Jennifer R Ovenden

List of Publications by Year in descending order

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133 papers 5,084 citations

147566 31 h-index 64 g-index

140 all docs 140 docs citations

140 times ranked 5507 citing authors

#	Article	IF	Citations
1	Fishing for DNA? Designing baits for population genetics in target enrichment experiments: Guidelines, considerations and the new tool supeRbaits. Molecular Ecology Resources, 2022, 22, 2105-2119.	2.2	5
2	Retrospective genomics highlights changes in genetic composition of tiger sharks (Galeocerdo) Tj ETQq0 0 0 rgBT	Overlock	. 10 Tf 50 70
3	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. Ecology and Evolution, 2021, 11, 186-198.	0.8	6
4	Spatial and temporal genetic variation in an exploited reef fish: The effects of exploitation on cohort genetic structure. Evolutionary Applications, 2021, 14, 1286-1300.	1.5	3
5	Global phylogeography of the smooth hammerhead shark: Glacial refugia and historical migration patterns. Aquatic Conservation: Marine and Freshwater Ecosystems, 2021, 31, 2348-2368.	0.9	6
6	Ocean currents and the population genetic signature of fish migrations. Ecology, 2020, 101, e02967.	1.5	14
7	A perfect storm of genetic drift and divergence may prevent the rebuilding of the gemfish (Rexea) Tj ETQq1 1 0.78	343]4 rgB	T/Overlock
8	Investigating the genetic stock structure of blue marlin (Makaira nigricans) in the Pacific Ocean. Fisheries Research, 2020, 228, 105565.	0.9	8
9	Assessment of genetic structure among Australian east coast populations of snapper Chrysophrys auratus (Sparidae). Marine and Freshwater Research, 2019, 70, 964.	0.7	11
10	Sweepstakes reproductive success is absent in a New Zealand snapper (<i>Chrysophrus auratus</i>) population protected from fishing despite "tiny― <i>N</i> _e / <i>N</i> ratios elsewhere. Molecular Ecology, 2019, 28, 2986-2995.	2.0	9
11	Development and characterization of 17 polymorphic microsatellite markers for the reef manta ray (Mobula alfredi). BMC Research Notes, 2019, 12, 233.	0.6	2
12	Novel multimarker comparisons address the genetic population structure of silvertip sharks (Carcharhinus albimarginatus). Marine and Freshwater Research, 2019, 70, 1007.	0.7	11
13	Breaking the myths (or how to have a successful career in science). ICES Journal of Marine Science, 2019, 76, 23-27.	1.2	3
14	<scp>neogen</scp> : A tool to predict genetic effective population size (<i>N</i> _e) for species with generational overlap and to assist empirical <i>N</i> _e study design. Molecular Ecology Resources, 2019, 19, 260-271.	2.2	15
15	Lack of multiple paternity in the oceanodromous tiger shark (Galeocerdo cuvier). Royal Society Open Science, 2018, 5, 171385.	1.1	12
16	Analysis of whole mitochondrial genome sequences increases phylogenetic resolution of istiophorid billfishes. Bulletin of Marine Science, 2018, 94, 73-84.	0.4	11
17	Population genetics of the endangered Maugean skate (Zearaja maugeana) in Macquarie Harbour, Tasmania. Conservation Genetics, 2018, 19, 1505-1512.	0.8	6
18	Misidentification of istiophorid billfishes by fisheries observers raises uncertainty over stock status. Journal of Fish Biology, 2018, 93, 415-419.	0.7	8

