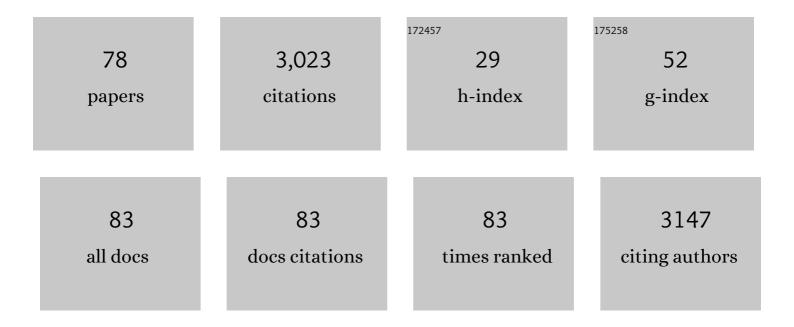
List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Inferring ancestral origin using a single multiplex assay of ancestry-informative marker SNPs. Forensic Science International: Genetics, 2007, 1, 273-280.	3.1	332
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	Development of a methylation marker set for forensic age estimation using analysis of public methylation data and the Agena Bioscience EpiTYPER system. Forensic Science International: Genetics, 2016, 24, 65-74.	3.1	127
4	Further development of forensic eye color predictive tests. Forensic Science International: Genetics, 2013, 7, 28-40.	3.1	119
5	Ancestry Analysis in the 11-M Madrid Bomb Attack Investigation. PLoS ONE, 2009, 4, e6583.	2.5	110
6	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
7	Analysis of global variability in 15 established and 5 new European Standard Set (ESS) STRs using the CEPH human genome diversity panel. Forensic Science International: Genetics, 2011, 5, 155-169.	3.1	103
8	A Microsatellite Genetic Map of the Turbot (<i>Scophthalmus maximus</i>). Genetics, 2007, 177, 2457-2467.	2.9	93
9	Detection of growth-related QTL in turbot (Scophthalmus maximus). BMC Genomics, 2011, 12, 473.	2.8	86
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 0.7843	14 rgBT /C)verjock 10 Tf
12	Molecular Characterization of Circulating Tumor Cells in Human Metastatic Colorectal Cancer. PLoS ONE, 2012, 7, e40476.	2.5	77
13	Development of a forensic skin colour predictive test. Forensic Science International: Genetics, 2014, 13, 34-44.	3.1	69
14	RNA-seq analysis reveals significant transcriptome changes in turbot (Scophthalmus maximus) suffering severe enteromyxosis. BMC Genomics, 2014, 15, 1149.	2.8	68
15	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
16	Expressed sequence tags (ESTs) from immune tissues of turbot (Scophthalmus maximus) challenged with pathogens. BMC Veterinary Research, 2008, 4, 37.	1.9	61
17	Centromere-linkage in the turbot (Scophthalmus maximus) through half-tetrad analysis in diploid meiogynogenetics. Aquaculture, 2008, 280, 81-88.	3.5	60
18	A multimarker panel for circulating tumor cells detection predicts patient outcome and therapy response in metastatic colorectal cancer. International Journal of Cancer, 2014, 135, 2633-2643.	5.1	55

#	Article	IF	CITATIONS
19	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
20	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
21	Targeted Proteomics Identifies Proteomic Signatures in Liquid Biopsies of the Endometrium to Diagnose Endometrial Cancer and Assist in the Prediction of the Optimal Surgical Treatment. Clinical Cancer Research, 2017, 23, 6458-6467.	7.0	50
22	Comprehensive transcriptomic analysis of the process of gonadal sex differentiation in the turbot () Tj ETQq0 0	0 rgBT /Ov	verlock 10 Tf 5 47
23	Fine Mapping and Evolution of the Major Sex Determining Region in Turbot (<i>Scophthalmus) Tj ETQq1 1 0.78</i>	4314 rgBT 1.8	Oyerlock 10
24	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 ETQqO	0 02:gBT /(Ovenkalock 10 T
25	Tracking age-correlated DNA methylation markers in the young. Forensic Science International: Genetics, 2018, 36, 50-59.	3.1	41
26	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
27	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
28	Automated Extraction Improves Multiplex Molecular Detection of Infection in Septic Patients. PLoS ONE, 2010, 5, e13387.	2.5	35
29	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
30	Exploring iris colour prediction and ancestry inference in admixed populations of South America. Forensic Science International: Genetics, 2014, 13, 3-9.	3.1	32
31	Exploration of SNP variants affecting hair colour prediction in Europeans. International Journal of Legal Medicine, 2015, 129, 963-975.	2.2	31
32	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 (0 rg₿∮ /Ov	erl ac k 10 Tf 5
33	Gene Expression Profiles of Spleen, Liver, and Head Kidney in Turbot (Scophthalmus maximus) Along the Infection Process with Philasterides dicentrarchi Using an Immune-Enriched Oligo-Microarray. Marine Biotechnology, 2012, 14, 570-582.	2.4	29
34	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
35	Inference of Ancestry in Forensic Analysis II: Analysis of Genetic Data. Methods in Molecular Biology, 2016, 1420, 255-285.	0.9	27
36	Turbot (Scophthalmus maximus) genomic resources: application for boosting aquaculture		26

production. , 2016, , 131-163.

