

Nicholas W Jeffery

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9212690/publications.pdf>

Version: 2024-02-01

38
papers

1,319
citations

394421

19
h-index

395702

33
g-index

39
all docs

39
docs citations

39
times ranked

2093
citing authors

#	ARTICLE	IF	CITATIONS
1	Integrating climate adaptation and biodiversity conservation in the global ocean. <i>Science Advances</i> , 2019, 5, eaay9969.	10.3	133
2	A climate-associated multispecies cryptic cline in the northwest Atlantic. <i>Science Advances</i> , 2018, 4, eaaq0929.	10.3	91
3	Identifying patterns of dispersal, connectivity and selection in the sea scallop, <i>Placopecten magellanicus</i> , using RAD sequencing-derived SNPs. <i>Evolutionary Applications</i> , 2017, 10, 102-117.	3.1	82
4	A guided tour of large genome size in animals: what we know and where we are heading. <i>Chromosome Research</i> , 2011, 19, 925-938.	2.2	77
5	Extensive hybridization following a large escape of domesticated Atlantic salmon in the Northwest Atlantic. <i>Communications Biology</i> , 2018, 1, 108.	4.4	68
6	Genotyping-by-sequencing of genome-wide microsatellite loci reveals fine-scale harvest composition in a coastal Atlantic salmon fishery. <i>Evolutionary Applications</i> , 2018, 11, 918-930.	3.1	60
7	genepopedit: a simple and flexible tool for manipulating multilocus molecular data in R. <i>Molecular Ecology Resources</i> , 2017, 17, 12-18.	4.8	52
8	Genomic signatures and correlates of widespread population declines in salmon. <i>Nature Communications</i> , 2019, 10, 2996.	12.8	52
9	hybriddetective: A workflow and package to facilitate the detection of hybridization using genomic data in R. <i>Molecular Ecology Resources</i> , 2017, 17, e275-e284.	4.8	49
10	parallelnewhybrid: an R package for the parallelization of hybrid detection using newhybrids. <i>Molecular Ecology Resources</i> , 2017, 17, 91-95.	4.8	46
11	Species Diversity and Phylogeographical Affinities of the Branchiopoda (Crustacea) of Churchill, Manitoba, Canada. <i>PLoS ONE</i> , 2011, 6, e18364.	2.5	43
12	Patterns of genome size variation in snapping shrimp. <i>Genome</i> , 2016, 59, 393-402.	2.0	42
13	RAD sequencing reveals genomewide divergence between independent invasions of the European green crab (<i>Carcinus maenas</i>) in the Northwest Atlantic. <i>Ecology and Evolution</i> , 2017, 7, 2513-2524.	1.9	42
14	Range-wide parallel climate-associated genomic clines in Atlantic salmon. <i>Royal Society Open Science</i> , 2017, 4, 171394.	2.4	35
15	The first genome size estimates for six species of krill (Malacostraca, Euphausiidae): large genomes at the north and south poles. <i>Polar Biology</i> , 2012, 35, 959-962.	1.2	34
16	Resolving fine-scale population structure and fishery exploitation using sequenced microsatellites in a northern fish. <i>Evolutionary Applications</i> , 2020, 13, 1055-1068.	3.1	32
17	Genomic evidence of hybridization between two independent invasions of European green crab (<i>Carcinus maenas</i>) in the Northwest Atlantic. <i>Heredity</i> , 2017, 119, 154-165.	2.6	31
18	Predicting the impacts of escaped farmed Atlantic salmon on wild salmon populations. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2018, 75, 506-512.	1.4	29

#	ARTICLE	IF	CITATIONS
19	Range-wide regional assignment of Atlantic salmon (<i>Salmo salar</i>) using genome wide single-nucleotide polymorphisms. <i>Fisheries Research</i> , 2018, 206, 163-175.	1.7	27
20	Latitudinal variation in genome size in crustaceans. <i>Biological Journal of the Linnean Society</i> , 2018, 123, 348-359.	1.6	24
21	Fine-scale temperature-associated genetic structure between inshore and offshore populations of sea scallop (<i>Placopecten magellanicus</i>). <i>Heredity</i> , 2019, 122, 69-80.	2.6	24
22	Nuclear DNA content correlates with depth, body size, and diversification rate in amphipod crustaceans from ancient Lake Baikal, Russia. <i>Genome</i> , 2017, 60, 303-309.	2.0	22
23	Genomewide evidence of environmentally mediated secondary contact of European green crab (<i>Carcinus maenas</i>) lineages in eastern North America. <i>Evolutionary Applications</i> , 2018, 11, 869-882.	3.1	22
24	Global marine biodiversity in the context of achieving the Aichi Targets: ways forward and addressing data gaps. <i>PeerJ</i> , 2019, 7, e7221.	2.0	22
25	A first exploration of genome size diversity in sponges. <i>Genome</i> , 2013, 56, 451-456.	2.0	21
26	Genome size estimates for crustaceans using Feulgen image analysis densitometry of ethanol-preserved tissues. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2014, 85, 862-868.	1.5	19
27	Temporal dynamics of genetic clines of invasive European green crab (<i>Carcinus maenas</i>) in eastern North America. <i>Evolutionary Applications</i> , 2018, 11, 1656-1670.	3.1	19
28	Eusociality in snapping shrimps is associated with larger genomes and an accumulation of transposable elements. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	19
29	Development and evaluation of SNP panels for the detection of hybridization between wild and escaped Atlantic salmon (<i>Salmo salar</i>) in the western Atlantic. <i>Canadian Journal of Fisheries and Aquatic Sciences</i> , 2019, 76, 695-704.	1.4	18
30	Insights into biodiversity sampling strategies for freshwater microinvertebrate faunas through bioblitz campaigns and DNA barcoding. <i>BMC Ecology</i> , 2013, 13, 13.	3.0	17
31	The Genome Sizes of Ostracod Crustaceans Correlate with Body Size and Evolutionary History, but not Environment. <i>Journal of Heredity</i> , 2017, 108, 701-706.	2.4	17
32	Genome size and chromosome number in velvet worms (Onychophora). <i>Genetica</i> , 2012, 140, 497-504.	1.1	16
33	Modeling demersal fish and benthic invertebrate assemblages in support of marine conservation planning. <i>Ecological Applications</i> , 2022, 32, e2546.	3.8	8
34	First estimates of genome size in ribbon worms (phylum Nemertea) using flow cytometry and Feulgen image analysis densitometry. <i>Canadian Journal of Zoology</i> , 2014, 92, 847-851.	1.0	6
35	Qualitative and quantitative analysis of the genomes and chromosomes of spider monkeys (Primates: <i>T. leucostictus</i>). <i>Journal of Heredity</i> , 2017, 108, 701-706.	1.6	6
36	Application of Omics Tools in Designing and Monitoring Marine Protected Areas For a Sustainable Blue Economy. <i>Frontiers in Genetics</i> , 0, 13, .	2.3	6

#	ARTICLE	IF	CITATIONS
37	Fish community surveys in eelgrass beds using both eDNA metabarcoding and seining: implications for biodiversity monitoring in the coastal zone. Canadian Journal of Fisheries and Aquatic Sciences, 2022, 79, 1335-1346.	1.4	5
38	Genome size estimates for Aplacophora, Polyplacophora and Scaphopoda: small solenogasters and sizeable scaphopods: TableA1.. Journal of Molluscan Studies, 2015, , eyv054.	1.2	3