Amy D Willis

List of Publications by Year
in descending order

31 papers	13,919 citations	394286 19 h-index	477173 29 g-index
47 all docs	47 docs citations	47 times ranked	17103 citing authors

#	Article	IF	Citations
1	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. Nature Biotechnology, 2019, 37, 852-857.	9.4	11,167
2	Community-led, integrated, reproducible multi-omics with anviâ€™o. Nature Microbiology, 2021, 6, 3-6.	5.9	370
3	Rarefaction, Alpha Diversity, and Statistics. Frontiers in Microbiology, 2019, 10, 2407.	1.5	366
4	Consistent and correctable bias in metagenomic sequencing experiments. ELife, 2019, 8, .	2.8	263
5	Modeling microbial abundances and dysbiosis with beta-binomial regression. Annals of Applied Statistics, 2020, 14, 94-115.	0.5	206
6	Estimating Diversity via Frequency Ratios. Biometrics, 2015, 71, 1042-1049.	0.8	145
7	Influencing the Tumor Microenvironment: A Phase II Study of Copper Depletion Using Tetrathiomolybdate in Patients with Breast Cancer at High Risk for Recurrence and in Preclinical Models of Lung Metastases. Clinical Cancer Research, 2017, 23, 666-676.	3.2	140
8	Functional and genetic markers of niche partitioning among enigmatic members of the human oral microbiome. Genome Biology, 2020, 21, 292.	3.8	132
9	Estimating diversity in networked ecological communities. Biostatistics, 2022, 23, 207-222.	0.9	92
10	Improved Detection of Changes in Species Richness in High Diversity Microbial Communities. Journal of the Royal Statistical Society Series C: Applied Statistics, 2017, 66, 963-977.	0.5	90
11	Estimating the Number of Species in Microbial Diversity Studies. Annual Review of Statistics and Its Application, 2014, 1, 427-445.	4.1	68
12	Segment number threshold determines juvenile onset of germline cluster expansion in <i>Platynereis dumerilii</i>. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2022, 338, 225-240.	0.6	50
13	Follicle number, not assessments of the ovarian stroma, represents the best ultrasonographic marker of polycystic ovary syndrome. Fertility and Sterility, 2014, 101, 280-287.e1.	0.5	41
14	Nonstandard regular variation of in-degree and out-degree in the preferential attachment model. Journal of Applied Probability, 2016, 53, 146-161.	0.4	33
15	Continental igneous rock composition: A major control of past global chemical weathering. Science Advances, 2017, 3, e1602183.	4.7	32
16	Clustering co-abundant genes identifies components of the gut microbiome that are reproducibly associated with colorectal cancer and inflammatory bowel disease. Microbiome, 2019, 7, 110.	4.9	31
17	Niche Separation Increases With Genetic Distance Among Bloom-Forming Cyanobacteria. Frontiers in Microbiology, 2018, 9, 438.	1.5	28
18	Lifetime mobility of an Arctic woolly mammoth. Science, 2021, 373, 806-808.	6.0	27

#	Article	IF	Citations
19	Extrapolating abundance curves has no predictive power for estimating microbial biodiversity. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E5096.	3.3	19
20	Confidence Sets for Phylogenetic Trees. Journal of the American Statistical Association, 2019, 114, 235-244.	1.8	17
21	Uncertainty in Phylogenetic Tree Estimates. Journal of Computational and Graphical Statistics, 2018, 27, 542-552.	0.9	15
22	Consistency of a phylogenetic tree maximum likelihood estimator. Journal of Statistical Planning and Inference, 2015, 161, 73-80.	0.4	14
23	A multiview model for relative and absolute microbial abundances. Biometrics, 2022, 78, 1181-1194.	0.8	14
24	geneshot: gene-level metagenomics identifies genome islands associated with immunotherapy response. Genome Biology, 2021, 22, 135.	3.8	12
25	Evaluating replicability in microbiome data. Biostatistics, 2022, 23, 1099-1114.	0.9	12
26	Sonographic markers of ovarian morphology, but not hirsutism indices, predict serum total testosterone in women with regular menstrual cycles. Fertility and Sterility, 2016, 105, 1322-1329.e1.	0.5	8
27	Rigorous Statistical Methods for Rigorous Microbiome Science. MSystems, 2019, 4, .	1.7	7
28	Strategies to Facilitate Translational Advances from Microbiome Surveys. Trends in Microbiology, 2020, 28, 329-330.	3.5	7
29	Tuning parameter selection for a penalized estimator of species richness. Journal of Applied Statistics, 2021, 48, 1053-1070.	0.6	0
30	Abstract CT309: Influencing the tumor microenvironment: A phase II study of copper-depletion using tetrathiomolybdate (TM) in patients (pts) with breast cancer (BC) at high risk for recurrence. , 2014, , .		0
31	Abstract LB-349: Copper depletion as a strategy to affect the tumor microenvironment in breast cancer patients at high risk of relapse and in triple negative preclinical models of breast cancer: Updated results of a phase II study of tetrathiomolybdate (TM) in breast cancer (BC) patients (pts) at high risk for recurrence. , 2016, , .		0