

# Zaid Abdo

## List of Publications by Year in descending order

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Version: 2024-02-01

71  
papers

10,041  
citations

136950

32  
h-index

95266

68  
g-index

76  
all docs

76  
docs citations

76  
times ranked

12476  
citing authors

#	ARTICLE	IF	CITATIONS
1	Accounting for animal movement improves vaccination strategies against wildlife disease in heterogeneous landscapes. <i>Ecological Applications</i> , 2022, 32, e2568.	3.8	10
2	Improved non-redundant species screening panels for benchmarking the performance of new investigational antibacterial candidates against Category A and B priority pathogens. <i>JAC-Antimicrobial Resistance</i> , 2022, 4, dlac028.	2.1	2
3	A Randomized Controlled Trial of Dietary Rice Bran Intake on Microbiota Diversity, Enteric Dysfunction, and Fecal Secretory IgA in Malian and Nicaraguan Infants. <i>Journal of Nutrition</i> , 2022, 152, 1792-1800.	2.9	7
4	Litter Commensal Bacteria Can Limit the Horizontal Gene Transfer of Antimicrobial Resistance to Salmonella in Chickens. <i>Applied and Environmental Microbiology</i> , 2022, 88, e0251721.	3.1	13
5	Transitions of foliar mycobiota community and transcriptome in response to pathogenic conifer needle interactions. <i>Scientific Reports</i> , 2022, 12, 7832.	3.3	3
6	Population genomic transformations induced by isolation of wild bird avian influenza viruses (Orthomyxoviridae) in embryonated chicken eggs. <i>Infection, Genetics and Evolution</i> , 2021, 90, 104505.	2.3	3
7	Temporal and Spatial Blood Feeding Patterns of Urban Mosquitoes in the San Juan Metropolitan Area, Puerto Rico. <i>Insects</i> , 2021, 12, 129.	2.2	4
8	Complete Genome Sequences of Eight <i>Streptococcus equi</i> subsp. <i>zooepidemicus</i> Strains Isolated from Mares in Estrus with Endometritis. <i>Microbiology Resource Announcements</i> , 2021, 10, e0132120.	0.6	0
9	Horizontal Gene Transfer Is the Main Driver of Antimicrobial Resistance in Broiler Chicks Infected with <i>Salmonella enterica</i> Serovar Heidelberg. <i>MSystems</i> , 2021, 6, e0072921.	3.8	8
10	Predicting whole genome sequencing success for archived avian influenza virus (Orthomyxoviridae) samples using real-time and droplet PCRs. <i>Journal of Virological Methods</i> , 2020, 276, 113777.	2.1	6
11	The emergence of microbiome centres. <i>Nature Microbiology</i> , 2020, 5, 2-3.	13.3	13
12	An Open-Source Program (Haplo-ST) for Whole-Genome Sequence Typing Shows Extensive Diversity among <i>Listeria monocytogenes</i> Isolates in Outdoor Environments and Poultry Processing Plants. <i>Applied and Environmental Microbiology</i> , 2020, 87, .	3.1	5
13	A comparative study of the gut microbiome in Egyptian patients with Type I and Type II diabetes. <i>PLoS ONE</i> , 2020, 15, e0238764.	2.5	27
14	Reused poultry litter microbiome with competitive exclusion potential against <i>Salmonella</i> Heidelberg. <i>Journal of Environmental Quality</i> , 2020, 49, 869-881.	2.0	39
15	Ecological drivers of African swine fever virus persistence in wild boar populations: Insight for control. <i>Ecology and Evolution</i> , 2020, 10, 2846-2859.	1.9	60
16	Hierarchical Hidden Markov models enable accurate and diverse detection of antimicrobial resistance sequences. <i>Communications Biology</i> , 2019, 2, 294.	4.4	31
17	Improving risk assessment of the emergence of novel influenza A viruses by incorporating environmental surveillance. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2019, 374, 20180346.	4.0	11
18	Responses of Bacterial and Fungal Community Structure to Different Rates of 1,3-Dichloropropene Fumigation. <i>Phytobiomes Journal</i> , 2019, 3, 212-223.	2.7	10

