

Paul P Gardner

List of Publications by Year in descending order

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Version: 2024-02-01

78
papers

7,773
citations

109137

35
h-index

71532

76
g-index

94
all docs

94
docs citations

94
times ranked

13001
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Rfam 12.0: updates to the RNA families database. <i>Nucleic Acids Research</i> , 2015, 43, D130-D137. | 6.5 | 1,000 |
| 2 | Comparative genomics reveals insights into avian genome evolution and adaptation. <i>Science</i> , 2014, 346, 1311-1320. | 6.0 | 895 |
| 3 | Rfam: updates to the RNA families database. <i>Nucleic Acids Research</i> , 2009, 37, D136-D140. | 6.5 | 820 |
| 4 | Rfam 11.0: 10 years of RNA families. <i>Nucleic Acids Research</i> , 2013, 41, D226-D232. | 6.5 | 745 |
| 5 | Rfam: Wikipedia, clans and the "decimal" release. <i>Nucleic Acids Research</i> , 2011, 39, D141-D145. | 6.5 | 355 |
| 6 | A comprehensive comparison of comparative RNA structure prediction approaches. <i>BMC Bioinformatics</i> , 2004, 5, 140. | 1.2 | 291 |
| 7 | An evaluation of the accuracy and speed of metagenome analysis tools. <i>Scientific Reports</i> , 2016, 6, 19233. | 1.6 | 278 |
| 8 | A benchmark of multiple sequence alignment programs upon structural RNAs. <i>Nucleic Acids Research</i> , 2005, 33, 2433-2439. | 6.5 | 242 |
| 9 | A Strand-Specific RNA-Seq Analysis of the Transcriptome of the Typhoid Bacillus <i>Salmonella Typhi</i> . <i>PLoS Genetics</i> , 2009, 5, e1000569. | 1.5 | 202 |
| 10 | Convergent regulatory evolution and loss of flight in paleognathous birds. <i>Science</i> , 2019, 364, 74-78. | 6.0 | 189 |
| 11 | Towards robust and repeatable sampling methods in eDNA-based studies. <i>Molecular Ecology Resources</i> , 2018, 18, 940-952. | 2.2 | 137 |
| 12 | 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. | 5.9 | 123 |
| 13 | 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. | 2.4 | 121 |
| 14 | Essential guidelines for computational method benchmarking. <i>Genome Biology</i> , 2019, 20, 125. | 3.8 | 114 |
| 15 | Identification of miRNA targets with stable isotope labeling by amino acids in cell culture. <i>Nucleic Acids Research</i> , 2006, 34, e107-e107. | 6.5 | 112 |
| 16 | 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. | 6.5 | 108 |
| 17 | The tuatara genome reveals ancient features of amniote evolution. <i>Nature</i> , 2020, 584, 403-409. | 13.7 | 105 |
| 18 | A comparison of RNA folding measures. <i>BMC Bioinformatics</i> , 2005, 6, 241. | 1.2 | 101 |

