Paulino MartÃ-nez

List of Publications by Year in descending order

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ΡΑΙΙΙΙΝΟ ΜΑΦΤΔΑΙΕΖ

#	Article	IF	CITATIONS
1	Applications of genotyping by sequencing in aquaculture breeding and genetics. Reviews in Aquaculture, 2018, 10, 670-682.	9.0	217
2	Whole genome sequencing of turbot (<i>Scophthalmus maximus</i> ; Pleuronectiformes): a fish adapted to demersal life. DNA Research, 2016, 23, 181-192.	3.4	150
3	Genetic architecture of sex determination in fish: applications to sex ratio control in aquaculture. Frontiers in Genetics, 2014, 5, 340.	2.3	139
4	Identification of the Major Sex-Determining Region of Turbot (<i>Scophthalmus maximus</i>). Genetics, 2009, 183, 1443-1452.	2.9	109
5	Analysis of qPCR reference gene stability determination methods and a practical approach for efficiency calculation on a turbot (Scophthalmus maximus) gonad dataset. BMC Genomics, 2014, 15, 648.	2.8	105
6	A Microsatellite Genetic Map of the Turbot (<i>Scophthalmus maximus</i>). Genetics, 2007, 177, 2457-2467.	2.9	93
7	Detection of growth-related QTL in turbot (Scophthalmus maximus). BMC Genomics, 2011, 12, 473.	2.8	86
8	Growth and gonadal development in diploid and triploid turbot (Scophthalmus maximus). Aquaculture, 2006, 251, 99-108.	3.5	82
9	Phylogeographic Congruence Between mtDNA and rDNA ITS Markers in Brown Trout. Molecular Biology and Evolution, 2002, 19, 2161-2175.	8.9	80
10	Gene Expression Profiles of the Spleen, Liver, and Head Kidney in Turbot (Scophthalmus maximus) Along the Infection Process with Aeromonas salmonicida Using an Immune-Enriched Oligo-microarray. Marine Biotechnology, 2011, 13, 1099-1114.	2.4	79
11	QTL detection for Aeromonas salmonicida resistance related traits in turbot (Scophthalmus) Tj ETQq1 1 0.78431	.4 rgBT /Ov	verlgck 10 Tf
12	Yessotoxin induces ER-stress followed by autophagic cell death in glioma cells mediated by mTOR and BNIP3. Cellular Signalling, 2014, 26, 419-432.	3.6	72
13	Localization of the repetitive telomeric sequence (TTAGGG)n in four salmonid species. Genome, 1996, 39, 1035-1038.	2.0	71
14	Genetic structure of brown trout, Salmo trutta L., at the southern limit of the distribution range of the anadromous form. Molecular Ecology, 1999, 8, 1991-2001.	3.9	70
15	Differential stocking incidence in brown trout (Salmo trutta) populations from Northwestern Spain. Aquaculture, 1993, 114, 203-216.	3.5	69
16	Induction of triploidy in the turbot (Scophthalmus maximus). Aquaculture, 2000, 188, 79-90.	3.5	68
17	RNA-seq analysis reveals significant transcriptome changes in turbot (Scophthalmus maximus) suffering severe enteromyxosis. BMC Genomics, 2014, 15, 1149.	2.8	68
18	Cytogenetic characterization of six species of flatfishes with comments to karyotype differentiation patterns in Pleuronectiformes (Teleostei). Journal of Fish Biology, 2007, 70, 1-15.	1.6	65