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19	Horizontal Gene Transfer and Acquired Antibiotic Resistance in <i>Salmonella enterica</i> Serovar Heidelberg following <i>In Vitro</i> Incubation in Broiler Ceca. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	39
20	Rice bran supplementation modulates growth, microbiota and metabolome in weaning infants: a clinical trial in Nicaragua and Mali. <i>Scientific Reports</i> , 2019, 9, 13919.	3.3	31
21	Effects of a <i>Saccharomyces cerevisiae</i> fermentation product on liver abscesses, fecal microbiome, and resistome in feedlot cattle raised without antibiotics. <i>Scientific Reports</i> , 2019, 9, 2559.	3.3	41
22	Impact of oral probiotic <i>Lactobacillus acidophilus</i> vaccine strains on the immune response and gut microbiome of mice. <i>PLoS ONE</i> , 2019, 14, e0225842.	2.5	15
23	Determining the distribution of fitness effects using a generalized Beta-Burr distribution. <i>Theoretical Population Biology</i> , 2018, 122, 88-96.	1.1	8
24	Applications of the FIV Model to Study HIV Pathogenesis. <i>Viruses</i> , 2018, 10, 206.	3.3	19
25	Associations between sexual habits, menstrual hygiene practices, demographics and the vaginal microbiome as revealed by Bayesian network analysis. <i>PLoS ONE</i> , 2018, 13, e0191625.	2.5	92
26	MEGARes: an antimicrobial resistance database for high throughput sequencing. <i>Nucleic Acids Research</i> , 2017, 45, D574-D580.	14.5	328
27	Whole-Genome Sequencing and Concordance Between Antimicrobial Susceptibility Genotypes and Phenotypes of Bacterial Isolates Associated with Bovine Respiratory Disease. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3059-3071.	1.8	19
28	Enrichment allows identification of diverse, rare elements in metagenomic resistome-virulome sequencing. <i>Microbiome</i> , 2017, 5, 142.	11.1	78
29	Subtyping of <i>Salmonella enterica</i> Subspecies I Using Single-Nucleotide Polymorphisms in Adenylate Cyclase. <i>Foodborne Pathogens and Disease</i> , 2016, 13, 350-362.	1.8	7
30	Derivation of chicken induced pluripotent stem cells tolerant to Newcastle disease virus-induced lysis through multiple rounds of infection. <i>Virology Journal</i> , 2016, 13, 205.	3.4	8
31	Trend Analysis and Forecast of Precipitation, Reference Evapotranspiration, and Rainfall Deficit in the Blackland Prairie of Eastern Mississippi. <i>Journal of Applied Meteorology and Climatology</i> , 2016, 55, 1425-1439.	1.5	60
32	Draft Genome Sequence of <i>Cercospora arachidicola</i> , Causal Agent of Early Leaf Spot in Peanuts. <i>Genome Announcements</i> , 2015, 3, .	0.8	10
33	Comparison of Resistance to Asiatic Citrus Canker Among Different Genotypes of <i>Citrus</i> in a Long-Term Canker-Resistance Field Screening Experiment in Brazil. <i>Plant Disease</i> , 2015, 99, 207-218.	1.4	36
34	Evaluation of disinfectants to prevent mechanical transmission of viruses and a viroid in greenhouse tomato production. <i>Virology Journal</i> , 2015, 12, 5.	3.4	37
35	The daily dynamics of cystic fibrosis airway microbiota during clinical stability and at exacerbation. <i>Microbiome</i> , 2015, 3, 12.	11.1	122
36	Maize death acids, 9-lipoxygenase-derived cyclopentane(a)nones, display activity as cytotoxic phytoalexins and transcriptional mediators. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 11407-11412.	7.1	128

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37	Mi-1-Mediated Nematode Resistance in Tomatoes is Broken by Short-Term Heat Stress but Recovers Over Time. <i>Journal of Nematology</i> , 2015, 47, 133-40.	0.9	19
38	Influence of brown stink bug feeding, planting date and sampling time on common smut infection of maize. <i>Insect Science</i> , 2014, 21, 564-571.	3.0	3
39	Differences in Stylet Sheath Occurrence and the Fibrous Ring (Sclerenchyma) between xCitroncirus Plants Relatively Resistant or Susceptible to Adults of the Asian Citrus Psyllid <i>Diaphorina citri</i> (Hemiptera: Liviidae). <i>PLoS ONE</i> , 2014, 9, e110919.	2.5	24
40	Microbiota of the seminal fluid from healthy and infertile men. <i>Fertility and Sterility</i> , 2013, 100, 1261-1269.e3.	1.0	190
41	The ABCs of Experimental Evolution. <i>ISRN Computational Biology</i> , 2013, 2013, 1-7.	0.3	0
42	Evaluation of Methods for the Extraction and Purification of DNA from the Human Microbiome. <i>PLoS ONE</i> , 2012, 7, e33865.	2.5	425
43	Association Between <i>Trichomonas vaginalis</i> and Vaginal Bacterial Community Composition Among Reproductive-Age Women. <i>Sexually Transmitted Diseases</i> , 2012, 39, 807-812.	1.7	138
44	The Role of Clonal Interference in the Evolutionary Dynamics of Plasmid-Host Adaptation. <i>MBio</i> , 2012, 3, e00077-12.	4.1	29
45	mcaGUI: microbial community analysis R-Graphical User Interface (GUI). <i>Bioinformatics</i> , 2012, 28, 2198-2199.	4.1	4
46	Increased rectal microbial richness is associated with the presence of colorectal adenomas in humans. <i>ISME Journal</i> , 2012, 6, 1858-1868.	9.8	195
47	Temporal Dynamics of the Human Vaginal Microbiota. <i>Science Translational Medicine</i> , 2012, 4, 132ra52.	12.4	1,168
48	Mucosal Adherent Bacteria, Inflammation and Colorectal Adenomas. <i>Gastroenterology</i> , 2011, 140, S-356.	1.3	0
49	Contrasting Codon Usage Patterns and Purifying Selection at the Mating Locus in Putatively Asexual <i>Alternaria</i> Fungal Species. <i>PLoS ONE</i> , 2011, 6, e20083.	2.5	22
50	Characterization of the Diversity and Temporal Stability of Bacterial Communities in Human Milk. <i>PLoS ONE</i> , 2011, 6, e21313.	2.5	630
51	Vaginal microbiome of reproductive-age women. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 4680-4687.	7.1	2,985
52	Caring about trees in the forest: incorporating frailty in risk analysis for personalized medicine. <i>Personalized Medicine</i> , 2011, 8, 681-688.	1.5	12
53	Bacterial diversity in a glacier foreland of the high Arctic. <i>Molecular Ecology</i> , 2010, 19, 54-66.	3.9	139
54	Shifts in the host range of a promiscuous plasmid through parallel evolution of its replication initiation protein. <i>ISME Journal</i> , 2010, 4, 1568-1580.	9.8	98

