

# Amy D Willis

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3737358/publications.pdf>

Version: 2024-02-01

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	A multiview model for relative and absolute microbial abundances. <i>Biometrics</i> , 2022, 78, 1181-1194.	0.8	14
2	Estimating diversity in networked ecological communities. <i>Biostatistics</i> , 2022, 23, 207-222.	0.9	92
3	Segment number threshold determines juvenile onset of germline cluster expansion in <i>Platynereis dumerilii</i> . <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2022, 338, 225-240.	0.6	50
4	Evaluating replicability in microbiome data. <i>Biostatistics</i> , 2022, 23, 1099-1114.	0.9	12
5	Tuning parameter selection for a penalized estimator of species richness. <i>Journal of Applied Statistics</i> , 2021, 48, 1053-1070.	0.6	0
6	Community-led, integrated, reproducible multi-omics with anvio™. <i>Nature Microbiology</i> , 2021, 6, 3-6.	5.9	370
7	geneshot: gene-level metagenomics identifies genome islands associated with immunotherapy response. <i>Genome Biology</i> , 2021, 22, 135.	3.8	12
8	Lifetime mobility of an Arctic woolly mammoth. <i>Science</i> , 2021, 373, 806-808.	6.0	27
9	Functional and genetic markers of niche partitioning among enigmatic members of the human oral microbiome. <i>Genome Biology</i> , 2020, 21, 292.	3.8	132
10	Strategies to Facilitate Translational Advances from Microbiome Surveys. <i>Trends in Microbiology</i> , 2020, 28, 329-330.	3.5	7
11	Modeling microbial abundances and dysbiosis with beta-binomial regression. <i>Annals of Applied Statistics</i> , 2020, 14, 94-115.	0.5	206
12	Clustering co-abundant genes identifies components of the gut microbiome that are reproducibly associated with colorectal cancer and inflammatory bowel disease. <i>Microbiome</i> , 2019, 7, 110.	4.9	31
13	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019, 37, 852-857.	9.4	11,167
14	Rigorous Statistical Methods for Rigorous Microbiome Science. <i>MSystems</i> , 2019, 4, .	1.7	7
15	Rarefaction, Alpha Diversity, and Statistics. <i>Frontiers in Microbiology</i> , 2019, 10, 2407.	1.5	366
16	Confidence Sets for Phylogenetic Trees. <i>Journal of the American Statistical Association</i> , 2019, 114, 235-244.	1.8	17
17	Consistent and correctable bias in metagenomic sequencing experiments. <i>ELife</i> , 2019, 8, .	2.8	263
18	Uncertainty in Phylogenetic Tree Estimates. <i>Journal of Computational and Graphical Statistics</i> , 2018, 27, 542-552.	0.9	15

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19	Niche Separation Increases With Genetic Distance Among Bloom-Forming Cyanobacteria. <i>Frontiers in Microbiology</i> , 2018, 9, 438.	1.5	28
20	Continental igneous rock composition: A major control of past global chemical weathering. <i>Science Advances</i> , 2017, 3, e1602183.	4.7	32
21	Improved Detection of Changes in Species Richness in High Diversity Microbial Communities. <i>Journal of the Royal Statistical Society Series C: Applied Statistics</i> , 2017, 66, 963-977.	0.5	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. <i>Clinical Cancer Research</i> , 2017, 23, 666-676.	3.2	140
23	Nonstandard regular variation of in-degree and out-degree in the preferential attachment model. <i>Journal of Applied Probability</i> , 2016, 53, 146-161.	0.4	33
24	Extrapolating abundance curves has no predictive power for estimating microbial biodiversity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E5096.	3.3	19
25	Sonographic markers of ovarian morphology, but not hirsutism indices, predict serum total testosterone in women with regular menstrual cycles. <i>Fertility and Sterility</i> , 2016, 105, 1322-1329.e1.	0.5	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. <i>Biometrics</i> , 2015, 71, 1042-1049.	0.8	145
28	Consistency of a phylogenetic tree maximum likelihood estimator. <i>Journal of Statistical Planning and Inference</i> , 2015, 161, 73-80.	0.4	14
29	Follicle number, not assessments of the ovarian stroma, represents the best ultrasonographic marker of polycystic ovary syndrome. <i>Fertility and Sterility</i> , 2014, 101, 280-287.e1.	0.5	41
30	Estimating the Number of Species in Microbial Diversity Studies. <i>Annual Review of Statistics and Its Application</i> , 2014, 1, 427-445.	4.1	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