#	Article	IF	CITATIONS
19	Potential sources of error in parentage assessment of turbot (Scophthalmus maximus) using microsatellite loci. Aquaculture, 2004, 242, 119-135.	3.5	63
20	An Expressed Sequence Tag (EST)-enriched genetic map of turbot (Scophthalmus maximus): a useful framework for comparative genomics across model and farmed teleosts. BMC Genetics, 2012, 13, 54.	2.7	62
21	Uncovering <scp>QTL</scp> for resistance and survival time to <i><scp>P</scp>hilasterides dicentrarchi</i> in turbot (<i><scp>S</scp>cophthalmus maximus</i>). Animal Genetics, 2013, 44, 149-157.	1.7	62
22	Phylogenetic analysis of flatfish (Order Pleuronectiformes) based on mitochondrial 16s rDNA sequences. Scientia Marina, 2005, 69, 531-543.	0.6	62
23	Expressed sequence tags (ESTs) from immune tissues of turbot (Scophthalmus maximus) challenged with pathogens. BMC Veterinary Research, 2008, 4, 37.	1.9	61
24	Allozyme and microsatellite diversity in natural and domestic populations of turbot (Scophthalmus) Tj ETQq0 0 0 Sciences, 2002, 59, 1460-1473.	rgBT /Ove 1.4	rlock 10 Tf 5 60
25	Centromere-linkage in the turbot (Scophthalmus maximus) through half-tetrad analysis in diploid meiogynogenetics. Aquaculture, 2008, 280, 81-88.	3.5	60
26	Karotypic characterization of turbot (Scophthalmus maximus) with conventional, fluorochrome and restriction endonuclease-banding techniques. Marine Biology, 1994, 120, 609-613.	1.5	59
27	Induction of gynogenesis in the turbot (Scophthalmus maximus):. Aquaculture, 2004, 238, 403-419.	3.5	59
28	The search for alternative aqueous film forming foams (AFFF) with a low environmental impact: Physiological and transcriptomic effects of two Forafac® fluorosurfactants in turbot. Aquatic Toxicology, 2011, 104, 168-176.	4.0	58
29	Cytogenetical characterization of hatchery stocks and natural populations of Sea and Brown Trout from northwestern Spain. Heredity, 1991, 66, 9-17.	2.6	57
30	Identification of Quantitative Trait Loci Associated with Resistance to Viral Haemorrhagic Septicaemia (VHS) in Turbot (Scophthalmus maximus): A Comparison Between Bacterium, Parasite and Virus Diseases. Marine Biotechnology, 2014, 16, 265-276.	2.4	54
31	Gene expression analysis at the onset of sex differentiation in turbot (Scophthalmus maximus). BMC Genomics, 2015, 16, 973.	2.8	54
32	Parallel evolution and adaptation to environmental factors in a marine flatfish: Implications for fisheries and aquaculture management of the turbot (<i>Scophthalmus maximus</i>). Evolutionary Applications, 2018, 11, 1322-1341.	3.1	54
33	Analysis of the structure and variability of nucleolar organizer regions of <i>Salmo trutta</i> by C-, Ag-, and restriction endonuclease banding. Cytogenetic and Genome Research, 1990, 54, 6-9.	1.1	52
34	Induction of triploidy in the turbot (Scophthalmus maximus) II. Effects of cold shock timing and induction of triploidy in a large volume of eggs. Aquaculture, 2003, 220, 821-831.	3.5	52
35	Heritability of skeleton abnormalities (lordosis, lack of operculum) in gilthead seabream (Sparus) Tj ETQq1 1 0.784	1314 rgBT 3.5	Overlock 51
36	Population analysis of an unusual NOR-site polymorphism in brown trout (Salmo trutta L.). Heredity, 2001, 86, 291-302.	2.6	50