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|----|--|-----|-----------|
| 19 | Third Report on Chicken Genes and Chromosomes 2015. <i>Cytogenetic and Genome Research</i> , 2015, 145, 78-179. | 0.6 | 97 |
| 20 | Genome-wide discovery and verification of novel structured RNAs in <i>Plasmodium falciparum</i> . <i>Genome Research</i> , 2008, 18, 281-292. | 2.4 | 81 |
| 21 | 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. | 1.0 | 75 |
| 22 | Machine learning identifies signatures of host adaptation in the bacterial pathogen <i>Salmonella enterica</i> . <i>PLoS Genetics</i> , 2018, 14, e1007333. | 1.5 | 73 |
| 23 | RNIE: genome-wide prediction of bacterial intrinsic terminators. <i>Nucleic Acids Research</i> , 2011, 39, 5845-5852. | 6.5 | 71 |
| 24 | MASTR: multiple alignment and structure prediction of non-coding RNAs using simulated annealing. <i>Bioinformatics</i> , 2007, 23, 3304-3311. | 1.8 | 67 |
| 25 | RNAcentral: A vision for an international database of RNA sequences. <i>Rna</i> , 2011, 17, 1941-1946. | 1.6 | 67 |
| 26 | The RNA WikiProject: Community annotation of RNA families. <i>Rna</i> , 2008, 14, 2462-2464. | 1.6 | 66 |
| 27 | 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. | 1.8 | 57 |
| 28 | A comprehensive benchmark of RNA-RNA interaction prediction tools for all domains of life. <i>Bioinformatics</i> , 2017, 33, 988-996. | 1.8 | 54 |
| 29 | Measuring covariation in RNA alignments: physical realism improves information measures. <i>Bioinformatics</i> , 2006, 22, 2988-2995. | 1.8 | 52 |
| 30 | Comparative Analysis of RNA Families Reveals Distinct Repertoires for Each Domain of Life. <i>PLoS Computational Biology</i> , 2012, 8, e1002752. | 1.5 | 50 |
| 31 | Robust Identification of Noncoding RNA from Transcriptomes Requires Phylogenetically-Informed Sampling. <i>PLoS Computational Biology</i> , 2014, 10, e1003907. | 1.5 | 49 |
| 32 | Letter from the Editor. <i>RNA Biology</i> , 2013, 10, 1-1. | 1.5 | 47 |
| 33 | Quantitative RNA-seq analysis of the <i>Campylobacter jejuni</i> transcriptome. <i>Microbiology (United Kingdom)</i> 153, 10, 2015, 2700-2714. doi:10.1099/mic/0/000000.0 | 0.7 | 44 |
| 34 | RNA Folding Argues Against a Hot-Start Origin of Life. <i>Journal of Molecular Evolution</i> , 2000, 51, 416-421. | 0.8 | 43 |
| 35 | Solubility-Weighted Index: fast and accurate prediction of protein solubility. <i>Bioinformatics</i> , 2020, 36, 4691-4698. | 1.8 | 40 |
| 36 | A search for H/ACA snoRNAs in yeast using MFE secondary structure prediction. <i>Bioinformatics</i> , 2003, 19, 865-873. | 1.8 | 38 |

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|----|--|------|-----------|
| 37 | Transcriptional noise and exaptation as sources for bacterial sRNAs. <i>Biochemical Society Transactions</i> , 2019, 47, 527-539. | 1.6 | 38 |
| 38 | SnoPatrol: how many snoRNA genes are there?. <i>Journal of Biology</i> , 2010, 9, 4. | 2.7 | 37 |
| 39 | Ten Simple Rules for Editing Wikipedia. <i>PLoS Computational Biology</i> , 2010, 6, e1000941. | 1.5 | 36 |
| 40 | Identifying accurate metagenome and amplicon software via a meta-analysis of sequence to taxonomy benchmarking studies. <i>PeerJ</i> , 2019, 7, e6160. | 0.9 | 34 |
| 41 | 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. | 5.9 | 32 |
| 42 | Making your database available through Wikipedia: the pros and cons. <i>Nucleic Acids Research</i> , 2012, 40, D9-D12. | 6.5 | 31 |
| 43 | RNASTAR: An RNA STRUCTURAL Alignment Repository that provides insight into the evolution of natural and artificial RNAs. <i>Rna</i> , 2012, 18, 1319-1327. | 1.6 | 30 |
| 44 | Long- and Short-Term Selective Forces on Malaria Parasite Genomes. <i>PLoS Genetics</i> , 2010, 6, e1001099. | 1.5 | 30 |
| 45 | 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. | 1.2 | 28 |
| 46 | 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. | 1.5 | 27 |
| 47 | 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. | 1.1 | 26 |
| 48 | Predicting RNA Structure Using Mutual Information. <i>Applied Bioinformatics</i> , 2005, 4, 53-59. | 1.7 | 25 |
| 49 | A profile-based method for identifying functional divergence of orthologous genes in bacterial genomes. <i>Bioinformatics</i> , 2016, 32, 3566-3574. | 1.8 | 25 |
| 50 | Avoidance of stochastic RNA interactions can be harnessed to control protein expression levels in bacteria and archaea. <i>ELife</i> , 2016, 5, . | 2.8 | 25 |
| 51 | A hidden Markov model approach for determining expression from genomic tiling micro arrays. <i>BMC Bioinformatics</i> , 2006, 7, 239. | 1.2 | 24 |
| 52 | Mutation of miRNA target sequences during human evolution. <i>Trends in Genetics</i> , 2008, 24, 262-265. | 2.9 | 23 |
| 53 | Annotating RNA motifs in sequences and alignments. <i>Nucleic Acids Research</i> , 2015, 43, 691-698. | 6.5 | 21 |
| 54 | 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 |

