Nicholas W Jeffery

List of Publications by Year
in descending order

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	Modeling demersal fish and benthic invertebrate assemblages in support of marine conservation planning. Ecological Applications, 2022, 32, e2546.	3.8	8
2	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
3	Eusociality in snapping shrimps is associated with larger genomes and an accumulation of transposable elements. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	19
4	Resolving fineâ€scale population structure and fishery exploitation using sequenced microsatellites in a northern fish. Evolutionary Applications, 2020, 13, 1055-1068.	3.1	32
5	Fine-scale temperature-associated genetic structure between inshore and offshore populations of sea scallop (Placopecten magellanicus). Heredity, 2019, 122, 69-80.	2.6	24
6	Development and evaluation of SNP panels for the detection of hybridization between wild and escaped Atlantic salmon (Salmo salar) in the western Atlantic. Canadian Journal of Fisheries and Aquatic Sciences, 2019, 76, 695-704.	1.4	18
7	Genomic signatures and correlates of widespread population declines in salmon. Nature Communications, 2019, 10, 2996.	12.8	52
8	Integrating climate adaptation and biodiversity conservation in the global ocean. Science Advances, 2019, 5, eaay9969.	10.3	133
9	Global marine biodiversity in the context of achieving the Aichi Targets: ways forward and addressing data gaps. PeerJ, 2019, 7, e7221.	2.0	22
10	Genomewide evidence of environmentally mediated secondary contact of European green crab (Carcinus maenas) lineages in eastern North America. Evolutionary Applications, 2018, 11, 869-882.	3.1	22
11	Latitudinal variation in genome size in crustaceans. Biological Journal of the Linnean Society, 2018, 123, 348-359.	1.6	24
12	Predicting the impacts of escaped farmed Atlantic salmon on wild salmon populations. Canadian Journal of Fisheries and Aquatic Sciences, 2018, 75, 506-512.	1.4	29
13	Genotypingâ€byâ€sequencing of genomeâ€wide microsatellite loci reveals fineâ€scale harvest composition in a coastal Atlantic salmon fishery. Evolutionary Applications, 2018, 11, 918-930.	3.1	60
14	A climate-associated multispecies cryptic cline in the northwest Atlantic. Science Advances, 2018, 4, eaaq0929.	10.3	91
15	Range-wide regional assignment of Atlantic salmon (Salmo salar) using genome wide single-nucleotide polymorphisms. Fisheries Research, 2018, 206, 163-175.	1.7	27
16	Temporal dynamics of genetic clines of invasive European green crab (Carcinus maenas) in eastern North America. Evolutionary Applications, 2018, 11, 1656-1670.	3.1	19
17	Extensive hybridization following a large escape of domesticated Atlantic salmon in the Northwest Atlantic. Communications Biology, 2018, 1, 108.	4.4	68
18	Genomic evidence of hybridization between two independent invasions of European green crab (Carcinus maenas) in the Northwest Atlantic. Heredity, 2017, 119, 154-165.	2.6	31

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19	The Genome Sizes of Ostracod Crustaceans Correlate with Body Size and Evolutionary History, but not Environment. Journal of Heredity, 2017, 108, 701-706.	2.4	17
20	<scp>RAD</scp> sequencing reveals genomewide divergence between independent invasions of the European green crab (Carcinus maenas) in the Northwest Atlantic. Ecology and Evolution, 2017, 7, 2513-2524.	1.9	42
21	<scp>hybriddetective</scp>: A workflow and package to facilitate the detection of hybridization using genomic data in <scp>r</scp>. Molecular Ecology Resources, 2017, 17, e275-e284.	4.8	49
22	Range-wide parallel climate-associated genomic clines in Atlantic salmon. Royal Society Open Science, 2017, 4, 171394.	2.4	35
23	Nuclear DNA content correlates with depth, body size, and diversification rate in amphipod crustaceans from ancient Lake Baikal, Russia. Genome, 2017, 60, 303-309.	2.0	22
24	<scp>genepopedit</scp>: a simple and flexible tool for manipulating multilocus molecular data in R. Molecular Ecology Resources, 2017, 17, 12-18.	4.8	52
25	parallelnewhybrid: an R package for the parallelization of hybrid detection using <scp>newhybrids</scp>. Molecular Ecology Resources, 2017, 17, 91-95.	4.8	46
26	Identifying patterns of dispersal, connectivity and selection in the sea scallop, Placopecten magellanicus, using <scp>RAD</scp>seqâ€derived <scp>SNP</scp>s. Evolutionary Applications, 2017, 10, 102-117.	3.1	82
27	Qualitative and quantitative analysis of the genomes and chromosomes of spider monkeys (Primates:) Tj ETQq1 1 0.784314 rgBT /Over	1.6	8
28	Patterns of genome size variation in snapping shrimp. Genome, 2016, 59, 393-402.	2.0	42
29	Genome size estimates for Aplacophora, Polyplacophora and Scaphopoda: small solenogasters and sizeable scaphopods: TableÂ1.. Journal of Molluscan Studies, 2015, , eyv054.	1.2	3
30	First estimates of genome size in ribbon worms (phylum Nemertea) using flow cytometry and Feulgen image analysis densitometry. Canadian Journal of Zoology, 2014, 92, 847-851.	1.0	6
31	Genome size estimates for crustaceans using Feulgen image analysis densitometry of ethanolâ€preserved tissues. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2014, 85, 862-868.	1.5	19
32	A first exploration of genome size diversity in sponges. Genome, 2013, 56, 451-456.	2.0	21
33	Insights into biodiversity sampling strategies for freshwater microinvertebrate faunas through bioblitz campaigns and DNA barcoding. BMC Ecology, 2013, 13, 13.	3.0	17
34	Genome size and chromosome number in velvet worms (Onychophora). Genetica, 2012, 140, 497-504.	1.1	16
35	The first genome size estimates for six species of krill (Malacostraca, Euphausiidae): large genomes at the north and south poles. Polar Biology, 2012, 35, 959-962.	1.2	34
36	A guided tour of large genome size in animals: what we know and where we are heading. Chromosome Research, 2011, 19, 925-938.	2.2	77

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37	Species Diversity and Phylogeographical Affinities of the Branchiopoda (Crustacea) of Churchill, Manitoba, Canada. PLoS ONE, 2011, 6, e18364.	2.5	43
38	Application of Omics Tools in Designing and Monitoring Marine Protected Areas For a Sustainable Blue Economy. Frontiers in Genetics, 0, 13, .	2.3	6