

# Jennifer R Ovenden

## List of Publications by Year in descending order

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133  
papers

5,084  
citations

147801

31  
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64  
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140  
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docs citations

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times ranked

5507  
citing authors

#	ARTICLE	IF	CITATIONS
1	NeEstimator v2: reimplementation of software for the estimation of contemporary effective population size ( $N_e$ ) from genetic data. <i>Molecular Ecology Resources</i> , 2014, 14, 209-214.	4.8	1,584
2	Harnessing the Power of Genomics to Secure the Future of Seafood. <i>Trends in Ecology and Evolution</i> , 2017, 32, 665-680.	8.7	202
3	A review of the application of molecular genetics for fisheries management and conservation of sharks and rays. <i>Journal of Fish Biology</i> , 2012, 80, 1789-1843.	1.6	190
4	Ocean's eleven: a critical evaluation of the role of population, evolutionary and molecular genetics in the management of wild fisheries. <i>Fish and Fisheries</i> , 2015, 16, 125-159.	5.3	141
5	Evidence for reproductive philopatry in the bull shark <i>Carcharhinus leucas</i> . <i>Journal of Fish Biology</i> , 2012, 80, 2140-2158.	1.6	103
6	Mitochondrial DNA analyses of the red rock lobster <i> Jasus edwardsii</i> supports an apparent absence of population subdivision throughout Australasia. <i>Marine Biology</i> , 1992, 112, 319-326.	1.5	102
7	The extent of population genetic subdivision differs among four co-distributed shark species in the Indo-Australian archipelago. <i>BMC Evolutionary Biology</i> , 2009, 9, 40.	3.2	100
8	Population genetics of Australian white sharks reveals fine-scale spatial structure, transoceanic dispersal events and low effective population sizes. <i>Marine Ecology - Progress Series</i> , 2012, 455, 229-244.	1.9	100
9	Application of environmental DNA to detect an endangered marine skate species in the wild. <i>PLoS ONE</i> , 2017, 12, e0178124.	2.5	98
10	Improved confidence intervals for the linkage disequilibrium method for estimating effective population size. <i>Heredity</i> , 2016, 117, 217-223.	2.6	91
11	The genetic effective and adult census size of an Australian population of tiger prawns ( <i>Penaeus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 227 T	3.9	88
12	IUCN classification zones concord with, but underestimate, the population genetic structure of the zebra shark <i>Stegostoma fasciatum</i> in the Indo-West Pacific. <i>Molecular Ecology</i> , 2009, 18, 248-261.	3.9	74
13	Accounting for missing data in the estimation of contemporary genetic effective population size ( $N_e$ ). <i>Molecular Ecology Resources</i> , 2013, 13, 243-253.	4.8	62
14	Pronounced genetic population structure in a potentially vagile fish species ( <i>Pristipomoides</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 227 T	3.9	60
15	Detection of interspecies hybridisation in Chondrichthyes: hybrids and hybrid offspring between Australian ( <i>Carcharhinus tilstoni</i> ) and common ( <i>C. limbatus</i> ) blacktip shark found in an Australian fishery. <i>Conservation Genetics</i> , 2012, 13, 455-463.	1.5	59
16	Accuracy of species identification by fisheries observers in a north Australian shark fishery. <i>Fisheries Research</i> , 2012, 127-128, 109-115.	1.7	58
17	Habitat segregation and mosaic sympatry of the two species of manta ray in the Indian and Pacific Oceans: <i>Manta alfredi</i> and <i>M. birostris</i> . <i>Marine Biodiversity Records</i> , 2011, 4, .	1.2	49
18	Crinkles in connectivity: combining genetics and other types of biological data to estimate movement and interbreeding between populations. <i>Marine and Freshwater Research</i> , 2013, 64, 201.	1.3	48