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|----|--|-----|-----------|
| 55 | On the optimistic performance evaluation of newly introduced bioinformatic methods. <i>Genome Biology</i> , 2021, 22, 152. | 3.8 | 20 |
| 56 | Optimal alphabets for an RNA world. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2003, 270, 1177-1182. | 1.2 | 19 |
| 57 | Conservation and Losses of Non-Coding RNAs in Avian Genomes. <i>PLoS ONE</i> , 2015, 10, e0121797. | 1.1 | 18 |
| 58 | The use of covariance models to annotate RNAs in whole genomes. <i>Briefings in Functional Genomics & Proteomics</i> , 2009, 8, 444-450. | 3.8 | 17 |
| 59 | TISIGNER.com: web services for improving recombinant protein production. <i>Nucleic Acids Research</i> , 2021, 49, W654-W661. | 6.5 | 15 |
| 60 | Molecular characterization of a new member of the lariat capping twin-ribozyme introns. <i>Mobile DNA</i> , 2014, 5, 25. | 1.3 | 14 |
| 61 | Use of tiling array data and RNA secondary structure predictions to identify noncoding RNA genes. <i>BMC Genomics</i> , 2007, 8, 244. | 1.2 | 12 |
| 62 | Two covariance models for iron-responsive elements. <i>RNA Biology</i> , 2011, 8, 792-801. | 1.5 | 11 |
| 63 | 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. | 1.5 | 9 |
| 64 | A home for RNA families at <i>RNA Biology</i> . <i>RNA Biology</i> , 2009, 6, 2-4. | 1.5 | 8 |
| 65 | 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, . | 1.4 | 8 |
| 66 | Sustained software development, not number of citations or journal choice, is indicative of accurate bioinformatic software. <i>Genome Biology</i> , 2022, 23, 56. | 3.8 | 8 |
| 67 | Sequence Diversity and Functional Conservation of the Origin of Replication in Lactococcal Prolate Phages. <i>Applied and Environmental Microbiology</i> , 2003, 69, 5104-5114. | 1.4 | 7 |
| 68 | An Introduction to RNA Databases. <i>Methods in Molecular Biology</i> , 2014, 1097, 107-123. | 0.4 | 7 |
| 69 | SorTn-seq: a high-throughput functional genomics approach to discovering regulators of bacterial gene expression. <i>Nature Protocols</i> , 2021, 16, 4382-4418. | 5.5 | 7 |
| 70 | Genomic correlates of extraintestinal infection are linked with changes in cell morphology in <i>Campylobacter jejuni</i> . <i>Microbial Genomics</i> , 2019, 5, . | 1.0 | 6 |
| 71 | 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. | 3.5 | 5 |
| 72 | Evolution of virulence in a novel family of transmissible megaplasmids. <i>Environmental Microbiology</i> , 2021, 23, 5289-5304. | 1.8 | 5 |

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|----|--|-----|-----------|
| 73 | CROWDSOURCING RNA STRUCTURAL ALIGNMENTS WITH AN ONLINE COMPUTER GAME. , 2014, , . | | 5 |
| 74 | Crowdsourcing RNA structural alignments with an online computer game. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2015, , 330-41. | 0.7 | 5 |
| 75 | Three years of RNA Families. RNA Biology, 2012, 9, 2-3. | 1.5 | 3 |
| 76 | Genomic, Transcriptomic, and Phenotypic Analyses of Neisseria meningitidis Isolates from Disease Patients and Their Household Contacts. MSystems, 2017, 2, . | 1.7 | 3 |
| 77 | Multiple alignment and structure prediction of non-coding RNA sequences. BMC Bioinformatics, 2007, 8, . | 1.2 | 2 |
| 78 | Complete Genome Sequences of Two Geographically Distinct Legionella micdadei Clinical Isolates. Genome Announcements, 2017, 5, . | 0.8 | 0 |