

Holly M Bik

List of Publications by Year in descending order

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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	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
2	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
3	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
4	Biodiversity monitoring using environmental DNA. <i>Molecular Ecology Resources</i> , 2021, 21, 1405-1409.	4.8	15
5	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
6	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
7	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
8	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
9	Microbial Metazoa Are Microbes Too. <i>MSystems</i> , 2019, 4, .	3.8	6
10	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
11	Host-associated microbiomes drive structure and function of marine ecosystems. <i>PLoS Biology</i> , 2019, 17, e3000533.	5.6	103
12	DNA metabarcoding—Need for robust experimental designs to draw sound ecological conclusions. <i>Molecular Ecology</i> , 2019, 28, 1857-1862.	3.9	300
13	Microbial Community Succession and Nutrient Cycling Responses following Perturbations of Experimental Saltwater Aquaria. <i>MSphere</i> , 2019, 4, .	2.9	14
14	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
15	Acidity promotes degradation of multi-species environmental DNA in lotic mesocosms. <i>Communications Biology</i> , 2018, 1, 4.	4.4	219
16	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
17	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
18	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

#	ARTICLE	IF	CITATIONS
19	Letâ€™s rise up to unite taxonomy and technology. PLoS Biology, 2017, 15, e2002231.	5.6	58
20	Coexisting cryptic species of the <i>Litoditis marina</i> complex (Nematoda) show differential resource use and have distinct microbiomes with high intraspecific variability. Molecular Ecology, 2016, 25, 2093-2110.	3.9	89
21	The ecologist's field guide to sequenceâ€based identification of biodiversity. Methods in Ecology and Evolution, 2016, 7, 1008-1018.	5.2	316
22	Microbial Community Patterns Associated with Automated Teller Machine Keypads in New York City. MSphere, 2016, 1, .	2.9	28
23	Evolution of the indoor biome. Trends in Ecology and Evolution, 2015, 30, 223-232.	8.7	75
24	Ten Simple Rules for Effective Online Outreach. PLoS Computational Biology, 2015, 11, e1003906.	3.2	42
25	Microbiota of the indoor environment: a meta-analysis. Microbiome, 2015, 3, 49.	11.1	216
26	microBEnet: Lessons Learned from Building an Interdisciplinary Scientific Community in the Online Sphere. PLoS Biology, 2014, 12, e1001884.	5.6	4
27	A molecularâ€based approach for examining responses of eukaryotes in microcosms to contaminantâ€spiked estuarine sediments. Environmental Toxicology and Chemistry, 2014, 33, 359-369.	4.3	48
28	Deciphering Diversity and Ecological Function From Marine Metagenomes. Biological Bulletin, 2014, 227, 107-116.	1.8	6
29	PhyloSift: phylogenetic analysis of genomes and metagenomes. PeerJ, 2014, 2, e243.	2.0	633
30	Phylotastic! Making tree-of-life knowledge accessible, reusable and convenient. BMC Bioinformatics, 2013, 14, 158.	2.6	33
31	Use of a novel sediment exposure to determine the effects of triclosan on estuarine benthic communities. Environmental Toxicology and Chemistry, 2013, 32, 384-392.	4.3	18
32	An Introduction to Social Media for Scientists. PLoS Biology, 2013, 11, e1001535.	5.6	291
33	Meeting Report: Fungal ITS Workshop (October 2012). Standards in Genomic Sciences, 2013, 8, 118-123.	1.5	34
34	Next-generation phenomics for the Tree of Life. PLOS Currents, 2013, 5, .	1.4	34
35	Intra-Genomic Variation in the Ribosomal Repeats of Nematodes. PLoS ONE, 2013, 8, e78230.	2.5	84
36	RCN4GSC Workshop Report: Managing Data at the Interface of Biodiversity and (Meta)Genomics, March 2011. Standards in Genomic Sciences, 2012, 7, 159-165.	1.5	5

#	ARTICLE	IF	CITATIONS
37	Sequencing our way towards understanding global eukaryotic biodiversity. Trends in Ecology and Evolution, 2012, 27, 233-243.	8.7	395
38	Metagenomics will highlight and drive links to taxonomic data: reply to Murray. Trends in Ecology and Evolution, 2012, 27, 652-653.	8.7	3
39	Metagenetic community analysis of microbial eukaryotes illuminates biogeographic patterns in deep-sea and shallow water sediments. Molecular Ecology, 2012, 21, 1048-1059.	3.9	162
40	Dramatic Shifts in Benthic Microbial Eukaryote Communities following the Deepwater Horizon Oil Spill. PLoS ONE, 2012, 7, e38550.	2.5	139
41	Digital Environmentalism: Tools and Strategies for the Evolving Online Ecosystem. , 2012, , 364-372.		14
42	Molecular Diversity of Fungal Phylotypes Co-Amplified Alongside Nematodes from Coastal and Deep-Sea Marine Environments. PLoS ONE, 2011, 6, e26445.	2.5	42
43	Small worms, big ideas: evolutionary inferences from nematode DNA. Journal of Biogeography, 2010, 37, 1-2.	3.0	2
44	Moving towards a complete molecular framework of the Nematoda: a focus on the Enoplida and early-branching clades. BMC Evolutionary Biology, 2010, 10, 353.	3.2	62
45	Low endemism, continued deep-shallow interchanges, and evidence for cosmopolitan distributions in free-living marine nematodes (order Enoplida). BMC Evolutionary Biology, 2010, 10, 389.	3.2	62
46	Rapid decline of PCR amplification from genomic extracts of DESS-preserved, slide-mounted nematodes. Nematology, 2009, 11, 827-834.	0.6	7
47	Unravelling post-glacial colonization through molecular techniques: new insight from estuarine invertebrates. Journal of Biogeography, 2009, 36, 16-17.	3.0	0
48	Perspective: Biodiversity and the (data) beast. , 0, , 154-174.		0
49	Complexity matters: Evaluating the impact of bioinformatics parameters on eukaryotic MOTU delimitation and taxonomy assignment. ARPHA Conference Abstracts, 0, 4, .	0.0	1