Amy D Willis

List of Publications by Year
in descending order

31 papers	13,919 citations	394421 19 h-index	477307 29 g-index
47 all docs	47 docs citations	47 times ranked	17103 citing authors

#	Article	IF	Citations
1	A multiview model for relative and absolute microbial abundances. Biometrics, 2022, 78, 1181-1194.	1.4	14
2	Estimating diversity in networked ecological communities. Biostatistics, 2022, 23, 207-222.	1.5	92
3	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.	1.3	50
4	Evaluating replicability in microbiome data. Biostatistics, 2022, 23, 1099-1114.	1.5	12
5	Tuning parameter selection for a penalized estimator of species richness. Journal of Applied Statistics, 2021, 48, 1053-1070.	1.3	0
6	Community-led, integrated, reproducible multi-omics with anviâ€™o. Nature Microbiology, 2021, 6, 3-6.	13.3	370
7	geneshot: gene-level metagenomics identifies genome islands associated with immunotherapy response. Genome Biology, 2021, 22, 135.	8.8	12
8	Lifetime mobility of an Arctic woolly mammoth. Science, 2021, 373, 806-808.	12.6	27
9	Functional and genetic markers of niche partitioning among enigmatic members of the human oral microbiome. Genome Biology, 2020, 21, 292.	8.8	132
10	Strategies to Facilitate Translational Advances from Microbiome Surveys. Trends in Microbiology, 2020, 28, 329-330.	7.7	7
11	Modeling microbial abundances and dysbiosis with beta-binomial regression. Annals of Applied Statistics, 2020, 14, 94-115.	1.1	206
12	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.	11.1	31
13	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. Nature Biotechnology, 2019, 37, 852-857.	17.5	11,167
14	Rigorous Statistical Methods for Rigorous Microbiome Science. MSystems, 2019, 4, .	3.8	7
15	Rarefaction, Alpha Diversity, and Statistics. Frontiers in Microbiology, 2019, 10, 2407.	3.5	366
16	Confidence Sets for Phylogenetic Trees. Journal of the American Statistical Association, 2019, 114, 235-244.	3.1	17
17	Consistent and correctable bias in metagenomic sequencing experiments. ELife, 2019, 8, .	6.0	263
18	Uncertainty in Phylogenetic Tree Estimates. Journal of Computational and Graphical Statistics, 2018, 27, 542-552.	1.7	15

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19	Niche Separation Increases With Genetic Distance Among Bloom-Forming Cyanobacteria. Frontiers in Microbiology, 2018, 9, 438.	3.5	28
20	Continental igneous rock composition: A major control of past global chemical weathering. Science Advances, 2017, 3, e1602183.	10.3	32
21	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.	1.0	90
22	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.	7.0	140
23	Nonstandard regular variation of in-degree and out-degree in the preferential attachment model. Journal of Applied Probability, 2016, 53, 146-161.	0.7	33
24	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.	7.1	19
25	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.	1.0	8
26	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
27	Estimating Diversity via Frequency Ratios. Biometrics, 2015, 71, 1042-1049.	1.4	145
28	Consistency of a phylogenetic tree maximum likelihood estimator. Journal of Statistical Planning and Inference, 2015, 161, 73-80.	0.6	14
29	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.	1.0	41
30	Estimating the Number of Species in Microbial Diversity Studies. Annual Review of Statistics and Its Application, 2014, 1, 427-445.	7.0	68
31	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