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19	Stock structure of Lethrinus laticaudis (Lethrinidae) across northern Australia determined using genetics, otolith microchemistry and parasite assemblage composition. Marine and Freshwater Research, 2018, 69, 487.	0.7	11
20	Switch from sexual to parthenogenetic reproduction in a zebra shark. Scientific Reports, 2017, 7, 40537.	1.6	32
21	Harnessing the Power of Genomics to Secure the Future of Seafood. Trends in Ecology and Evolution, 2017, 32, 665-680.	4.2	202
22	Variability in multiple paternity rates for grey reef sharks (Carcharhinus amblyrhynchos) and scalloped hammerheads (Sphyrna lewini). Scientific Reports, 2017, 7, 1528.	1.6	12
23	Strong population structure deduced from genetics, otolith chemistry and parasite abundances explains vulnerability to localized fishery collapse in a large Sciaenid fish, <i>ProtonibeaÂdiacanthus</i> . Evolutionary Applications, 2017, 10, 978-993.	1.5	33
24	Population structure and connectivity of tiger sharks (<i>Galeocerdo cuvier</i>) across the Indo-Pacific Ocean basin. Royal Society Open Science, 2017, 4, 170309.	1.1	29
25	A novel field method to distinguish between cryptic carcharhinid sharks, <scp>A</scp> ustralian blacktip shark <i>Carcharhinus tilstoni</i> and common blacktip shark <i>C. limbatus</i> , despite the presence of hybrids. Journal of Fish Biology, 2017, 90, 39-60.	0.7	14
26	Extracting <scp>DNA</scp> from â€~jaws': high yield and quality from archived tiger shark (<i>Galeocerdo cuvier</i>) skeletal material. Molecular Ecology Resources, 2017, 17, 431-442.	2.2	12
27	Towards sustainable fishery management for skates in South America: The genetic population structure of Zearaja chilensis and Dipturus trachyderma (Chondrichthyes, Rajiformes) in the south-east Pacific Ocean. PLoS ONE, 2017, 12, e0172255.	1.1	16
28	Application of environmental DNA to detect an endangered marine skate species in the wild. PLoS ONE, 2017, 12, e0178124.	1.1	98
29	Population genetics of Southern Hemisphere tope shark (Galeorhinus galeus): Intercontinental divergence and constrained gene flow at different geographical scales. PLoS ONE, 2017, 12, e0184481.	1.1	22
30	The complete mitochondrial genome of the sandbar sharkCarcharhinus plumbeus. Mitochondrial DNA, 2016, 27, 923-924.	0.6	5
31	The complete validated mitochondrial genome of the yellownose skate <i>Zearaja chilensis</i> (Guichenot 1848) (Rajiformes, Rajidae). Mitochondrial DNA, 2016, 27, 1227-1228.	0.6	8
32	The complete validated mitochondrial genome of the silver gemfish <i>Rexea solandri</i> (Cuvier, 1832) (Perciformes, Gempylidae). Mitochondrial DNA, 2016, 27, 405-406.	0.6	4
33	Genetype and phylogenomic position of the frilled shark <i>Chlamydoselachus anguineus (i) inferred from the mitochondrial genome. Mitochondrial DNA Part B: Resources, 2016, 1, 18-20.</i>	0.2	1
34	The complete mitochondrial genome of the grass emperor, Lethrinus laticaudis (Perciformes:) Tj ETQq0 0 0 rgBT	/Oyerlock	10 Tf 50 142
35	Spatial genetic subdivision among populations of the highly migratory black marlin Istiompax indica within the central Indo-Pacific. Marine and Freshwater Research, 2016, 67, 1205.	0.7	19
36	Stirred but not shaken: population and recruitment genetics of the scallop (Pecten fumatus) in Bass Strait, Australia. ICES Journal of Marine Science, 2016, 73, 2333-2341.	1.2	2

