-1083. doi:10.1099/mic/0/000000.0	1.8	44
54	SnoPatrol: how many snoRNA genes are there?. <i>Journal of Biology</i> , 2010, 9, 4.	2.7	37

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55	Ten Simple Rules for Editing Wikipedia. <i>PLoS Computational Biology</i> , 2010, 6, e1000941.	3.2	36
56	Long- and Short-Term Selective Forces on Malaria Parasite Genomes. <i>PLoS Genetics</i> , 2010, 6, e1001099.	3.5	30
57	The use of covariance models to annotate RNAs in whole genomes. <i>Briefings in Functional Genomics &amp; Proteomics</i> , 2009, 8, 444-450.	3.8	17
58	A home for RNA families at <i>RNA Biology</i> . <i>RNA Biology</i> , 2009, 6, 2-4.	3.1	8
59	Rfam: updates to the RNA families database. <i>Nucleic Acids Research</i> , 2009, 37, D136-D140.	14.5	820
60	A Strand-Specific RNA-Seq Analysis of the Transcriptome of the Typhoid Bacillus <i>Salmonella Typhi</i> . <i>PLoS Genetics</i> , 2009, 5, e1000569.	3.5	202
61	Mutation of miRNA target sequences during human evolution. <i>Trends in Genetics</i> , 2008, 24, 262-265.	6.7	23
62	Genome-wide discovery and verification of novel structured RNAs in <i>Plasmodium falciparum</i> . <i>Genome Research</i> , 2008, 18, 281-292.	5.5	81
63	The RNA WikiProject: Community annotation of RNA families. <i>Rna</i> , 2008, 14, 2462-2464.	3.5	66
64	MASTR: multiple alignment and structure prediction of non-coding RNAs using simulated annealing. <i>Bioinformatics</i> , 2007, 23, 3304-3311.	4.1	67
65	Multiple alignment and structure prediction of non-coding RNA sequences. <i>BMC Bioinformatics</i> , 2007, 8, .	2.6	2
66	Use of tiling array data and RNA secondary structure predictions to identify noncoding RNA genes. <i>BMC Genomics</i> , 2007, 8, 244.	2.8	12
67	Identification of miRNA targets with stable isotope labeling by amino acids in cell culture. <i>Nucleic Acids Research</i> , 2006, 34, e107-e107.	14.5	112
68	A hidden Markov model approach for determining expression from genomic tiling micro arrays. <i>BMC Bioinformatics</i> , 2006, 7, 239.	2.6	24
69	Exploring genomic dark matter: A critical assessment of the performance of homology search methods on noncoding RNA. <i>Genome Research</i> , 2006, 17, 117-125.	5.5	121
70	Measuring covariation in RNA alignments: physical realism improves information measures. <i>Bioinformatics</i> , 2006, 22, 2988-2995.	4.1	52
71	A comparison of RNA folding measures. <i>BMC Bioinformatics</i> , 2005, 6, 241.	2.6	101
72	A benchmark of multiple sequence alignment programs upon structural RNAs. <i>Nucleic Acids Research</i> , 2005, 33, 2433-2439.	14.5	242

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73	Predicting RNA Structure Using Mutual Information. <i>Applied Bioinformatics</i> , 2005, 4, 53-59.	1.6	25
74	A comprehensive comparison of comparative RNA structure prediction approaches. <i>BMC Bioinformatics</i> , 2004, 5, 140.	2.6	291
75	Optimal alphabets for an RNA world. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2003, 270, 1177-1182.	2.6	19
76	A search for H/ACA snoRNAs in yeast using MFE secondary structure prediction. <i>Bioinformatics</i> , 2003, 19, 865-873.	4.1	38
77	Sequence Diversity and Functional Conservation of the Origin of Replication in Lactococcal Prolate Phages. <i>Applied and Environmental Microbiology</i> , 2003, 69, 5104-5114.	3.1	7
78	RNA Folding Argues Against a Hot-Start Origin of Life. <i>Journal of Molecular Evolution</i> , 2000, 51, 416-421.	1.8	43