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19	Evidence of stock separation in southern hemisphere orange roughy ( <i>Hoplostethus atlanticus</i> ). <i>Tj ETQq1 1 0.784314 rgBT /Overlock</i> 219-230.	1.5	46
20	Mitochondrial DNA phylogeny of red and green rock lobsters (genus <i>Jasus</i> ). <i>Marine and Freshwater Research</i> , 1997, 48, 1131.	1.3	46
21	The genetic signature of recent speciation in manta rays ( <i>Manta alfredi</i> and <i>M. birostris</i> ). <i>Molecular Phylogenetics and Evolution</i> , 2012, 64, 212-218.	2.7	46
22	Genetic subdivision of Australian and New Zealand populations of <i>Jasus verreauxi</i> (Decapoda: Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 and <i>Freshwater Research</i> , 1992, 26, 53-58.	2.0	43
23	Population-Genetic Structure of a Philopatric, Colonially Nesting Seabird, the Short-Tailed Shearwater ( <i>Puffinus tenuirostris</i> ). <i>Auk</i> , 1994, 111, 70-79.	1.4	43
24	Towards better management of Australia's shark fishery: genetic analyses reveal unexpected ratios of cryptic blacktip species <i>Carcharhinus tilstoni</i> and <i>C. limbatus</i> . <i>Marine and Freshwater Research</i> , 2010, 61, 253.	1.3	43
25	Mitochondrial DNA variation and phylogenetic relationships of <i>Jasus</i> spp. (Decapoda: Palinuridae). <i>Journal of Zoology</i> , 1992, 227, 1-16.	1.7	40
26	Distribution of <i>Jasus</i> spp. (Decapoda:Palinuridae) phyllosomas in southern waters:implications for larval recruitment. <i>Marine Ecology - Progress Series</i> , 2000, 200, 241-255.	1.9	39
27	Spatial genetic subdivision between northern Australian and southeast Asian populations of <i>Pristipomoides multidens</i> : a tropical marine reef fish species. <i>Fisheries Research</i> , 2002, 59, 57-69.	1.7	38
28	New SNP's for population genetic analysis reveal possible cryptic speciation of eastern Australian sea mullet ( <i>Mugil cephalus</i> ). <i>Molecular Ecology Resources</i> , 2013, 13, 715-725.	4.8	35
29	Negligible evidence for regional genetic population structure for two shark species <i>Rhizoprionodon acutus</i> (Rä¼ppell, 1837) and <i>Sphyrna lewini</i> (Griffith & Smith, 1834) with contrasting biology. <i>Marine Biology</i> , 2011, 158, 1497-1509.	1.5	33
30	The relationship between abundance and genetic effective population size in elasmobranchs: an example from the globally threatened zebra shark <i>Stegostoma fasciatum</i> within its protected range. <i>Conservation Genetics</i> , 2015, 16, 1443-1454.	1.5	33
31	Strong population structure deduced from genetics, otolith chemistry and parasite abundances explains vulnerability to localized fishery collapse in a large Sciaenid fish, <i>Protonibea adianthus</i> . <i>Evolutionary Applications</i> , 2017, 10, 978-993.	3.1	33
32	Evolutionary relationships of <i>Gadopsis</i> spp. inferred from restriction enzyme analysis of their mitochondrial DNA. <i>Journal of Fish Biology</i> , 1988, 32, 137-148.	1.6	32
33	Switch from sexual to parthenogenetic reproduction in a zebra shark. <i>Scientific Reports</i> , 2017, 7, 40537.	3.3	32
34	Mitochondrial DNA restriction site variation in Tasmanian populations of Orange Roughy ( <i>Hoplostethus atlanticus</i> ), a deep-water marine teleost. <i>Marine and Freshwater Research</i> , 1989, 40, 1.	1.3	31
35	Population genetic evidence for the east-west division of the narrow-barred Spanish mackerel ( <i>Scomberomorus commerson</i> , Perciformes: Teleostei) along Wallace's Line. <i>Biodiversity and Conservation</i> , 2010, 19, 563-574.	2.6	29
36	Evidence for extensive population structure in the white-spotted eagle ray within the Indo-Pacific inferred from mitochondrial gene sequences. <i>Journal of Zoology</i> , 2010, 281, 46-55.	1.7	29

