

Holly M Bik

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4481591/publications.pdf>

Version: 2024-02-01

49
papers

5,005
citations

236925

25
h-index

223800

46
g-index

52
all docs

52
docs citations

52
times ranked

8019
citing authors

#	ARTICLE	IF	CITATIONS
1	Environmental <sc>DNA</sc> metabarcoding: Transforming how we survey animal and plant communities. <i>Molecular Ecology</i> , 2017, 26, 5872-5895.	3.9	1,210
2	PhyloSift: phylogenetic analysis of genomes and metagenomes. <i>PeerJ</i> , 2014, 2, e243.	2.0	633
3	Sequencing our way towards understanding global eukaryotic biodiversity. <i>Trends in Ecology and Evolution</i> , 2012, 27, 233-243.	8.7	395
4	The ecologist's field guide to sequence-based identification of biodiversity. <i>Methods in Ecology and Evolution</i> , 2016, 7, 1008-1018.	5.2	316
5	DNA metabarcoding—Need for robust experimental designs to draw sound ecological conclusions. <i>Molecular Ecology</i> , 2019, 28, 1857-1862.	3.9	300
6	An Introduction to Social Media for Scientists. <i>PLoS Biology</i> , 2013, 11, e1001535.	5.6	291
7	Acidity promotes degradation of multi-species environmental DNA in lotic mesocosms. <i>Communications Biology</i> , 2018, 1, 4.	4.4	219
8	Microbiota of the indoor environment: a meta-analysis. <i>Microbiome</i> , 2015, 3, 49.	11.1	216
9	Metagenetic community analysis of microbial eukaryotes illuminates biogeographic patterns in deep-sea and shallow water sediments. <i>Molecular Ecology</i> , 2012, 21, 1048-1059.	3.9	162
10	Dramatic Shifts in Benthic Microbial Eukaryote Communities following the Deepwater Horizon Oil Spill. <i>PLoS ONE</i> , 2012, 7, e38550.	2.5	139
11	Host-associated microbiomes drive structure and function of marine ecosystems. <i>PLoS Biology</i> , 2019, 17, e3000533.	5.6	103
12	Coexisting cryptic species of the <i>Litoditis marina</i> complex (Nematoda) show differential resource use and have distinct microbiomes with high intraspecific variability. <i>Molecular Ecology</i> , 2016, 25, 2093-2110.	3.9	89
13	Intra-Genomic Variation in the Ribosomal Repeats of Nematodes. <i>PLoS ONE</i> , 2013, 8, e78230.	2.5	84
14	Evolution of the indoor biome. <i>Trends in Ecology and Evolution</i> , 2015, 30, 223-232.	8.7	75
15	Moving towards a complete molecular framework of the Nematoda: a focus on the Enoplida and early-branching clades. <i>BMC Evolutionary Biology</i> , 2010, 10, 353.	3.2	62
16	Low endemism, continued deep-shallow interchanges, and evidence for cosmopolitan distributions in free-living marine nematodes (order Enoplida). <i>BMC Evolutionary Biology</i> , 2010, 10, 389.	3.2	62
17	Let's rise up to unite taxonomy and technology. <i>PLoS Biology</i> , 2017, 15, e2002231.	5.6	58
18	Sample size effects on the assessment of eukaryotic diversity and community structure in aquatic sediments using high-throughput sequencing. <i>Scientific Reports</i> , 2018, 8, 11737.	3.3	55

