

Nicholas M Sard

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1290610/publications.pdf>

Version: 2024-02-01

16
papers

237
citations

1163117

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996975

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17
docs citations

17
times ranked

277
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparison of fish detections, community diversity, and relative abundance using environmental DNA metabarcoding and traditional gears. <i>Environmental DNA</i> , 2019, 1, 368-384.	5.8	65
2	RAPTURE (RAD capture) panel facilitates analyses characterizing sea lamprey reproductive ecology and movement dynamics. <i>Ecology and Evolution</i> , 2020, 10, 1469-1488.	1.9	29
3	Factors influencing spawner success in a spring Chinook salmon (<i>Oncorhynchus tshawytscha</i>) reintroduction program. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2015, 72, 1390-1397.	1.4	28
4	eDNA metabarcoding outperforms traditional fisheries sampling and reveals fine-scale heterogeneity in a temperate freshwater lake. <i>Environmental DNA</i> , 2021, 3, 912-929.	5.8	20
5	eDNA metabarcoding in lakes to quantify influences of landscape features and human activity on aquatic invasive species prevalence and fish community diversity. <i>Diversity and Distributions</i> , 2021, 27, 2016-2031.	4.1	18
6	Grandparentage assignments identify unexpected adfluvial life history tactic contributing offspring to a reintroduced population. <i>Ecology and Evolution</i> , 2016, 6, 6773-6783.	1.9	12
7	Genetic Family Reconstruction Characterizes Lake Sturgeon Use of Newly Constructed Spawning Habitat and Larval Dispersal. <i>Transactions of the American Fisheries Society</i> , 2020, 149, 266-283.	1.4	12
8	Contemporary spatial extent and environmental drivers of larval coregonine distributions across Lake Ontario. <i>Journal of Great Lakes Research</i> , 2022, 48, 359-370.	1.9	12
9	Evaluation of Effective Number of Breeders and Coancestry among Progeny Produced Using Common Hatchery Mating Strategies. <i>Transactions of the American Fisheries Society</i> , 2018, 147, 185-194.	1.4	8
10	Adaptive genetic management: assessing the benefits of translocations. <i>Conservation Genetics</i> , 2020, 21, 277-287.	1.5	7
11	Coalescent models characterize sources and demographic history of recent round goby colonization of Great Lakes and inland waters. <i>Evolutionary Applications</i> , 2019, 12, 1034-1049.	3.1	6
12	Pedigree accumulation analysis: Combining methods from community ecology and population genetics for breeding adult estimation. <i>Methods in Ecology and Evolution</i> , 2021, 12, 2388-2396.	5.2	5
13	Pedigree-based decadal estimates of lake sturgeon adult spawning numbers and genetic diversity of stream-side hatchery produced offspring. <i>Journal of Great Lakes Research</i> , 2022, 48, 551-564.	1.9	5
14	Evaluating sources of bias in pedigree-based estimates of breeding population size. <i>Ecological Applications</i> , 2022, 32, e2602.	3.8	5
15	RAD-tag and mitochondrial DNA sequencing reveal the genetic structure of a widespread and regionally imperiled freshwater mussel, <i>Obovaria olivaria</i> (Bivalvia: Unionidae). <i>Ecology and Evolution</i> , 2022, 12, e8560.	1.9	3
16	Functional gene diversity and migration timing in reintroduced Chinook salmon. <i>Conservation Genetics</i> , 2015, 16, 1455-1464.	1.5	1