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37	Population structure and connectivity of tiger sharks ( <i>Galeocerdo cuvier</i> ) across the Indo-Pacific Ocean basin. <i>Royal Society Open Science</i> , 2017, 4, 170309.	2.4	29
38	Can estimates of genetic effective population size contribute to fisheries stock assessments?. <i>Journal of Fish Biology</i> , 2016, 89, 2505-2518.	1.6	28
39	Venereal Transmission of Sindbis Virus Between Individuals of <i>Aedes Australis</i> (Diptera: Culicidae). <i>Journal of Medical Entomology</i> , 1984, 21, 292-295.	1.8	27
40	Mitochondrial and allozyme genetics of two Tasmanian galaxiids ( <i>Galaxias auratus</i> and <i>G.</i> )	2.6	27
41	Population structure, effective population size and adverse effects of stocking in the endangered Australian eastern freshwater cod <i>Maccullochella ikei</i> . <i>Journal of Fish Biology</i> , 2011, 78, 303-321.	1.6	27
42	Integrating different approaches in the definition of biological stocks: A northern Australian multi-jurisdictional fisheries example using grey mackerel, <i>Scomberomorus semifasciatus</i> . <i>Marine Policy</i> , 2015, 55, 73-80.	3.2	27
43	Genetic population structure of mangrove jack, <i>Lutjanus argentimaculatus</i> (Forsskål). <i>Marine and Freshwater Research</i> , 2003, 54, 127.	1.3	26
44	Multi-gene barcoding to discriminate sibling species within a morphologically difficult fish genus ( <i>Sillago</i> ). <i>Fisheries Research</i> , 2013, 143, 39-46.	1.7	26
45	Contrasting Genetic Structure among Populations of Two Amphidromous Fish Species ( <i>Sicydiinae</i> ) in the Central West Pacific. <i>PLoS ONE</i> , 2013, 8, e75465.	2.5	26
46	Genetic population structure of grey mackerel <i>Scomberomorus semifasciatus</i> in northern Australia. <i>Journal of Fish Biology</i> , 2011, 79, 633-661.	1.6	25
47	Pleistocene isolation, secondary introgression and restricted contemporary gene flow in the pig-eye shark, <i>Carcharhinus amboinensis</i> across northern Australia. <i>Conservation Genetics</i> , 2012, 13, 99-115.	1.5	24
48	Extensive genetic population structure in the Indo-West Pacific spot-tail shark, <i>Carcharhinus sorrah</i> . <i>Bulletin of Marine Science</i> , 2014, 90, 427-454.	0.8	23
49	Restriction Fragment Length Polymorphisms in Chloroplast DNA From Six Species of <i>Eucalyptus</i> . <i>Australian Journal of Botany</i> , 1991, 39, 399.	0.6	22
50	Mitochondrial DNA nucleotide sequence variation in Atlantic salmon ( <i>Salmo salar</i> ), brown trout ( <i>S.</i> )	3.5	22
51	Australia. <i>Aquaculture</i> , 1993, 114, 217-227.	1.6	22
52	Genetic population structure of red snappers ( <i>Lutjanus malabaricus</i> Bloch & Schneider, 1801 and)	1.0	22
53	Stock structure of Grey Mackerel, <i>Scomberomorus semifasciatus</i> (Pisces: Scombridae) across northern Australia, based on otolith stable isotope chemistry. <i>Environmental Biology of Fishes</i> , 2010, 89, 357-367.	2.1	22
54	Evolution of Diadromy in Fish: Insights from a Tropical Genus ( <i>Kuhlia</i> Species). <i>American Naturalist</i> , 2013, 181, 52-63.	2.5	22
54	Population genetics of Southern Hemisphere tope shark ( <i>Galeorhinus galeus</i> ): Intercontinental divergence and constrained gene flow at different geographical scales. <i>PLoS ONE</i> , 2017, 12, e0184481.		

