

Erik Scott Wright

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3093119/publications.pdf>

Version: 2024-02-01

23
papers

1,076
citations

933447

10
h-index

794594

19
g-index

26
all docs

26
docs citations

26
times ranked

1972
citing authors

#	ARTICLE	IF	CITATIONS
1	IDTAXA: a novel approach for accurate taxonomic classification of microbiome sequences. <i>Microbiome</i> , 2018, 6, 140.	11.1	336
2	DECIPHER: harnessing local sequence context to improve protein multiple sequence alignment. <i>BMC Bioinformatics</i> , 2015, 16, 322.	2.6	271
3	Quality filtering of Illumina index reads mitigates sample cross-talk. <i>BMC Genomics</i> , 2016, 17, 876.	2.8	103
4	Inhibitory interactions promote frequent bistability among competing bacteria. <i>Nature Communications</i> , 2016, 7, 11274.	12.8	82
5	Exploiting extension bias in polymerase chain reaction to improve primer specificity in ensembles of nearly identical <sc>DNA</sc> templates. <i>Environmental Microbiology</i> , 2014, 16, 1354-1365.	3.8	72
6	Automated Design of Probes for rRNA-Targeted Fluorescence <i>In Situ</i> Hybridization Reveals the Advantages of Using Dual Probes for Accurate Identification. <i>Applied and Environmental Microbiology</i> , 2014, 80, 5124-5133.	3.1	39
7	RNAconTest: comparing tools for noncoding RNA multiple sequence alignment based on structural consistency. <i>Rna</i> , 2020, 26, 531-540.	3.5	37
8	Identification of antibiotic pairs that evade concurrent resistance via a retrospective analysis of antimicrobial susceptibility test results. <i>Lancet Microbe</i> , The, 2021, 2, e545-e554.	7.3	26
9	Stochastic exits from dormancy give rise to heavy-tailed distributions of descendants in bacterial populations. <i>Molecular Ecology</i> , 2019, 28, 3915-3928.	3.9	21
10	Modeling Formamide Denaturation of Probe-Target Hybrids for Improved Microarray Probe Design in Microbial Diagnostics. <i>PLoS ONE</i> , 2012, 7, e43862.	2.5	16
11	Exclusivity offers a sound yet practical species criterion for bacteria despite abundant gene flow. <i>BMC Genomics</i> , 2018, 19, 724.	2.8	14
12	Parallel evolution between genomic segments of seasonal human influenza viruses reveals RNA-RNA relationships. <i>ELife</i> , 2021, 10, .	6.0	11
13	DesignSignatures: a tool for designing primers that yields amplicons with distinct signatures. <i>Bioinformatics</i> , 2016, 32, 1565-1567.	4.1	10
14	AssessORF: combining evolutionary conservation and proteomics to assess prokaryotic gene predictions. <i>Bioinformatics</i> , 2020, 36, 1022-1029.	4.1	10
15	Multi-stable bacterial communities exhibit extreme sensitivity to initial conditions. <i>FEMS Microbiology Ecology</i> , 2021, 97, .	2.7	10
16	Ten simple rules for hitting a home run with your elevator pitch. <i>PLoS Computational Biology</i> , 2021, 17, e1008756.	3.2	6
17	Capturing the Complex Interplay Between Drugs and the Intestinal Microbiome. <i>Clinical Pharmacology and Therapeutics</i> , 2019, 106, 501-504.	4.7	5
18	SubTap, a Versatile 3D Printed Platform for Eavesdropping on Extracellular Interactions. <i>MSystems</i> , 2021, 6, e0090221.	3.8	1

#	ARTICLE	IF	CITATIONS
19	Discordance Among Antibiotic Prescription Guidelines Reflects a Lack of Clear Best Practices. Open Forum Infectious Diseases, 2021, 8, ofaa571.	0.9	1
20	Accurate annotation of protein coding sequences with IDTAXA. NAR Genomics and Bioinformatics, 2021, 3, lqab080.	3.2	0
21	FindNonCoding: rapid and simple detection of non-coding RNAs in genomes. Bioinformatics, 2022, 38, 841-843.	4.1	0
22	Identification of antibiotic pairs with disjoint resistance: innovative progress made but questions remain – Authors' reply. Lancet Microbe, The, 2021, 2, e653.	7.3	0
23	Sample-efficient identification of high-dimensional antibiotic synergy with a normalized diagonal sampling design. PLoS Computational Biology, 2022, 18, e1010311.	3.2	0