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37	Can estimates of genetic effective population size contribute to fisheries stock assessments?. Journal of Fish Biology, 2016, 89, 2505-2518.	0.7	28
38	Improved confidence intervals for the linkage disequilibrium method for estimating effective population size. Heredity, 2016, 117, 217-223.	1.2	91
39	The phylogenetic position of the giant devil ray <i>Mobula mobular</i> (Bonnaterre, 1788) (Myliobatiformes, Myliobatidae) inferred from the mitochondrial genome. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 3540-3541.	0.7	8
40	The complete validated mitochondrial genome of the black marlinistiompax indica(Cuvier, 1832). Mitochondrial DNA, 2016, 27, 418-419.	0.6	2
41	The complete mitochondrial genome of the black jewfishProtonibea diacanthus(Perciformes:) Tj ETQq1 1 0.78431	4 rgBT /O	verlock 10
42	The phylogenomic position of the grey nurse shark Carcharias taurus Rafinesque, 1810 (Lamniformes,) Tj ETQq0 0 Sequencing, and Analysis, 2016, 27, 4328-4330.	0 rgBT /C 0.7	Overlock 10 5
43	The phylogenetic position of the roughskin skate <i>Dipturus trachyderma</i> (Krefft & Dipturus trachyderma (Krefft &	0.7843 0.7	814 rgBT /0 8
44	The complete mitochondrial genome of the golden snapper <i>Lutjanus johnii</i> (Perciformes:) Tj ETQq0 0 0 rgBT	/Oyerlock	10 Tf 50 4
45	Genetic and phenotypic diversity in the wedgefish Rhynchobatus australiae, a threatened ray of high value in the shark fin trade. Marine Ecology - Progress Series, 2016, 548, 165-180.	0.9	21
46	Characterization, development and multiplexing of microsatellite markers in three commercially exploited reef fish and their application for stock identification. PeerJ, 2016, 4, e2418.	0.9	4
47	Integrating different approaches in the definition of biological stocks: A northern Australian multi-jurisdictional fisheries example using grey mackerel, Scomberomorus semifasciatus. Marine Policy, 2015, 55, 73-80.	1.5	27
48	Population Genetic Diversity in the Australian â€~Seascape': A Bioregion Approach. PLoS ONE, 2015, 10, e0136275.	1.1	14
49	The relationship between abundance and genetic effective population size in elasmobranchs: an example from the globally threatened zebra shark Stegostoma fasciatum within its protected range. Conservation Genetics, 2015, 16, 1443-1454.	0.8	33
50	Translocation between freshwater catchments has facilitated the spread of tilapia in eastern Australia. Biological Invasions, 2015, 17, 637-650.	1.2	4
51	Isolation and characterisation of 18 polymorphic microsatellite loci for black marlin (Istiompax) Tj ETQq1 1 0.7843	14.rgBT /0	Oyerlock 10
52	Characterisation and cross-amplification of 21 novel microsatellite loci for the dusky shark, Carcharhinus obscurus. Conservation Genetics Resources, 2015, 7, 909-912.	0.4	3
53	Characterisation and cross-amplification of 19 novel microsatellite loci for the sandbar shark, Carcharhinus plumbeus. Conservation Genetics Resources, 2015, 7, 913-915.	0.4	О
54	Parental contribution to progeny during experimental spawning of jungle perch, Kuhlia rupestris. Marine and Freshwater Research, 2015, 66, 375.	0.7	3

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#	Article	lF	Citations
55	Ocean's eleven: a critical evaluation of the role of population, evolutionary and molecular genetics in the management of wild fisheries. Fish and Fisheries, 2015, 16, 125-159.	2.7	141
56	Extensive genetic population structure in the Indo–West Pacific spot-tail shark, <i>Carcharhinus sorrah</i> . Bulletin of Marine Science, 2014, 90, 427-454.	0.4	23
57	<scp>NeEstimator</scp> v2: reâ€implementation of software for the estimation of contemporary effective population size (<i>N</i> _{<i>e</i>}) from genetic data. Molecular Ecology Resources, 2014, 14, 209-214.	2.2	1,584
58	Fine scale population structure of dugongs (Dugong dugon) implies low gene flow along the southern Queensland coastline. Conservation Genetics, 2014, 15, 1381-1392.	0.8	21
59	Genetic structure and diversity of two highly vulnerable carcharhinids in Australian waters. Endangered Species Research, 2014, 24, 45-60.	1.2	19
60	Hybridisation, paternal leakage and mitochondrial DNA linearization in three anomalous fish (Scombridae). Mitochondrion, 2013, 13, 852-861.	1.6	11
61	Accounting for missing data in the estimation of contemporary genetic effective population size (N _e). Molecular Ecology Resources, 2013, 13, 243-253.	2.2	62
62	Evolution of Diadromy in Fish: Insights from a Tropical Genus (<i>Kuhlia</i> Species). American Naturalist, 2013, 181, 52-63.	1.0	22
63	Crinkles in connectivity: combining genetics and other types of biological data to estimate movement and interbreeding between populations. Marine and Freshwater Research, 2013, 64, 201.	0.7	48
64	Stretched to the limit; can a short pelagic larval duration connect adult populations of an <scp>I</scp> ndoâ€ <scp>P</scp> acific diadromous fish (<i><scp>K</scp>uhlia rupestris</i>)?. Molecular Ecology, 2013, 22, 1518-1530.	2.0	19
65	The complete mitochondrial genome of the dusky shark <i>Carcharhinus obscurus</i> DNA, 2013, 24, 619-621.	0.6	13
66	New <scp>SNP</scp> s for population genetic analysis reveal possible cryptic speciation of eastern Australian sea mullet (<i>Mugil cephalus</i>). Molecular Ecology Resources, 2013, 13, 715-725.	2.2	35
67	Multi-gene barcoding to discriminate sibling species within a morphologically difficult fish genus (Sillago). Fisheries Research, 2013, 143, 39-46.	0.9	26
68	Linkage Disequilibrium Estimation of Effective Population Size with Immigrants from Divergent Populations: A Case Study on Spanish Mackerel (<i>Scomberomorus commerson</i>). G3: Genes, Genomes, Genetics, 2013, 3, 709-717.	0.8	14
69	Population Expansion and Genetic Structure in Carcharhinus brevipinna in the Southern Indo-Pacific. PLoS ONE, 2013, 8, e75169.	1.1	21
70	Contrasting Genetic Structure among Populations of Two Amphidromous Fish Species (Sicydiinae) in the Central West Pacific. PLoS ONE, 2013, 8, e75465.	1.1	26
71	Pelagic larval duration of two diadromous species of Kuhliidae (Teleostei: Percoidei) from Indo-Pacific insular systems. Marine and Freshwater Research, 2012, 63, 397.	0.7	11
72	Comparison of the reproductive ecology of two sympatric blacktip sharks (<i>Carcharhinus) Tj ETQq0 0 0 rgBT /</i>	Overlock :	10 Tf 50 67 Td 15