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55	Title is missing!. Conservation Genetics, 2001, 2, 63-67.	1.5	21
56	Spatial subdivision among assemblages of Spanish mackerel, <i>Scomberomorus commerson</i> (Pisces: Scombridae) across northern Australia: implications for fisheries management. Global Ecology and Biogeography, 2009, 18, 711-723.	5.8	21
57	Likelihood-based genetic mark-recapture estimates when genotype samples are incomplete and contain typing errors. Theoretical Population Biology, 2011, 80, 185-196.	1.1	21
58	Population Expansion and Genetic Structure in <i>Carcharhinus brevipinna</i> in the Southern Indo-Pacific. PLoS ONE, 2013, 8, e75169.	2.5	21
59	Fine scale population structure of dugongs ( <i>Dugong dugon</i> ) implies low gene flow along the southern Queensland coastline. Conservation Genetics, 2014, 15, 1381-1392.	1.5	21
60	Genetic and phenotypic diversity in the wedgetfish <i>Rhynchobatus australiae</i> , a threatened ray of high value in the shark fin trade. Marine Ecology - Progress Series, 2016, 548, 165-180.	1.9	21
61	A mitochondrial species identification assay for Australian blacktip sharks ( <i>Carcharhinus</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 147 T melt analysis. Molecular Ecology Resources, 2011, 11, 813-819.	4.8	19
62	Stretched to the limit; can a short pelagic larval duration connect adult populations of an Indo-Pacific diadromous fish ( <i>Chelodactylus rupestris</i> )?. Molecular Ecology, 2013, 22, 1518-1530.	3.9	19
63	Genetic structure and diversity of two highly vulnerable carcharhinids in Australian waters. Endangered Species Research, 2014, 24, 45-60.	2.4	19
64	Spatial genetic subdivision among populations of the highly migratory black marlin <i>Istiompax indica</i> within the central Indo-Pacific. Marine and Freshwater Research, 2016, 67, 1205.	1.3	19
65	Characterization of 26 new microsatellite loci in the dugong ( <i>Dugong dugon</i> ). Molecular Ecology Notes, 2007, 7, 1275-1277.	1.7	18
66	Characterization of highly informative cross-species microsatellite panels for the Australian dugong ( <i>Dugong dugon</i> ) and Florida manatee ( <i>Trichechus manatus latirostris</i> ) including five novel primers. Molecular Ecology Resources, 2010, 10, 368-377.	4.8	18
67	Towards sustainable fishery management for skates in South America: The genetic population structure of <i>Zearaja chilensis</i> and <i>Dipturus trachyderma</i> (Chondrichthyes, Rajiformes) in the south-east Pacific Ocean. PLoS ONE, 2017, 12, e0172255.	2.5	16
68	New microsatellite loci for Carcharhinid sharks ( <i>Carcharhinus tilstoni</i> and <i>C. sorrah</i> ) and their cross-amplification in other shark species. Molecular Ecology Notes, 2006, 6, 415-418.	1.7	15
69	Identification of small juvenile scombrids from northwest tropical Australia using mitochondrial DNA cytochrome b sequences. Ichthyological Research, 2007, 54, 246-252.	0.8	15
70	Comparison of the reproductive ecology of two sympatric blacktip sharks ( <i>Carcharhinus</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 147 T inferred from vertebral counts. Journal of Fish Biology, 2012, 81, 1225-1233.	1.6	15
71	neogen: A tool to predict genetic effective population size ( $N_e$ ) for species with generational overlap and to assist empirical $N_e$ study design. Molecular Ecology Resources, 2019, 19, 260-271.	4.8	15
72	Evidence for a stock discontinuity of snapper ( <i>Pagrus auratus</i> ) on the east coast of Australia. Fisheries Research, 2008, 94, 92-98.	1.7	14