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#	Article	IF	CITATIONS
37	RNA-seq analysis of early enteromyxosis in turbot (Scophthalmus maximus): new insights into parasite invasion and immune evasion strategies. International Journal for Parasitology, 2016, 46, 507-517.	3.1	50
38	Disentangling Genetic Variation for Resistance and Endurance to Scuticociliatosis in Turbot Using Pedigree and Genomic Information. Frontiers in Genetics, 2019, 10, 539.	2.3	49
39	Body pigmentation pattern to assess introgression by hatchery stocks in native Salmo trutta from Mediterranean streams. Journal of Fish Biology, 2005, 67, 931-949.	1.6	47
40	Comprehensive transcriptomic analysis of the process of gonadal sex differentiation in the turbot () Tj ETQq0 0	0 rgBT /Ov 3.2	verlock 10 Tf 5
41	Fine Mapping and Evolution of the Major Sex Determining Region in Turbot (<i>Scophthalmus) Tj ETQq1 1 0.78</i>	4314 rgB1 1.8	[/Oyerlock 10
42	A microsatellite marker tool for parentage analysis in Senegal sole (Solea senegalensis): Genotyping errors, null alleles and conformance to theoretical assumptions. Aquaculture, 2006, 261, 1194-1203.	3.5	45
43	Variation in anonymous and EST-microsatellites suggests adaptive population divergence in turbot. Marine Ecology - Progress Series, 2010, 420, 231-239.	1.9	45
44	Integrative Transcriptome, Genome and Quantitative Trait Loci Resources Identify Single Nucleotide Polymorphisms in Candidate Genes for Growth Traits in Turbot. International Journal of Molecular Sciences, 2016, 17, 243.	4.1	45
45	A combined strategy involving Sanger and 454 pyrosequencing increases genomic resources to aid in the management of reproduction, disease control and genetic selection in the turbot (Scophthalmus) Tj ETQq1	1 02788431	l4 rg&T /Overl
46	Highly dense linkage maps from 31 full-sibling families of turbot (Scophthalmus maximus) provide insights into recombination patterns and chromosome rearrangements throughout a newly refined genome assembly. DNA Research, 2018, 25, 439-450.	3.4	44
47	Regional environmental pressure influences population differentiation in turbot (<i><scp>S</scp>cophthalmus maximus</i>). Molecular Ecology, 2014, 23, 618-636.	3.9	43
48	Mapping of DNA Sex-Specific Markers and Genes Related to Sex Differentiation in Turbot (Scophthalmus maximus). Marine Biotechnology, 2012, 14, 655-663.	2.4	42
49	Gene diversity analysis in natural populations and cultured stocks of turbot (Scophthalmus maximus) Tj ETQq1	1 0,7843 1.7	14 rgBT /Over 41
50	Phylogenetic analysis of the order Pleuronectiformes (Teleostei) based on sequences of 12S and 16S mitochondrial genes. Genetics and Molecular Biology, 2008, 31, 284-292.	1.3	41
51	A genome scan for candidate genes involved in the adaptation of turbot (Scophthalmus maximus). Marine Genomics, 2015, 23, 77-86.	1.1	41
52	Characterization of an atypical NOR site polymorphism in brown trout (Salmo trutta) with Ag- and CMA ₃ -staining, and fluorescent in situ hybridization. Cytogenetic and Genome Research, 1996, 75, 234-239.	1.1	40
53	A sex-associated sequence identified by RAPD screening in gynogenetic individuals of turbot (Scophthalmus maximus). Molecular Biology Reports, 2014, 41, 1501-1509.	2.3	40
54	Validation of single nucleotide polymorphism (SNP) markers from an immune Expressed Sequence Tag (EST) turbot, Scophthalmus maximus, database. Aquaculture, 2011, 313, 31-41.	3.5	39

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55	Permanent Genetic Resources added to Molecular Ecology Resources Database 1 December 2010–31 January 2011. Molecular Ecology Resources, 2011, 11, 586-589.	4.8	38
56	Low stocking incidence in brown trout populations from northwestern Spain monitored by LDH-5* diagnostic marker. Journal of Fish Biology, 1995, 47, 170-176.	1.6	37
57	Design and Performance of a Turbot (Scophthalmus maximus) Oligo-microarray Based on ESTs from Immune Tissues. Marine Biotechnology, 2010, 12, 452-465.	2.4	37
58	Compilation of mapping resources in turbot (Scophthalmus maximus): A new integrated consensus genetic map. Aquaculture, 2013, 414-415, 19-25.	3.5	37
59	>Localization of ribosomal genes in Pleuronectiformes using Ag-, CMA3-banding and in situ hybridization. Heredity, 2001, 86, 531-536.	2.6	36
60	Permanent Genetic Resources added to Molecular Ecology Resources Database 1 December 2012–31 January 2013. Molecular Ecology Resources, 2013, 13, 546-549.	4.8	36
61	A microsatellite marker tool for parentage assessment in gilthead seabream (Sparus aurata). Aquaculture, 2007, 272, S210-S216.	3.5	35
62	Signatures of selection for bonamiosis resistance in European flat oyster (Ostrea edulis): New genomic tools for breeding programs and management of natural resources. Evolutionary Applications, 2019, 12, 1781-1796.	3.1	35
63	Genetic Identification of F1 and Post-F1 Serrasalmid Juvenile Hybrids in Brazilian Aquaculture. PLoS ONE, 2014, 9, e89902.	2.5	34
64	Characterization of ESTâ€derived microsatellites for gene mapping and evolutionary genomics in turbot. Animal Genetics, 2008, 39, 666-670.	1.7	33
65	Development and Validation of Single Nucleotide Polymorphisms (SNPs) Markers from Two Transcriptome 454-Runs of Turbot (Scophthalmus maximus) Using High-Throughput Genotyping. International Journal of Molecular Sciences, 2013, 14, 5694-5711.	4.1	33
66	Quantitative analysis of the variability of nucleolar organizer regions in Salmo trutta. Genome, 1993, 36, 1119-1123.	2.0	32
67	Threatened freshwater pearl mussel Margaritifera margaritifera L. in NW Spain: low and very structured genetic variation in southern peripheral populations assessed using microsatellite markers. Conservation Genetics, 2007, 8, 937-948.	1.5	32
68	Gynogenesis Assessment Using Microsatellite Genetic Markers in Turbot (Scophthalmus maximus). Marine Biotechnology, 2003, 5, 584-592.	2.4	31
69	Current genetic status, temporal stability and structure of the remnant wild European flat oyster populations: conservation and restoring implications. Marine Biology, 2016, 163, 1.	1.5	30
70	A genome-wide association study, supported by a new chromosome-level genome assembly, suggests sox2 as a main driver of the undifferentiatiated ZZ/ZW sex determination of turbot (Scophthalmus) Tj ETQq0 0 () rgB¶ /Ov	erl ac k 10 Tf 5
71	Allozymic evidence of parapatric differentiation of brown trout (Salmo trutta L.) within an Atlantic river basin of the Iberian Peninsula. Molecular Ecology, 2001, 10, 1455-1469.	3.9	29

