

# Masaki Miya

## List of Publications by Year in descending order

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Version: 2024-02-01

39  
papers

3,278  
citations

279798

23  
h-index

361022

35  
g-index

45  
all docs

45  
docs citations

45  
times ranked

2733  
citing authors

#	ARTICLE	IF	CITATIONS
1	MitoFish and MitoAnnotator: A Mitochondrial Genome Database of Fish with an Accurate and Automatic Annotation Pipeline. <i>Molecular Biology and Evolution</i> , 2013, 30, 2531-2540.	8.9	651
2	Environmental DNA metabarcoding reveals local fish communities in a species-rich coastal sea. <i>Scientific Reports</i> , 2017, 7, 40368.	3.3	348
3	Environmental DNA as a "Snapshot"™ of Fish Distribution: A Case Study of Japanese Jack Mackerel in Maizuru Bay, Sea of Japan. <i>PLoS ONE</i> , 2016, 11, e0149786.	2.5	192
4	MitoFish and MiFish Pipeline: A Mitochondrial Genome Database of Fish with an Analysis Pipeline for Environmental DNA Metabarcoding. <i>Molecular Biology and Evolution</i> , 2018, 35, 1553-1555.	8.9	169
5	Molecular phylogeny and evolution of the freshwater eels genus <i>Anguilla</i> based on the whole mitochondrial genome sequences. <i>Molecular Phylogenetics and Evolution</i> , 2005, 34, 134-146.	2.7	159
6	Environmental <i>scp</i> DNA enables detection of terrestrial mammals from forest pond water. <i>Molecular Ecology Resources</i> , 2017, 17, e63-e75.	4.8	158
7	Evolutionary Origin of the Scombridae (Tunas and Mackerels): Members of a Paleogene Adaptive Radiation with 14 Other Pelagic Fish Families. <i>PLoS ONE</i> , 2013, 8, e73535.	2.5	136
8	Deep-ocean origin of the freshwater eels. <i>Biology Letters</i> , 2010, 6, 363-366.	2.3	127
9	MiFish metabarcoding: a high-throughput approach for simultaneous detection of multiple fish species from environmental DNA and other samples. <i>Fisheries Science</i> , 2020, 86, 939-970.	1.6	117
10	An illustrated manual for environmental DNA research: Water sampling guidelines and experimental protocols. <i>Environmental DNA</i> , 2021, 3, 8-13.	5.8	102
11	Explosive Speciation of Takifugu: Another Use of Fugu as a Model System for Evolutionary Biology. <i>Molecular Biology and Evolution</i> , 2008, 26, 623-629.	8.9	89
12	Comparing local and regional scale estimations of the diversity of stream fish using <i>scp</i> eDNA metabarcoding and conventional observation methods. <i>Freshwater Biology</i> , 2018, 63, 569-580.	2.4	88
13	Evaluation of detection probabilities at the water-filtering and initial PCR steps in environmental DNA metabarcoding using a multispecies site occupancy model. <i>Scientific Reports</i> , 2019, 9, 3581.	3.3	81
14	Demonstration of the potential of environmental DNA as a tool for the detection of avian species. <i>Scientific Reports</i> , 2018, 8, 4493.	3.3	78
15	Sedimentary eDNA provides different information on timescale and fish species composition compared with aqueous eDNA. <i>Environmental DNA</i> , 2020, 2, 505-518.	5.8	77
16	Environmental DNA metabarcoding for biodiversity monitoring of a highly diverse tropical fish community in a coral reef lagoon: Estimation of species richness and detection of habitat segregation. <i>Environmental DNA</i> , 2021, 3, 55-69.	5.8	65
17	Use of a Filter Cartridge for Filtration of Water Samples and Extraction of Environmental DNA. <i>Journal of Visualized Experiments</i> , 2016, , .	0.3	60
18	Mitogenomic evaluation of the unique facial nerve pattern as a phylogenetic marker within the perciform fishes (Teleostei: Percomorpha). <i>Molecular Phylogenetics and Evolution</i> , 2009, 53, 258-266.	2.7	55