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73	The stock structure of grey mackerel <i>Scomberomorus semifasciatus</i> in Australia as inferred from its parasite fauna. <i>Fisheries Research</i> , 2010, 101, 94-99.	1.7	14
74	Linkage Disequilibrium Estimation of Effective Population Size with Immigrants from Divergent Populations: A Case Study on Spanish Mackerel ( <i>Scomberomorus commerson</i> ). <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 709-717.	1.8	14
75	Population Genetic Diversity in the Australian "Seascape": A Bioregion Approach. <i>PLoS ONE</i> , 2015, 10, e0136275.	2.5	14
76	A novel field method to distinguish between cryptic carcharhinid sharks, Australian blacktip shark <i>Carcharhinus tilstoni</i> and common blacktip shark <i>C. limbatus</i> , despite the presence of hybrids. <i>Journal of Fish Biology</i> , 2017, 90, 39-60.	1.6	14
77	Ocean currents and the population genetic signature of fish migrations. <i>Ecology</i> , 2020, 101, e02967.	3.2	14
78	Population genetic structure of the brown tiger prawn, <i>Penaeus esculentus</i> , in tropical northern Australia. <i>Marine Biology</i> , 2006, 148, 599-607.	1.5	13
79	A PCR assay for gender assignment in dugong ( <i>Dugong dugon</i> ) and West Indian manatee ( <i>Trichechus</i> )	4.8	13
80	The complete mitochondrial genome of the dusky shark <i>Carcharhinus obscurus</i> . <i>Mitochondrial DNA</i> , 2013, 24, 619-621.	0.6	13
81	Sexing Sirenians: Validation of Visual and Molecular Sex Determination in Both Wild Dugongs (<i>Dugong dugon</i>) and Florida Manatees (<i>Trichechus manatus</i>)	0.784314	10
82	Variability in multiple paternity rates for grey reef sharks ( <i>Carcharhinus amblyrhynchos</i> ) and scalloped hammerheads ( <i>Sphyrna lewini</i> ). <i>Scientific Reports</i> , 2017, 7, 1528.	3.3	12
83	Extracting DNA from "jaws": high yield and quality from archived tiger shark ( <i>Galeocerdo cuvier</i> ) skeletal material. <i>Molecular Ecology Resources</i> , 2017, 17, 431-442.	4.8	12
84	Lack of multiple paternity in the oceanodromous tiger shark ( <i>Galeocerdo cuvier</i> ). <i>Royal Society Open Science</i> , 2018, 5, 171385.	2.4	12
85	Polymorphic microsatellite loci for the zebra shark <i>Stegostoma fasciatum</i> . <i>Molecular Ecology Notes</i> , 2006, 6, 1086-1088.	1.7	11
86	Pelagic larval duration of two diadromous species of Kuhlidae (Teleostei: Percoidei) from Indo-Pacific insular systems. <i>Marine and Freshwater Research</i> , 2012, 63, 397.	1.3	11
87	Hybridisation, paternal leakage and mitochondrial DNA linearization in three anomalous fish (Scombridae). <i>Mitochondrion</i> , 2013, 13, 852-861.	3.4	11
88	Analysis of whole mitochondrial genome sequences increases phylogenetic resolution of istiophorid billfishes. <i>Bulletin of Marine Science</i> , 2018, 94, 73-84.	0.8	11
89	Stock structure of <i>Lethrinus laticaudis</i> (Lethrinidae) across northern Australia determined using genetics, otolith microchemistry and parasite assemblage composition. <i>Marine and Freshwater Research</i> , 2018, 69, 487.	1.3	11
90	Assessment of genetic structure among Australian east coast populations of snapper <i>Chrysophrys auratus</i> (Sparidae). <i>Marine and Freshwater Research</i> , 2019, 70, 964.	1.3	11