Gene Expression Profiles of Spleen, Liver, and Head Kidney in Turbot (Scophthalmus maximus) Along72the Infection Process with Philasterides dicentrarchi Using an Immune-Enriched Oligo-Microarray.2.429Marine Biotechnology, 2012, 14, 570-582.2.429

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73	Tracing the genetic impact of farmed turbot Scophthalmus maximus on wild populations. Aquaculture Environment Interactions, 2018, 10, 447-463.	1.8	29
74	Very low microsatellite polymorphism and large heterozygote deficits suggest founder effects and cryptic structure in the parasite Perkinsus olseni. Infection, Genetics and Evolution, 2011, 11, 904-911.	2.3	28
75	Turbot (Scophthalmus maximus) genomic resources: application for boosting aquaculture production. , 2016, , 131-163.		26
76	Sex-dependent synaptic behaviour in triploid turbot, Scophthalmus maximus (Pisces, Scophthalmidae). Heredity, 2002, 89, 460-464.	2.6	25
77	Localization of rDNA genes in European eel (Anguilla anguilla) by FISH. Genome, 1996, 39, 1220-1223.	2.0	24
78	A population analysis of the structure and variability of NOR in Salmo trutta by Ag, CMA3 and ISH. Genetica, 2000, 108, 113-118.	1.1	24
79	Ribosomal genes in Coregonid fishes (Coregonus lavaretus, C. albula and C. peled) (Salmonidae): single and multiple nucleolus organizer regions. Heredity, 2001, 87, 672-679.	2.6	24
80	Development and characterization of 248 novel microsatellite markers in turbot (Scophthalmus) Tj ETQq0 0 0	rgBT_/Overl 2.0	lock 10 Tf 50 4
81	Mitochondrial haplotype variability of brown trout populations from Northwestern Iberian Peninsula, a secondary contact area between lineages. Conservation Genetics, 2008, 9, 917-920.	1.5	24
82	Synaptonemal complex analysis in spermatocytes and oocytes of turbot, <i>Scophthalmus maximus</i> (Pisces, Scophthalmidae). Genome, 2001, 44, 1143-1147.	2.0	23
83	Growth and gonadal development of gynogenetic diploid Scophthalmus maximus. Journal of Fish Biology, 2006, 68, 401-413.	1.6	23
84	Diversity in isochore structure among cold-blooded vertebrates based on GC content of coding and non-coding sequences. Genetica, 2007, 129, 281-289.	1.1	23
85	Phylogeography, genetic structure, and conservation of the endangered Caspian brown trout, Salmo trutta caspius (Kessler, 1877), from Iran. Hydrobiologia, 2011, 664, 51-67.	2.0	23
86	Consolidation of the genetic and cytogenetic maps of turbot (Scophthalmus maximus) using FISH with BAC clones. Chromosoma, 2014, 123, 281-291.	2.2	23
87	Differential gene expression and SNP association between fast- and slow-growing turbot (Scophthalmus maximus). Scientific Reports, 2017, 7, 12105.	3.3	23
88	Identification and validation of single nucleotide polymorphisms as tools to detect hybridization and population structure in freshwater stingrays. Molecular Ecology Resources, 2017, 17, 550-556.	4.8	23
89	Hybridization and genetic introgression patterns between two South American catfish along their sympatric distribution range. Hydrobiologia, 2017, 788, 319-343.	2.0	23
90	Integrating Genomic and Morphological Approaches in Fish Pathology Research: The Case of Turbot (Scophthalmus maximus) Enteromyxosis. Frontiers in Genetics, 2019, 10, 26.	2.3	23