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inferred from vertebral counts. Journal of Fish Biology, 2012, 81, 1225-1233.

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73	Development and characterization of ten microsatellite loci for the reef manta ray Manta alfredi. Conservation Genetics Resources, 2012, 4, 1055-1058.	0.4	5
74	The genetic signature of recent speciation in manta rays (Manta alfredi and M. birostris). Molecular Phylogenetics and Evolution, 2012, 64, 212-218.	1.2	46
75	Accuracy of species identification by fisheries observers in a north Australian shark fishery. Fisheries Research, 2012, 127-128, 109-115.	0.9	58
76	Detection of interspecies hybridisation in Chondrichthyes: hybrids and hybrid offspring between Australian (Carcharhinus tilstoni) and common (C. limbatus) blacktip shark found in an Australian fishery. Conservation Genetics, 2012, 13, 455-463.	0.8	59
77	Evidence for reproductive philopatry in the bull shark <i>Carcharhinus leucas</i> . Journal of Fish Biology, 2012, 80, 2140-2158.	0.7	103
78	A review of the application of molecular genetics for fisheries management and conservation of sharks and rays. Journal of Fish Biology, 2012, 80, 1789-1843.	0.7	190
79	Telomere dynamics in the Sydney rock oyster (Saccostrea glomerata): an investigation into the effects of age, tissue type, location and time of sampling. Marine Biology, 2012, 159, 77-86.	0.7	9
80	Pleistocene isolation, secondary introgression and restricted contemporary gene flow in the pig-eye shark, Carcharhinus amboinensis across northern Australia. Conservation Genetics, 2012, 13, 99-115.	0.8	24
81	Population genetics of Australian white sharks reveals fine-scale spatial structure, transoceanic dispersal events and low effective population sizes. Marine Ecology - Progress Series, 2012, 455, 229-244.	0.9	100
82	A mitochondrial species identification assay for Australian blacktip sharks (<i>Carcharhinus) Tj ETQq0 0 0 rgBT / melt analysis. Molecular Ecology Resources, 2011, 11, 813-819.</i>	Overlock 1 2.2	0 Tf 50 387 ⁻ 19
83	Population structure, effective population size and adverse effects of stocking in the endangered Australian eastern freshwater cod Maccullochella ikei. Journal of Fish Biology, 2011, 78, 303-321.	0.7	27
84	Genetic population structure of grey mackerel Scomberomorus semifasciatus in northern Australia. Journal of Fish Biology, 2011, 79, 633-661.	0.7	25
85	Likelihood-based genetic mark–recapture estimates when genotype samples are incomplete and contain typing errors. Theoretical Population Biology, 2011, 80, 185-196.	0.5	21
86	Negligible evidence for regional genetic population structure for two shark species Rhizoprionodon acutus (Rüppell, 1837) and Sphyrna lewini (Griffith & Smith, 1834) with contrasting biology. Marine Biology, 2011, 158, 1497-1509.	0.7	33
87	Habitat segregation and mosaic sympatry of the two species of manta ray in the Indian and Pacific Oceans: Manta alfredi and M. birostris—CORRIGENDUM. Marine Biodiversity Records, 2011, 4, .	1.2	2
88	Telomere length analysis in crustacean species: Metapenaeus macleayi, Sagmariasus verreauxi, and Jasus edwardsii. ICES Journal of Marine Science, 2011, 68, 2053-2058.	1.2	10
89	Habitat segregation and mosaic sympatry of the two species of manta ray in the Indian and Pacific Oceans: Manta alfredi and M. birostris. Marine Biodiversity Records, 2011, 4, .	1.2	49
90	Towards better management of Australia's shark fishery: genetic analyses reveal unexpected ratios of cryptic blacktip species Carcharhinus tilstoni and C. limbatus. Marine and Freshwater Research, 2010, 61, 253.	0.7	43