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91	Novel multimer comparisons address the genetic population structure of silvertip sharks ( <i>Carcharhinus albimarginatus</i> ). <i>Marine and Freshwater Research</i> , 2019, 70, 1007.	1.3	11
92	Telomere length analysis in crustacean species: <i>Metapenaeus macleayi</i> , <i>Sagmariasus verreauxi</i> , and <i>Jasus edwardsii</i> . <i>ICES Journal of Marine Science</i> , 2011, 68, 2053-2058.	2.5	10
93	locuseater and shadowboxer: programs to optimize experimental design and multiplexing strategies for genetic mark-recapture. <i>Molecular Ecology Notes</i> , 2005, 5, 974-976.	1.7	9
94	Telomere dynamics in the Sydney rock oyster ( <i>Saccostrea glomerata</i> ): an investigation into the effects of age, tissue type, location and time of sampling. <i>Marine Biology</i> , 2012, 159, 77-86.	1.5	9
95	Isolation and characterisation of 18 polymorphic microsatellite loci for black marlin ( <i>Istiompax</i> ) Tj ETQq1 1 0.784314 rgBT /Oyerlock 10	1.7	9
96	Sweepstakes reproductive success is absent in a New Zealand snapper ( <i>Chrysophrus auratus</i> ) population protected from fishing despite $\frac{N_e}{N}$ ratios elsewhere. <i>Molecular Ecology</i> , 2019, 28, 2986-2995.	3.9	9
97	The complete validated mitochondrial genome of the yellownose skate ( <i>Zearaja chilensis</i> ) (Guichenot 1848) (Rajiformes, Rajidae). <i>Mitochondrial DNA</i> , 2016, 27, 1227-1228.	0.6	8
98	The phylogenetic position of the giant devil ray ( <i>Mobula mobular</i> ) (Bonnaterre, 1788) (Myliobatiformes, Myliobatidae) inferred from the mitochondrial genome. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 3540-3541.	0.7	8
99	The phylogenetic position of the roughskin skate ( <i>Dipturus trachyderma</i> ) (Krefft & Stehmann,) Tj ETQq1 1 0.784314 rgBT /Oyerlock 10 Mapping, Sequencing, and Analysis, 2016, 27, 2965-2966.	0.7	8
100	Misidentification of istiophorid billfishes by fisheries observers raises uncertainty over stock status. <i>Journal of Fish Biology</i> , 2018, 93, 415-419.	1.6	8
101	Investigating the genetic stock structure of blue marlin ( <i>Makaira nigricans</i> ) in the Pacific Ocean. <i>Fisheries Research</i> , 2020, 228, 105565.	1.7	8
102	A Program for the Estimation of Restriction Endonuclease Site Positions from Restriction Fragment Size and Number: An Aid for Mitochondrial DNA Analysis. <i>Journal of Heredity</i> , 1992, 83, 240-241.	2.4	6
103	Fifteen microsatellite loci for the jungle perch, ( <i>Kuhlia rupestris</i> ). <i>Molecular Ecology Resources</i> , 2009, 9, 1467-1469.	4.8	6
104	Population genetics of the endangered Maugean skate ( <i>Zearaja maugeana</i> ) in Macquarie Harbour, Tasmania. <i>Conservation Genetics</i> , 2018, 19, 1505-1512.	1.5	6
105	Effective number of white shark ( <i>Carcharodon carcharias</i> , Linnaeus) breeders is stable over four successive years in the population adjacent to eastern Australia and New Zealand. <i>Ecology and Evolution</i> , 2021, 11, 186-198.	1.9	6
106	Global phylogeography of the smooth hammerhead shark: Glacial refugia and historical migration patterns. <i>Aquatic Conservation: Marine and Freshwater Ecosystems</i> , 2021, 31, 2348-2368.	2.0	6
107	Effect of DNA extraction on ageing success in coral trout ( <i>Plectropomus leopardus</i> ) otoliths. <i>Journal of Fish Biology</i> , 2007, 71, 302-307.	1.6	5
108	Characterization of four tetranucleotide and six dinucleotide microsatellite markers for use in the tropical freshwater fish <i>Telmatherina antoniae</i> and related species. <i>Molecular Ecology Notes</i> , 2007, 7, 651-653.	1.7	5