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91	Estimates of recent and historical effective population size in turbot, seabream, seabass and carp selective breeding programmes. Genetics Selection Evolution, 2021, 53, 85.	3.0	23
92	A set of highly polymorphic microsatellites useful for kinship and population analysis in turbot (Scophthalmus maximus L.). Aquaculture Research, 2006, 37, 1578-1582.	1.8	22
93	Chromosomal heterochromatin differentiation in Salmo trutta with restriction enzymes. Heredity, 1991, 66, 241-249.	2.6	21
94	Integrating genomic resources of flatfish (Pleuronectiformes) to boost aquaculture production. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2017, 21, 41-55.	1.0	21
95	Estimation of genetic parameters for growth traits in a hatchery population of gilthead sea bream (Sparus aurata L.). Aquaculture International, 2017, 25, 499-514.	2.2	21
96	Performance and precision of double digestion RAD (ddRAD) genotyping in large multiplexed datasets of marine fish species. Marine Genomics, 2018, 39, 64-72.	1.1	21
97	Validation of growth-related quantitative trait loci markers in turbot (Scophthalmus maximus) families as a step toward marker assisted selection. Aquaculture, 2018, 495, 602-610.	3.5	21
98	Comparative expression analysis in mature gonads, liver and brain of turbot (Scophthalmus maximus) by cDNA-AFLPS. Gene, 2012, 492, 250-261.	2.2	20
99	Ecological Factors and Diversification among Neotropical Characiforms. International Journal of Ecology, 2012, 2012, 1-20.	0.8	20
100	Evolution of egg production and parental contribution in Senegalese sole, Solea senegalensis, during four consecutive spawning seasons. Aquaculture, 2014, 424-425, 45-52.	3.5	20
101	Oral immunostimulation of the oyster Ostrea edulis: Impacts on the parasite Bonamia ostreae. Fish and Shellfish Immunology, 2015, 45, 43-51.	3.6	20
102	Construction of an Ostrea edulis database from genomic and expressed sequence tags (ESTs) obtained from Bonamia ostreae infected haemocytes: Development of an immune-enriched oligo-microarray. Fish and Shellfish Immunology, 2016, 59, 331-344.	3.6	20
103	SNP discovery from liver transcriptome in the fish Piaractus mesopotamicus. Conservation Genetics Resources, 2016, 8, 109-114.	0.8	20
104	Long-term affected flat oyster (Ostrea edulis) haemocytes show differential gene expression profiles from naÃ ⁻ ve oysters in response to Bonamia ostreae. Genomics, 2018, 110, 390-398.	2.9	20
105	A population analysis of Robertsonian and Ag-NOR polymorphisms in brown trout (Salmo trutta). Theoretical and Applied Genetics, 1994, 89, 105-111.	3.6	19
106	A NOR-associated repetitive element present in the genome of two <i>Salmo</i> species (<i>salmo) Tj ETQq0 0</i>	0 rgBT /Ov	verlock 10 Tf
107	Analysis of a secondary contact between divergent lineages of brown trout Salmo trutta L. from Duero basin using microsatellites and mtDNA RFLPs. Journal of Fish Biology, 2007, 71, 195-213.	1.6	19

108 Identification and conservation of remnant genetic resources of brown trout in relict populations from Western Mediterranean streams. Hydrobiologia, 2013, 707, 29-45.