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91	Population genetic evidence for the east–west division of the narrow-barred Spanish mackerel (Scomberomorus commerson, Perciformes: Teleostei) along Wallace's Line. Biodiversity and Conservation, 2010, 19, 563-574.	1.2	29
92	Stock structure of Grey Mackerel, Scomberomorus semifasciatus (Pisces: Scombridae) across northern Australia, based on otolith stable isotope chemistry. Environmental Biology of Fishes, 2010, 89, 357-367.	0.4	22
93	Evidence for extensive population structure in the whiteâ€spotted eagle ray within the Indoâ€Pacific inferred from mitochondrial gene sequences. Journal of Zoology, 2010, 281, 46-55.	0.8	29
94	The stock structure of grey mackerel Scomberomorus semifasciatus in Australia as inferred from its parasite fauna. Fisheries Research, 2010, 101, 94-99.	0.9	14
95	Characterization of highly informative crossâ€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.	2.2	18
96	Sexing Sirenians: Validation of Visual and Molecular Sex Determination in Both Wild Dugongs (<i>Dugong dugon</i>) and Florida Manatees (<i>Trichechus manatus) Tj ETQq0 0 0 rgBT /Overlo</i>	oc lo.14 0 Tf 5	01 5 37 Td (lat
97	The extent of population genetic subdivision differs among four co-distributed shark species in the Indo-Australian archipelago. BMC Evolutionary Biology, 2009, 9, 40.	3.2	100
98	IUCN classification zones concord with, but underestimate, the population genetic structure of the zebra shark <i>Stegostoma fasciatum</i> i> in the Indoâ€West Pacific. Molecular Ecology, 2009, 18, 248-261.	2.0	74
99	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.	2.7	21
100	Fifteen microsatellite loci for the jungle perch, <i>Kuhlia rupestris</i> . Molecular Ecology Resources, 2009, 9, 1467-1469.	2.2	6
101	Population genetic evidence for the east–west division of the narrow-barred Spanish mackerel (Scomberomorus commerson, Perciformes: Teleostei) along Wallace's Line. Topics in Biodiversity and Conservation, 2009, , 251-262.	0.3	0
102	A PCR assay for gender assignment in dugong (Dugong dugon) and West Indian manatee (Trichechus) Tj ETQq0	0 <u>9 rg</u> BT /0	Overlock 10 T
103	Evidence for a stock discontinuity of snapper (Pagrus auratus) on the east coast of Australia. Fisheries Research, 2008, 94, 92-98.	0.9	14
104	Effect of DNA extraction on ageing success in coral trout (Plectropomus leopardus) otoliths. Journal of Fish Biology, 2007, 71, 302-307.	0.7	5
105	Characterization of four tetranucleotide and six dinucleotide microsatellite markers for use in the tropical freshwater fishTelmatherina antoniaeand related species. Molecular Ecology Notes, 2007, 7, 651-653.	1.7	5
106	Characterization of 26 new microsatellite loci in the dugong (Dugong dugon). Molecular Ecology Notes, 2007, 7, 1275-1277.	1.7	18
107	Identification of small juvenile scombrids from northwest tropical Australia using mitochondrial DNA cytochrome b sequences. Ichthyological Research, 2007, 54, 246-252.	0.5	15
108	Genetic population structure of red snappers (Lutjanus malabaricus Bloch & Schneider, 1801 and) Tj ETQq0 0 0 r of Fish Biology, 2006, 68, 217-234.	gBT /Overlo 0.7	ock 10 Tf 50 22

of Fish Biology, 2006, 68, 217-234.