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109	Development and characterization of ten microsatellite loci for the reef manta ray <i>Manta alfredi</i> . <i>Conservation Genetics Resources</i> , 2012, 4, 1055-1058.	0.8	5
110	The complete mitochondrial genome of the sandbar shark <i>Carcharhinus plumbeus</i> . <i>Mitochondrial DNA</i> , 2016, 27, 923-924.	0.6	5
111	The phylogenomic position of the grey nurse shark <i>Carcharias taurus</i> Rafinesque, 1810 (Lamniformes, <i>Tj ETQq1 1 0.784314 rgBT /O</i> Sequencing, and Analysis, 2016, 27, 4328-4330.	0.7	5
112	Fishing for DNA? Designing baits for population genetics in target enrichment experiments: Guidelines, considerations and the new tool superBaits. <i>Molecular Ecology Resources</i> , 2022, 22, 2105-2119.	4.8	5
113	Translocation between freshwater catchments has facilitated the spread of tilapia in eastern Australia. <i>Biological Invasions</i> , 2015, 17, 637-650.	2.4	4
114	The complete validated mitochondrial genome of the silver gemfish <i>Rexea solandri</i> (Cuvier, 1832) (Perciformes, Gempylidae). <i>Mitochondrial DNA</i> , 2016, 27, 405-406.	0.6	4
115	Characterization, development and multiplexing of microsatellite markers in three commercially exploited reef fish and their application for stock identification. <i>PeerJ</i> , 2016, 4, e2418.	2.0	4
116	Preliminary investigation of mitochondrial DNA variation in jack mackerel ( <i>Trachurus declivis</i> , <i>Tj ETQq0 0 0 rgBT /O</i> verlock 10 Tf 50 462	1.3	3
117	Characterisation and cross-amplification of 21 novel microsatellite loci for the dusky shark, <i>Carcharhinus obscurus</i> . <i>Conservation Genetics Resources</i> , 2015, 7, 909-912.	0.8	3
118	Parental contribution to progeny during experimental spawning of jungle perch, <i>Kuhlia rupestris</i> . <i>Marine and Freshwater Research</i> , 2015, 66, 375.	1.3	3
119	Breaking the myths (or how to have a successful career in science). <i>ICES Journal of Marine Science</i> , 2019, 76, 23-27.	2.5	3
120	Spatial and temporal genetic variation in an exploited reef fish: The effects of exploitation on cohort genetic structure. <i>Evolutionary Applications</i> , 2021, 14, 1286-1300.	3.1	3
121	Retrospective genomics highlights changes in genetic composition of tiger sharks ( <i>Galeocerdo</i> ) <i>Tj ETQq1 1 0.784314 rgBT /O</i> verlock 10 Tf 50 462	3.3	3
122	Mitochondrial DNA restriction site map for <i>Gadopsis marmoratus</i> . <i>Biochemical Systematics and Ecology</i> , 1988, 16, 355-357.	1.3	2
123	Habitat segregation and mosaic sympatry of the two species of manta ray in the Indian and Pacific Oceans: <i>Manta alfredi</i> and <i>M. birostris</i> CORRIGENDUM. <i>Marine Biodiversity Records</i> , 2011, 4, .	1.2	2
124	Stirred but not shaken: population and recruitment genetics of the scallop ( <i>Pecten fumatus</i> ) in Bass Strait, Australia. <i>ICES Journal of Marine Science</i> , 2016, 73, 2333-2341.	2.5	2
125	The complete validated mitochondrial genome of the black marlin <i>Istiompax indica</i> (Cuvier, 1832). <i>Mitochondrial DNA</i> , 2016, 27, 418-419.	0.6	2
126	The complete mitochondrial genome of the golden snapper <i>Lutjanus johnii</i> (Perciformes:) <i>Tj ETQq0 0 0 rgBT /O</i> verlock 10 Tf 50 462	0.6	2



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127	Development and characterization of 17 polymorphic microsatellite markers for the reef manta ray ( <i>Mobula alfredi</i> ). <i>BMC Research Notes</i> , 2019, 12, 233.	1.4	2
128	Genotype and phylogenomic position of the frilled shark <i>Chlamydoselachus anguineus</i> inferred from the mitochondrial genome. <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 18-20.	0.4	1
129	The complete mitochondrial genome of the grass emperor, <i>Lethrinus laticaudis</i> (Perciformes:). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 622</i>	0.4	1
130	The complete mitochondrial genome of the black jewfish <i>Protonibea diacanthus</i> (Perciformes:). <i>Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 622</i>	0.6	1
131	A perfect storm of genetic drift and divergence may prevent the rebuilding of the gemfish ( <i>Rexea</i> ). <i>Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 622</i>	1.7	1
132	Characterisation and cross-amplification of 19 novel microsatellite loci for the sandbar shark, <i>Carcharhinus plumbeus</i> . <i>Conservation Genetics Resources</i> , 2015, 7, 913-915.	0.8	0
133	Population genetic evidence for the east-west division of the narrow-barred Spanish mackerel ( <i>Scomberomorus commerson</i> , Perciformes: Teleostei) along Wallace's Line. <i>Topics in Biodiversity and Conservation</i> , 2009, , 251-262.	1.0	0