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55	Effects of parameter estimation on maximum-likelihood bootstrap analysis. <i>Molecular Phylogenetics and Evolution</i> , 2010, 56, 642-648.	2.7	2
56	Molecular characterization of mucosal adherent bacteria and associations with colorectal adenomas. <i>Gut Microbes</i> , 2010, 1, 138-147.	9.8	355
57	Recent Advances in Understanding the Microbiology of the Female Reproductive Tract and the Causes of Premature Birth. <i>Infectious Diseases in Obstetrics and Gynecology</i> , 2010, 2010, 1-10.	1.5	70
58	Estimation of Selection Intensity under Overdominance by Bayesian Methods. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2009, 8, 1-22.	0.6	6
59	The Genetics of Adaptation for Eight Microvirid Bacteriophages. <i>Journal of Molecular Evolution</i> , 2009, 69, 229-239.	1.8	65
60	Bacterial succession in a glacier foreland of the High Arctic. <i>ISME Journal</i> , 2009, 3, 1258-1268.	9.8	102
61	Advances in the use of terminal restriction fragment length polymorphism (T-RFLP) analysis of 16S rRNA genes to characterize microbial communities. <i>Applied Microbiology and Biotechnology</i> , 2008, 80, 365-380.	3.6	318
62	Patchy distribution of flexible genetic elements in bacterial populations mediates robustness to environmental uncertainty. <i>FEMS Microbiology Ecology</i> , 2008, 65, 361-371.	2.7	59
63	A Step Toward Barcoding Life: A Model-Based, Decision-Theoretic Method to Assign Genes to Preexisting Species Groups. <i>Systematic Biology</i> , 2007, 56, 44-56.	5.6	79
64	Differences in the composition of vaginal microbial communities found in healthy Caucasian and black women. <i>ISME Journal</i> , 2007, 1, 121-133.	9.8	470
65	Statistical methods for characterizing diversity of microbial communities by analysis of terminal restriction fragment length polymorphisms of 16S rRNA genes. <i>Environmental Microbiology</i> , 2006, 8, 929-938.	3.8	369
66	Modeling the impact of periodic bottlenecks, unidirectional mutation, and observational error in experimental evolution. <i>Journal of Mathematical Biology</i> , 2005, 50, 645-662.	1.9	14
67	Accounting for Uncertainty in the Tree Topology Has Little Effect on the Decision-Theoretic Approach to Model Selection in Phylogeny Estimation. <i>Molecular Biology and Evolution</i> , 2005, 22, 691-703.	8.9	68
68	Evaluating the Performance of a Successive-Approximations Approach to Parameter Optimization in Maximum-Likelihood Phylogeny Estimation. <i>Molecular Biology and Evolution</i> , 2005, 22, 1386-1392.	8.9	115
69	Combining Mathematical Models and Statistical Methods to Understand and Predict the Dynamics of Antibiotic-Sensitive Mutants in a Population of Resistant Bacteria During Experimental Evolution. <i>Genetics</i> , 2004, 168, 1131-1144.	2.9	68
70	Evaluating the performance of likelihood methods for detecting population structure and migration. <i>Molecular Ecology</i> , 2004, 13, 837-851.	3.9	72
71	Performance-Based Selection of Likelihood Models for Phylogeny Estimation. <i>Systematic Biology</i> , 2003, 52, 674-683.	5.6	386