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19	The mitogenomic contributions to molecular phylogenetics and evolution of fishes: a 15-year retrospect. <i>Ichthyological Research</i> , 2015, 62, 29-71.	0.8	55
20	Tropical-forest mammals as detected by environmental DNA at natural saltlicks in Borneo. <i>Biological Conservation</i> , 2017, 210, 281-285.	4.1	54
21	Environmental DNA Metabarcoding: A Novel Method for Biodiversity Monitoring of Marine Fish Communities. <i>Annual Review of Marine Science</i> , 2022, 14, 161-185.	11.6	52
22	Evaluating intraspecific genetic diversity using environmental DNA and denoising approach: A case study using tank water. <i>Environmental DNA</i> , 2020, 2, 42-52.	5.8	47
23	Determining an effective sampling method for eDNA metabarcoding: a case study for fish biodiversity monitoring in a small, natural river. <i>Limnology</i> , 2021, 22, 221-235.	1.5	34
24	Development of a new set of PCR primers for eDNA metabarcoding decapod crustaceans. <i>Metabarcoding and Metagenomics</i> , 0, 3, .	0.0	34
25	Environmental DNA analysis shows high potential as a tool for estimating intraspecific genetic diversity in a wild fish population. <i>Molecular Ecology Resources</i> , 2020, 20, 1248-1258.	4.8	29
26	Effects of sampling seasons and locations on fish environmental DNA metabarcoding in dam reservoirs. <i>Ecology and Evolution</i> , 2020, 10, 5354-5367.	1.9	27
27	Optimization of environmental DNA extraction and amplification methods for metabarcoding of deep-sea fish. <i>MethodsX</i> , 2021, 8, 101238.	1.6	21
28	Ongoing localized extinctions of stream-dwelling white-spotted charr populations in small dammed-off habitats of Hokkaido Island, Japan. <i>Hydrobiologia</i> , 2019, 840, 207-213.	2.0	20
29	New PCR primers for metabarcoding environmental DNA from freshwater eels, genus <i>Anguilla</i> . <i>Scientific Reports</i> , 2019, 9, 7977.	3.3	18
30	Environmental DNA metabarcoding reveals the presence of a small, quick-moving, nocturnal water shrew in a forest stream. <i>Conservation Genetics</i> , 2020, 21, 1079-1084.	1.5	16
31	»¿The use of citizen science in fish eDNA metabarcoding for evaluating regional biodiversity in a coastal marine region: A pilot study. <i>Metabarcoding and Metagenomics</i> , 0, 6, .	0.0	15
32	Preservation Obscures Pelagic Deep-Sea Fish Diversity: Doubling the Number of Sole-Bearing Opisthoproctids and Resurrection of the Genus <i>Monacoa</i> (Opisthoproctidae, Argentiniformes). <i>PLoS ONE</i> , 2016, 11, e0159762.	2.5	11
33	Detection of the Largest Deep-Sea-Endemic Teleost Fish at Depths of Over 2,000 m Through a Combination of eDNA Metabarcoding and Baited Camera Observations. <i>Frontiers in Marine Science</i> , 0, 9, .	2.5	9
34	»¿Development and evaluation of PCR primers for environmental DNA (eDNA) metabarcoding of Amphibia. <i>Metabarcoding and Metagenomics</i> , 0, 6, .	0.0	8
35	Multilocus phylogenetic analysis of the first molecular data from the rare and monotypic Amarsipidae places the family within the Pelagia and highlights limitations of existing data sets in resolving pelagian interrelationships. <i>Molecular Phylogenetics and Evolution</i> , 2018, 124, 172-180.	2.7	7
36	Discovery of a colossal slickhead (Alepocephaliformes: Alepocephalidae): an active-swimming top predator in the deep waters of Suruga Bay, Japan. <i>Scientific Reports</i> , 2021, 11, 2490.	3.3	6

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37	Phylogenomic resolution of the monotypic and enigmatic <i>Amarsipus</i> , the Bagless Glassfish (Teleostei), Tj ETQq1 1 0.784314 <sub>5</sub> rgBT /Over	1.7	5
38	Decadal vision in oceanography 2021: New methods and problems. <i>Oceanography in Japan</i> , 2021, 30, 227-253.	0.5	5
39	<i>Bajacalifornia aequatoris</i> , New Species of Alepocephalid Fish (Pisces: Salmoniformes) from the Central Equatorial Pacific. <i>Copeia</i> , 1993, 1993, 743.	1.3	4