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109	Assessing Genetic Diversity for a Pre-Breeding Program in Piaractus mesopotamicus by SNPs and SSRs. Genes, 2019, 10, 668.	2.4	19
110	Induction of G-bands on <i>Anguilla anguilla</i> chromosomes by the restriction endonucleases Haelll, <i>Hinf</i> I, and <i>Mse</i> I. Cytogenetic and Genome Research, 1994, 65, 79-81.	1.1	18
111	Promiscuous Speciation with Gene Flow in Silverside Fish Genus Odontesthes (Atheriniformes,) Tj ETQq1 1 0.784	314 rgBT 2.5	/Overlock 10
112	First characterization and validation of turbot microRNAs. Aquaculture, 2017, 472, 76-83.	3.5	18
113	Molecular analysis of a NOR site polymorphism in brown trout (<i>Salmo trutta</i>): organization of rDNA intergenic spacers. Genome, 1997, 40, 916-922.	2.0	17
114	Development and validation of a molecular tool for assessing triploidy in turbot (Scophthalmus) Tj ETQq0 0 0 rgE	BT JOverlo	ck 10 Tf 50 5 17
115	First Haploid Genetic Map Based on Microsatellite Markers in Senegalese Sole (Solea senegalensis,) Tj ETQq1 1 0	.784314 ı 2.4	gBT /Overloc
116	Chromosomal characteristics of rDNA in European grayling Thymallus thymallus (Salmonidae). Genetica, 2003, 119, 219-224.	1.1	16
117	Genomic Organization, Molecular Diversification, and Evolution of Antimicrobial Peptide Myticin-C Genes in the Mussel (Mytilus galloprovincialis). PLoS ONE, 2011, 6, e24041.	2.5	16
118	First identification of interspecies hybridization in the freshwater stingrays Potamotrygon motoro and P. falkneri (Myliobatiformes, Potamotrygonidae). Conservation Genetics, 2015, 16, 241-245.	1.5	16
119	Genomics advances for boosting aquaculture breeding programs in Spain. Aquaculture, 2017, 472, 4-7.	3.5	16
120	New microsatellite markers in turbot (Scophthalmus maximus) derived from an enriched genomic library and sequence databases. Molecular Ecology Notes, 2005, 5, 62-64.	1.7	15
121	Characterization of single-nucleotide polymorphism markers in the Mediterranean mussel, <i>Mytilus galloprovincialis</i> . Aquaculture Research, 2010, 41, e568-e575.	1.8	15
122	Exploitation of a turbot (<i>Scophthalmus maximus</i> L.) immuneâ€related expressed sequence tag (EST) database for microsatellite screening and validation. Molecular Ecology Resources, 2012, 12, 706-716.	4.8	15
123	Transcriptomic profile of Manila clam (Ruditapes philippinarum) haemocytes in response to Perkinsus olseni infection. Aquaculture, 2017, 467, 170-181.	3.5	15
124	Stocking impact, population structure and conservation of wild brown trout populations in inner Galicia (NW Spain), an unstable hydrologic region. Aquatic Conservation: Marine and Freshwater Ecosystems, 2018, 28, 435-443.	2.0	15
125	Evolution and conservation of Characidium sex chromosomes. Heredity, 2017, 119, 237-244.	2.6	15
126	Characterization of a New Hpal Centromeric Satellite DNA in Salmo salar. Genetica, 2004, 121, 81-87.	1.1	14

