

Kristine Bohmann

List of Publications by Year in descending order

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Version: 2024-02-01

39
papers

3,895
citations

257450

24
h-index

345221

36
g-index

49
all docs

49
docs citations

49
times ranked

5398
citing authors

#	ARTICLE	IF	CITATIONS
1	Environmental DNA for wildlife biology and biodiversity monitoring. <i>Trends in Ecology and Evolution</i> , 2014, 29, 358-367.	8.7	920
2	Tag jumps illuminated “reducing sequence-to-sample misidentifications in metabarcoding studies. <i>Molecular Ecology Resources</i> , 2015, 15, 1289-1303.	4.8	429
3	Scrutinizing key steps for reliable metabarcoding of environmental samples. <i>Methods in Ecology and Evolution</i> , 2018, 9, 134-147.	5.2	425
4	Ancient and modern environmental DNA. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20130383.	4.0	292
5	Do Vertebrate Gut Metagenomes Confer Rapid Ecological Adaptation?. <i>Trends in Ecology and Evolution</i> , 2016, 31, 689-699.	8.7	235
6	Molecular Diet Analysis of Two African Free-Tailed Bats (Molossidae) Using High Throughput Sequencing. <i>PLoS ONE</i> , 2011, 6, e21441.	2.5	175
7	Connecting Earth observation to high-throughput biodiversity data. <i>Nature Ecology and Evolution</i> , 2017, 1, 176.	7.8	156
8	Promises and pitfalls of using high-throughput sequencing for diet analysis. <i>Molecular Ecology Resources</i> , 2019, 19, 327-348.	4.8	138
9	Hologenomic adaptations underlying the evolution of sanguivory in the common vampire bat. <i>Nature Ecology and Evolution</i> , 2018, 2, 659-668.	7.8	124
10	Airborne environmental DNA for terrestrial vertebrate community monitoring. <i>Current Biology</i> , 2022, 32, 701-707.e5.	3.9	91
11	Second generation sequencing and morphological faecal analysis reveal unexpected foraging behaviour by <i>Myotis nattereri</i> (Chiroptera, Vespertilionidae) in winter. <i>Frontiers in Zoology</i> , 2014, 11, 39.	2.0	75
12	Using <i>scp</i> -DNA metabarcoding for simultaneous inference of common vampire bat diet and population structure. <i>Molecular Ecology Resources</i> , 2018, 18, 1050-1063.	4.8	70
13	Skmer: assembly-free and alignment-free sample identification using genome skims. <i>Genome Biology</i> , 2019, 20, 34.	8.8	70
14	Beyond DNA barcoding: The unrealized potential of genome skim data in sample identification. <i>Molecular Ecology</i> , 2020, 29, 2521-2534.	3.9	58
15	A practical guide to DNA-based methods for biodiversity assessment. , 2021, , .		57
16	DAME: a toolkit for the initial processing of datasets with PCR replicates of double-tagged amplicons for DNA metabarcoding analyses. <i>BMC Research Notes</i> , 2016, 9, 255.	1.4	45
17	Debugging diversity “a pancontinental exploration of the potential of terrestrial blood-feeding leeches as a vertebrate monitoring tool. <i>Molecular Ecology Resources</i> , 2018, 18, 1282-1298.	4.8	45
18	An appetite for pests: Synanthropic insectivorous bats exploit cotton pest irruptions and consume various deleterious arthropods. <i>Molecular Ecology</i> , 2020, 29, 1185-1198.	3.9	41

#	ARTICLE	IF	CITATIONS
19	Tagsteady: A metabarcoding library preparation protocol to avoid false assignment of sequences to samples. <i>Molecular Ecology Resources</i> , 2020, 20, 1620-1631.	4.8	40
20	Strategies for sample labelling and library preparation in DNA metabarcoding studies. <i>Molecular Ecology Resources</i> , 2022, 22, 1231-1246.	4.8	40
21	A simplified DNA extraction protocol for unsorted bulk arthropod samples that maintains exoskeletal integrity. <i>Environmental DNA</i> , 2019, 1, 144-154.	5.8	34
22	Using metabarcoding to compare the suitability of two blood-feeding leech species for sampling mammalian diversity in North Borneo. <i>Molecular Ecology Resources</i> , 2019, 19, 105-117.	4.8	31
23	Molossid bats in an African agro-ecosystem select sugarcane fields as foraging habitat. <i>African Zoology</i> , 2012, 47, 1-11.	0.4	30
24	Molossid Bats in an African Agro-Ecosystem Select Sugarcane Fields as Foraging Habitat. <i>African Zoology</i> , 2012, 47, 1-11.	0.4	27
25	Vertebrate diversity revealed by metabarcoding of bulk arthropod samples from tropical forests. <i>Environmental DNA</i> , 2019, 1, 329-341.	5.8	27
26	Connecting high-throughput biodiversity inventories: Opportunities for a site-based genomic framework for global integration and synthesis. <i>Molecular Ecology</i> , 2021, 30, 1120-1135.	3.9	26
27	Diet Determined by Next Generation Sequencing Reveals Pest Consumption and Opportunistic Foraging by Bats in Macadamia Orchards in South Africa. <i>Acta Chiropterologica</i> , 2017, 19, 239-254.	0.6	24
28	Mitochondrial genomes of Danish vertebrate species generated for the national DNA reference database, DNAMark. <i>Environmental DNA</i> , 2021, 3, 472-480.	5.8	24
29	Biodiversity Soup II: A bulk-sample metabarcoding pipeline emphasizing error reduction. <i>Methods in Ecology and Evolution</i> , 2021, 12, 1252-1264.	5.2	21
30	When bugs reveal biodiversity. <i>Molecular Ecology</i> , 2013, 22, 909-911.	3.9	20
31	DNA metabarcoding reveals that African leopard diet varies between habitats. <i>African Journal of Ecology</i> , 2021, 59, 37-50.	0.9	17
32	Metagenomics: A viable tool for reconstructing herbivore diet. <i>Molecular Ecology Resources</i> , 2021, 21, 2249-2263.	4.8	16
33	Molecular dietary analyses of western capercaillies (<i>Tetrao urogallus</i>) reveal a diverse diet. <i>Environmental DNA</i> , 2021, 3, 1156-1171.	5.8	9
34	The potential of aquatic bloodfeeding and nonbloodfeeding leeches as a tool for iDNA characterisation. <i>Molecular Ecology Resources</i> , 2022, 22, 539-553.	4.8	8
35	DNA-Net conference unites participants from around the world with the quest to standardize and implement DNA-based aquatic biomonitoring. <i>Environmental DNA</i> , 2021, 3, 884-888.	5.8	7
36	DNA-Based Arthropod Diversity Assessment in Amazonian Iron Mine Lands Show Ecological Succession Towards Undisturbed Reference Sites. <i>Frontiers in Ecology and Evolution</i> , 2020, 8, .	2.2	5

#	ARTICLE	IF	CITATIONS
37	Labelling strategies in metabarcoding studies & how to ensure that nucleotide tags stay in place. ARPHA Conference Abstracts, 0, 4, .	0.0	1
38	A two-step metagenomics approach for the identification and mitochondrial DNA contig assembly of vertebrate prey from the blood meals of common vampire bats (<i>Desmodus rotundus</i>). Metabarcoding and Metagenomics, 0, 6, .	0.0	1
39	Shunning the scoop: Sidestepping the race to publish. IScience, 2022, 25, 104080.	4.1	0