

# Michael E Pfrender

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/890525/publications.pdf>

Version: 2024-02-01

20  
papers

3,048  
citations

567281

15  
h-index

794594

19  
g-index

22  
all docs

22  
docs citations

22  
times ranked

3848  
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	Quantification of mesocosm fish and amphibian species diversity via environmental <sc>DNA</sc> metabarcoding. <i>Molecular Ecology Resources</i> , 2016, 16, 29-41.	4.8	311
3	Conservation in a cup of water: estimating biodiversity and population abundance from environmental DNA. <i>Molecular Ecology</i> , 2012, 21, 2555-2558.	3.9	248
4	Estimating species richness using environmental <sc>DNA</sc>. <i>Ecology and Evolution</i> , 2016, 6, 4214-4226.	1.9	169
5	Fish community assessment with eDNA metabarcoding: effects of sampling design and bioinformatic filtering. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2017, 74, 1362-1374.	1.4	161
6	Gene content evolution in the arthropods. <i>Genome Biology</i> , 2020, 21, 15.	8.8	150
7	Constraint shapes convergence in tetrodotoxin-resistant sodium channels of snakes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 4556-4561.	7.1	139
8	Effects of sampling effort on biodiversity patterns estimated from environmental DNA metabarcoding surveys. <i>Scientific Reports</i> , 2018, 8, 8843.	3.3	113
9	The evolutionary origins of beneficial alleles during the repeated adaptation of garter snakes to deadly prey. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 13415-13420.	7.1	109
10	Calibrating Environmental DNA Metabarcoding to Conventional Surveys for Measuring Fish Species Richness. <i>Frontiers in Ecology and Evolution</i> , 2020, 8, .	2.2	74
11	Molecular Adaptations for Sensing and Securing Prey and Insight into Amniote Genome Diversity from the Garter Snake Genome. <i>Genome Biology and Evolution</i> , 2018, 10, 2110-2129.	2.5	72
12	Parallel Evolution of Tetrodotoxin Resistance in Three Voltage-Gated Sodium Channel Genes in the Garter Snake <i>Thamnophis sirtalis</i> . <i>Molecular Biology and Evolution</i> , 2014, 31, 2836-2846.	8.9	60
13	Optimising the detection of marine taxonomic richness using environmental DNA metabarcoding: the effects of filter material, pore size and extraction method. <i>Metabarcoding and Metagenomics</i> , 0, 2, .	0.0	55
14	Estimating fish alpha- and beta-diversity along a small stream with environmental DNA metabarcoding. <i>Metabarcoding and Metagenomics</i> , 0, 2, e24262.	0.0	48
15	Historical Contingency in a Multigene Family Facilitates Adaptive Evolution of Toxin Resistance. <i>Current Biology</i> , 2016, 26, 1616-1621.	3.9	47
16	Genetic architecture of a feeding adaptation: garter snake ( <i>Thamnophis</i> ) resistance to tetrodotoxin bearing prey. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2010, 277, 3317-3325.	2.6	43
17	The geographic mosaic in parallel: Matching patterns of newt tetrodotoxin levels and snake resistance in multiple predator-prey pairs. <i>Journal of Animal Ecology</i> , 2020, 89, 1645-1657.	2.8	22
18	The road not taken: Evolution of tetrodotoxin resistance in the Sierra garter snake ( <i>Thamnophis</i> )	3.9	10

#	ARTICLE	IF	CITATIONS
19	Uncovering Effects from the Structure of Metabarcoding Sequences for Metagenetic and Microbiome Analysis. <i>Methods and Protocols</i> , 2020, 3, 22.	2.0	6
20	Combining natural language processing and metabarcoding to reveal pathogen-environment associations. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0008755.	3.0	3