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127	Accuracy of pairwise methods in the reconstruction of family relationships, using molecular information from turbot (Scophthalmus maximus). Aquaculture, 2007, 273, 434-442.	3.5	14
128	Novel microsatellite loci in the threatened European long-snouted seahorse (Hippocampus) Tj ETQq0 0 0 rgBT /O	verlock 10	T_{14}^{f} 50 702 To
129	De novo transcriptome assembly of Perkinsus olseni trophozoite stimulated in vitro with Manila clam (Ruditapes philippinarum) plasma. Journal of Invertebrate Pathology, 2016, 135, 22-33.	3.2	14
130	Morphological variation in a secondary contact between divergent lineages of brown trout (Salmo) Tj ETQq0 0 0	rgBT /Ove 1.3	rlock 10 Tf 5
131	Species identification and genetic structure of threatened seahorses in Gran Canaria Island (Spain) using mitochondrial and microsatellite markers. Conservation Genetics, 2010, 11, 2431-2436.	1.5	13
132	Microarray analysis of the inflammatory and immune responses in head kidney turbot leucocytes treated with resveratrol. International Immunopharmacology, 2013, 15, 588-596.	3.8	13
133	First genetic linkage map for comparative mapping and QTL screening of brill (Scophthalmus) Tj ETQq1 1 0.7843	14 rgBT /0 3.9	Overlock 10 T
134	Heritability estimation for okadaic acid algal toxin accumulation, mantle color and growth traits in Mediterranean mussel (Mytilus galloprovincialis). Aquaculture, 2015, 440, 32-39.	3.5	13
135	Isolation and characterization of 20 polymorphic microsatellite loci in the migratory freshwater fish <i>Leporinus obtusidens</i> (Characiformes: Anostomidae) using 454 shotgun pyrosequencing. Journal of Fish Biology, 2015, 86, 1209-1217.	1.6	13
136	A molecular tool for parentage analysis in the Mediterranean mussel (<i>Mytilus) Tj ETQq0 0 0 rgBT /Overlock 10</i>	Tf 50 382 1.8	Td (gallopro
137	Genetic structure and evidence of anthropogenic effects on wild populations of two Neotropical catfishes: baselines for conservation. Journal of Fish Biology, 2018, 92, 55-72.	1.6	13
138	Genomic survey of edible cockle (<i>Cerastoderma edule</i>) in the Northeast Atlantic: A baseline for sustainable management of its wild resources. Evolutionary Applications, 2022, 15, 262-285.	3.1	13
139	Brief communication. Analysis of the inheritance of NOR size variants in brown trout (Salmo trutta). Journal of Heredity, 1998, 89, 264-266.	2.4	12
140	Localization of 5S rRNA loci in three coregonid species (Salmonidae). Genetica, 2003, 119, 183-186.	1.1	12
141	Screening of repetitive motifs inside the genome of the flat oyster (Ostrea edulis): Transposable elements and short tandem repeats. Marine Genomics, 2015, 24, 335-341.	1.1	12
142	SNP identification and validation on genomic DNA for studying genetic diversity in Thunnus albacares and Scomberomorus brasiliensis by combining RADseq and long read high throughput sequencing. Fisheries Research, 2018, 198, 189-194.	1.7	12
143	Genetic Characterization of the Fish Piaractus brachypomus by Microsatellites Derived from Transcriptome Sequencing. Frontiers in Genetics, 2018, 9, 46.	2.3	12

Genomic Signatures After Five Generations of Intensive Selective Breeding: Runs of Homozygosity and Genetic Diversity in Representative Domestic and Wild Populations of Turbot (Scophthalmus) Tj ETQq0 0 0 rgBT / Overlock 10 If 50 57 T

#	Article	IF	CITATIONS
145	Analysis of centromere size in human chromosomes 1, 9, 15, and 16 by electron microscopy. Genome, 1991, 34, 710-713.	2.0	11
146	Development and characterization of 16 microsatellites for the Neotropical catfish Pseudoplatystoma reticulatum and cross species analysis. Conservation Genetics Resources, 2014, 6, 679-681.	0.8	11
147	Management units of brown trout from Galicia (NW: Spain) based on spatial genetic structure analysis. Conservation Genetics, 2010, 11, 897-906.	1.5	10
148	Insights into Mussel Microbiome. , 2019, , 95-120.		10
149	The Teleost Thymus in Health and Disease: New Insights from Transcriptomic and Histopathological Analyses of Turbot, Scophthalmus maximus. Biology, 2020, 9, 221.	2.8	10
150	Evaluating different genomic coancestry matrices for managing genetic variability in turbot. Aquaculture, 2020, 520, 734985.	3.5	10
151	Analysis of the vomeronasal organ transcriptome reveals variable gene expression depending on age and function in rabbits. Genomics, 2021, 113, 2240-2252.	2.9	10
152	Restriction endonuclease/nick translation procedure on fixed chromosomes of the Atlantic salmon fish cell line. Chromosome Research, 1995, 3, 379-385.	2.2	9
153	Chromosome Banding and 18S rDNA in situ Hybridization Analysis of Seven Species of the Family Achiridae (Teleostei: Pleuronectiformes). Genetica, 2005, 125, 125-132.	1.1	9
154	Phylogenetic diversity within the endemic brown trout Duero lineage: implications for conservation and management. Marine and Freshwater Research, 2015, 66, 1066.	1.3	9
155	Reproductive performance of captive Senegalese sole, Solea senegalensis, according to the origin (wild or cultured) and gender. Spanish Journal of Agricultural Research, 2020, 17, e0608.	0.6	9
156	rRNA genes map to chromosomes 10, 11 and 12 in European whitefish (Coregonus lavaretus) and to chromosomes 1, 5, 9 and 10 in vendace (Coregonus albula). Chromosome Research, 2000, 8, 455-455.	2.2	8
157	High Ag-NOR-site variation associated to a secondary contact in brown trout from the Iberian Peninsula. Genetica, 2009, 136, 419-427.	1.1	8
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