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19	Nematode-associated microbial taxa do not correlate with host phylogeny, geographic region or feeding morphology in marine sediment habitats. <i>Molecular Ecology</i> , 2018, 27, 1930-1951.	3.9	49
20	A molecular-based approach for examining responses of eukaryotes in microcosms to contaminant-spiked estuarine sediments. <i>Environmental Toxicology and Chemistry</i> , 2014, 33, 359-369.	4.3	48
21	Ten Simple Rules for Effective Online Outreach. <i>PLoS Computational Biology</i> , 2015, 11, e1003906.	3.2	42
22	Molecular Diversity of Fungal Phylotypes Co-Amplified Alongside Nematodes from Coastal and Deep-Sea Marine Environments. <i>PLoS ONE</i> , 2011, 6, e26445.	2.5	42
23	Meeting Report: Fungal ITS Workshop (October 2012). <i>Standards in Genomic Sciences</i> , 2013, 8, 118-123.	1.5	34
24	Next-generation phenomics for the Tree of Life. <i>PLOS Currents</i> , 2013, 5, .	1.4	34
25	Phylotastic! Making tree-of-life knowledge accessible, reusable and convenient. <i>BMC Bioinformatics</i> , 2013, 14, 158.	2.6	33
26	Microbial Community Patterns Associated with Automated Teller Machine Keypads in New York City. <i>MSphere</i> , 2016, 1, .	2.9	28
27	Antarctic ecosystem responses following ice-shelf collapse and iceberg calving: Science review and future research. <i>Wiley Interdisciplinary Reviews: Climate Change</i> , 2021, 12, .	8.1	25
28	Use of a novel sediment exposure to determine the effects of triclosan on estuarine benthic communities. <i>Environmental Toxicology and Chemistry</i> , 2013, 32, 384-392.	4.3	18
29	Natural experiments and long-term monitoring are critical to understand and predict marine host-microbe ecology and evolution. <i>PLoS Biology</i> , 2021, 19, e3001322.	5.6	17
30	Widespread prevalence but contrasting patterns of intragenomic rRNA polymorphisms in nematodes: Implications for phylogeny, species delimitation and life history inference. <i>Molecular Ecology Resources</i> , 2020, 20, 318-332.	4.8	16
31	Biodiversity monitoring using environmental DNA. <i>Molecular Ecology Resources</i> , 2021, 21, 1405-1409.	4.8	15
32	Microbial Community Succession and Nutrient Cycling Responses following Perturbations of Experimental Saltwater Aquaria. <i>MSphere</i> , 2019, 4, .	2.9	14
33	Digital Environmentalism: Tools and Strategies for the Evolving Online Ecosystem. , 2012, , 364-372.		14
34	Spatial and temporal variation of intertidal nematodes in the northern Gulf of Mexico after the Deepwater Horizon oil spill. <i>Marine Environmental Research</i> , 2017, 130, 200-212.	2.5	10
35	The impact of intragenomic rRNA variation on metabarcoding-derived diversity estimates: A case study from marine nematodes. <i>Environmental DNA</i> , 2020, 2, 519-534.	5.8	8
36	Just keep it simple? Benchmarking the accuracy of taxonomy assignment software in metabarcoding studies. <i>Molecular Ecology Resources</i> , 2021, 21, 2187-2189.	4.8	8

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37	Rapid decline of PCR amplification from genomic extracts of DESS-preserved, slide-mounted nematodes. <i>Nematology</i> , 2009, 11, 827-834.	0.6	7
38	Dataset complexity impacts both MOTU delimitation and biodiversity estimates in eukaryotic 18S rRNA metabarcoding studies. <i>Environmental DNA</i> , 2022, 4, 363-384.	5.8	7
39	Deciphering Diversity and Ecological Function From Marine Metagenomes. <i>Biological Bulletin</i> , 2014, 227, 107-116.	1.8	6
40	Microbial Metazoa Are Microbes Too. <i>MSystems</i> , 2019, 4, .	3.8	6
41	Above-below surface interactions mediate effects of seagrass disturbance on meiobenthic diversity, nematode and polychaete trophic structure. <i>Communications Biology</i> , 2019, 2, 362.	4.4	6
42	RCN4GSC Workshop Report: Managing Data at the Interface of Biodiversity and (Meta)Genomics, March 2011. <i>Standards in Genomic Sciences</i> , 2012, 7, 159-165.	1.5	5
43	Composition of marine nematode communities across broad longitudinal and bathymetric gradients in the Northeast Chukchi and Beaufort Seas. <i>Polar Biology</i> , 2021, 44, 85-103.	1.2	5
44	microBEnet: Lessons Learned from Building an Interdisciplinary Scientific Community in the Online Sphere. <i>PLoS Biology</i> , 2014, 12, e1001884.	5.6	4
45	Metagenomics will highlight and drive links to taxonomic data: reply to Murray. <i>Trends in Ecology and Evolution</i> , 2012, 27, 652-653.	8.7	3
46	Small worms, big ideas: evolutionary inferences from nematode DNA. <i>Journal of Biogeography</i> , 2010, 37, 1-2.	3.0	2
47	Complexity matters: Evaluating the impact of bioinformatics parameters on eukaryotic MOTU delimitation and taxonomy assignment. <i>ARPHA Conference Abstracts</i> , 0, 4, .	0.0	1
48	Unravelling post-glacial colonization through molecular techniques: new insight from estuarine invertebrates. <i>Journal of Biogeography</i> , 2009, 36, 16-17.	3.0	0
49	Perspective: Biodiversity and the (data) beast. , 0, , 154-174.		0