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37	A Comparison of Forensic Age Prediction Models Using Data From Four DNA Methylation Technologies. Frontiers in Genetics, 2020, 11, 932.	2.3	26
38	Consolidation of the genetic and cytogenetic maps of turbot (Scophthalmus maximus) using FISH with BAC clones. Chromosoma, 2014, 123, 281-291.	2.2	23
39	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
40	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
41	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
42	Molecular Profiling of Circulating Tumour Cells Identifies Notch1 as a Principal Regulator in Advanced Non-Small Cell Lung Cancer. Scientific Reports, 2016, 6, 37820.	3.3	22
43	Improving circulating tumor cells enumeration and characterization to predict outcome in first line chemotherapy mCRPC patients. Oncotarget, 2017, 8, 54708-54721.	1.8	22
44	A logistic model for the detection of circulating tumour cells in human metastatic colorectal cancer. Journal of Cellular and Molecular Medicine, 2012, 16, 2342-2349.	3.6	21
45	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
46	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
47	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
48	Rational homotopy theory for non-simply connected spaces. Transactions of the American Mathematical Society, 1999, 352, 1493-1525.	0.9	18
49	Broadening the Applicability of a Custom Multi-Platform Panel of Microhaplotypes: Bio-Geographical Ancestry Inference and Expanded Reference Data. Frontiers in Genetics, 2020, 11, 581041.	2.3	17
50	Characterization of single-nucleotide polymorphism markers in the Mediterranean mussel, <i>Mytilus galloprovincialis</i> . Aquaculture Research, 2010, 41, e568-e575.	1.8	15
51	Transcriptomic profile of Manila clam (Ruditapes philippinarum) haemocytes in response to Perkinsus olseni infection. Aquaculture, 2017, 467, 170-181.	3.5	15
52	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
53	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
54	Immunohistochemical detection and gene expression of TNFα in turbot (Scophthalmus maximus) enteromyxosis. Fish and Shellfish Immunology, 2015, 47, 368-376.	3.6	13

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55	The Lusternik-Schnirelmann category of \$operatorname {Sp}(3)\$. Proceedings of the American Mathematical Society, 2003, 132, 587-595.	0.8	12
56	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
57	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
58	Hepatitis B virus genotyping based on cluster analysis of the region involved in lamivudine resistance. Journal of Virological Methods, 2004, 115, 9-17.	2.1	10
59	An assessment of Bayesian and multinomial logistic regression classification systems to analyse admixed individuals. Forensic Science International: Genetics Supplement Series, 2013, 4, e63-e64.	0.3	10
60	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
61	Implication of p38 mitogen-activated protein kinase isoforms (α, β, γ and Î) in CD4+ T-cell infection with human immunodeficiency virus type I. Journal of General Virology, 2008, 89, 1661-1671.	2.9	9
62	Trace map, Cayley transform and LS category of Lie groups. Annals of Global Analysis and Geometry, 2011, 39, 325-335.	0.6	9
63	Vaccine-induced modulation of gene expression in turbot peritoneal cells. A microarray approach. Molecular Immunology, 2016, 75, 188-199.	2.2	8
64	A multidisciplinary approach to identify priority areas for the monitoring of a vulnerable family of fishes in Spanish Marine National Parks. Bmc Ecology and Evolution, 2021, 21, 4.	1.6	8
65	Hepatic gene transcription profiles in turbot (Scophthalmus maximus) experimentally exposed to heavy fuel oil nº 6 and to styrene. Marine Environmental Research, 2017, 123, 14-24.	2.5	7
66	Global Gene Expression Characterization of Circulating Tumor Cells in Metastasic Castration-Resistant Prostate Cancer Patients. Journal of Clinical Medicine, 2020, 9, 2066.	2.4	7
67	Blood Transcriptomics of Turbot Scophthalmus maximus: A Tool for Health Monitoring and Disease Studies. Animals, 2021, 11, 1296.	2.3	7
68	Hopf–Ganea invariants and weak LS category. Topology and Its Applications, 2001, 115, 305-316.	0.4	5
69	Microsatellite marker development in the protozoan parasite Perkinsus olseni. Diseases of Aquatic Organisms, 2011, 94, 161-165.	1.0	5
70	Gene expression analysis of Ruditapes philippinarum haemocytes after experimental Perkinsus olseni zoospore challenge and infection in the wild. Fish and Shellfish Immunology, 2018, 72, 611-621.	3.6	5
71	Species identification of two closely exploited flatfish, turbot (<scp><i>Scophthalmus) Tj ETQq1 1 0.784314 rgBT approach. Aquatic Conservation: Marine and Freshwater Ecosystems, 2018, 28, 1253-1260.</i></scp>	- /Overlock 2.0	10 Tf 50 10 4
72	Theorie De Sullivan Pour La Cohomologie a Coefficients Locaux. Transactions of the American Mathematical Society, 1992, 330, 295.	0.9	3

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73	New insights into the Manila clam – Perkinsus olseni interaction based on gene expression analysis of clam hemocytes and parasite trophozoites through in vitro challenges. International Journal for Parasitology, 2020, 50, 195-208.	3.1	3
74	Identification of Bacillus and Yersinia species and hoax agents by protein profiling using microfluidic capillary electrophoresis with peak detection algorithms. Australian Journal of Forensic Sciences, 2021, 53, 2-15.	1.2	2
75	Théorie de Sullivan pour la cohomologie à coefficients locaux. Transactions of the American Mathematical Society, 1992, 330, 235-305.	0.9	2
76	Homologie de L'Espace des Lacets des Intersections Completes. American Journal of Mathematics, 1995, 117, 635.	1.1	0
77	A compact population analysis test using 32 SNPs with highly diverse allele frequency distributions. International Congress Series, 2006, 1288, 58-60.	0.2	0
78	Molecular characterization of circulating tumor cells in human metastatic colorectal cancer Journal of Clinical Oncology, 2012, 30, 10534-10534.	1.6	0