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109	New microsatellite loci for Carcharhinid sharks (Carcharhinus tilstoni and C. sorrah) and their cross-amplification in other shark species. Molecular Ecology Notes, 2006, 6, 415-418.	1.7	15
110	Polymorphic microsatellite loci for the zebra shark Stegostoma fasciatum. Molecular Ecology Notes, 2006, 6, 1086-1088.	1.7	11
111	The genetic effective and adult census size of an Australian population of tiger prawns (Penaeus) Tj ETQq $1\ 1\ 0.78$	34314 rgBT 2.0	 Overlock
112	Population genetic structure of the brown tiger prawn, Penaeus esculentus, in tropical northern Australia. Marine Biology, 2006, 148, 599-607.	0.7	13
113	locuseater and shadowboxer: programs to optimize experimental design and multiplexing strategies for genetic mark-recapture. Molecular Ecology Notes, 2005, 5, 974-976.	1.7	9
114	Pronounced genetic population structure in a potentially vagile fish species (Pristipomoides) Tj ETQq0 0 0 rgBT /0 13, 1991-1999.	Overlock 10 2.0) Tf 50 547 T 60
115	Genetic population structure of mangrove jack, Lutjanus argentimaculatus (ForsskåI). Marine and Freshwater Research, 2003, 54, 127.	0.7	26
116	Spatial genetic subdivision between northern Australian and southeast Asian populations of Pristipomoides multidens: a tropical marine reef fish species. Fisheries Research, 2002, 59, 57-69.	0.9	38
117	Title is missing!. Conservation Genetics, 2001, 2, 63-67.	0.8	21
118	Distribution of Jasus spp. (Decapoda:Palinuridae) phyllosomas in southern waters:implications for larval recruitment. Marine Ecology - Progress Series, 2000, 200, 241-255.	0.9	39
119	Mitochondrial DNA phylogeny of red and green rock lobsters (genus Jasus). Marine and Freshwater Research, 1997, 48, 1131.	0.7	46
120	Population-Genetic Structure of a Philopatric, Colonially Nesting Seabird, the Short-Tailed Shearwater (Puffinus tenuirostris). Auk, 1994, 111, 70-79.	0.7	43
121	Preliminary investigation of mitochondrial DNA variation in jack mackerel (Trachurus declivis,) Tj ETQq $1\ 1\ 0.7843$	14 rgBT /Ov	vgrlock 10 T
122	Evidence of stock separation in southern hemisphere organge roughy (Hoplostethus atlanticus,) Tj ETQq0 0 0 rgE 219-230.	3T /Overloc 0.7	k 10 Tf 50 2 46
123	Mitochondrial and allozyme genetics of two Tasmanian galaxiids (Galaxias auratus and G.) Tj ETQq1 1 0.784314 i	gBT/Overl	ock 10 Tf <mark>50</mark> 27
124	Mitochondrial DNA nucleotide sequence variation in Atlantic salmon (Salmo salar), brown trout (S.) Tj ETQq0 0 0 Australia. Aquaculture, 1993, 114, 217-227.	rgBT /Over 1.7	lock 10 Tf 50 22
125	A Program for the Estimation of Restriction Endonuclease Site Positions from Restriction Fragment Size and Number: An Aid for Mitochondrial DNA Analysis. Journal of Heredity, 1992, 83, 240-241.	1.0	6
126	Genetic subdivision of Australian and New Zealand populations of <i>Jasus verreauxi </i> Decapoda:	rgBT /Over	rlock 10 Tf 5 43

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127	Mitochondrial DNA variation and phylogenetic relationships of Jasusspp. (Decapoda: Palinuridae). Journal of Zoology, 1992, 227, 1-16.	0.8	40
128	Mitochondrial DNA analyses of the red rock lobsterJasus edwardsii supports an apparent absence of population subdivision throughout Australasia. Marine Biology, 1992, 112, 319-326.	0.7	102
129	Restriction Fragment Length Polymorphisms in Chloroplast DNA From Six Species of Eucalyptus. Australian Journal of Botany, 1991, 39, 399.	0.3	22
130	Mitochondrial DNA restriction site variation in Tasmanian populations of Orange Roughy (Hoplostethus atlanticus), a deep-water marine teleost. Marine and Freshwater Research, 1989, 40, 1.	0.7	31
131	Evolutionary relationships of Gadopsis spp. inferred from restriction enzyme analysis of their mitochondrial DNA. Journal of Fish Biology, 1988, 32, 137-148.	0.7	32
132	Mitochondrial DNA restriction site map for Gadopsis marmoratus. Biochemical Systematics and Ecology, 1988, 16, 355-357.	0.6	2
133	Venereal Transmission of Sindbis Virus Between Individuals of Aedes Australis (Diptera: Culicidae). Journal of Medical Entomology, 1984, 21, 292-295.	0.9	27