José M Yáñez

List of Publications by Year
in descending order

86 papers	**3,410** citations	147726 **31** h-index	175177 **52** g-index
112 all docs	**112** docs citations	**112** times ranked	**1796** citing authors

#	Article	IF	Citations
1	Increased accuracy of genomic predictions for growth under chronic thermal stress in rainbow trout by prioritizing variants from GWAS using imputed sequence data. Evolutionary Applications, 2022, 15, 537-552.	1.5	33
2	Microbiota composition and susceptibility to florfenicol and oxytetracycline of bacterial isolates from mussels (Mytilus spp.) reared on different years and distance from salmon farms. Environmental Research, 2022, 204, 112068.	3.7	8
3	Infectious pancreatic necrosis virus in salmonids: Molecular epidemiology and host response to infection. Reviews in Aquaculture, 2022, 14, 751-769.	4.6	9
4	Genotype-by-environment interaction for growth in seawater and freshwater in Atlantic salmon (Salmo salar). Aquaculture, 2022, 548, 737674.	1.7	2
5	Accuracy of genotype imputation to whole genome sequencing level using different populations of Nile tilapia. Aquaculture, 2022, 551, 737947.	1.7	6
6	The impact of genetic relationship between training and validation populations on genomic prediction accuracy in Atlantic salmon. Aquaculture Reports, 2022, 23, 101033.	0.7	12
7	Genomics applied to livestock and aquaculture breeding. Evolutionary Applications, 2022, 15, 517-522.	1.5	11
8	Differential Transcriptomic Response of Rainbow Trout to Infection with Two Strains of IPNV. Viruses, 2022, 14, 21.	1.5	7
9	Linkage map for chromosome-level genome anchoring and genome-wide association study for resistance to Aeromonas hydrophila in Colossoma macropomum. Aquaculture, 2022, 560, 738462.	1.7	5
10	Genetics of growth and survival under chronic heat stress and trade-offs with growth- and robustness-related traits in rainbow trout. Aquaculture, 2021, 531, 735685.	1.7	17
11	Investigating mechanisms underlying genetic resistance to Salmon Rickettsial Syndrome in Atlantic salmon using RNA sequencing. BMC Genomics, 2021, 22, 156.	1.2	15
12	Detection of selection signatures in farmed coho salmon (Oncorhynchus kisutch) using dense genome-wide information. Scientific Reports, 2021, 11, 9685.	1.6	15
13	Genome-scale comparative analysis for host resistance against sea lice between Atlantic salmon and rainbow trout. Scientific Reports, 2021, 11, 13231.	1.6	9
14	Application of a novel 50K SNP genotyping array to assess the genetic diversity and linkage disequilibrium in a farmed Pacific white shrimp (Litopenaeus vannamei) population. Aquaculture Reports, 2021, 20, 100691.	0.7	6
15	Detection of selection signatures in the genome of a farmed population of anadromous rainbow trout (Oncorhynchus mykiss). Genomics, 2021, 113, 3395-3404.	1.3	11
16	Development of a multi-species SNP array for serrasalmid fish Colossoma macropomum and Piaractus mesopotamicus. Scientific Reports, 2021, 11, 19289.	1.6	12
17	Multi-trait GWAS using imputed high-density genotypes from whole-genome sequencing identifies genes associated with body traits in Nile tilapia. BMC Genomics, 2021, 22, 57.	1.2	39
18	Comparison of mortality and viral load in rainbow trout (*Oncorhynchus mykiss*) infected with infectious pancreatic necrosis virus (IPNV) genogroups 1 and 5. Journal of Fish Diseases, 2020, 43, 139-146.	0.9	11

#	ARTICLE	IF	CITATIONS
19	Development of a SNP linkage map and genome-wide association study for resistance to Aeromonas hydrophila in pacu (Piaractus mesopotamicus). BMC Genomics, 2020, 21, 672.	1.2	8
20	Whole genome re-sequencing reveals recent signatures of selection in three strains of farmed Nile tilapia (Oreochromis niloticus). Scientific Reports, 2020, 10, 11514.	1.6	34
21	Genomics to accelerate genetic improvement in tilapia. Animal Genetics, 2020, 51, 658-674.	0.6	33
22	Pharmacological iron-chelation as an assisted nutritional immunity strategy against Piscirickettsia salmonis infection. Veterinary Research, 2020, 51, 134.	1.1	3
23	Quantitative genetic variation for resistance to the parasite Ichthyophthirius multifiliis in the Neotropical fish tambaqui (Colossoma macropomum). Aquaculture Reports, 2020, 17, 100338.	0.7	7
24	Estimates of Autozygosity Through Runs of Homozygosity in Farmed Coho Salmon. Genes, 2020, 11, 490.	1.0	10
25	Opportunities and challenges of phenomics applied to livestock and aquaculture breeding in South America. Animal Frontiers, 2020, 10, 45-52.	0.8	18
26	High-Throughput Single Nucleotide Polymorphism (SNP) Discovery and Validation Through Whole-Genome Resequencing in Nile Tilapia (Oreochromis niloticus). Marine Biotechnology, 2020, 22, 109-117.	1.1	25
27	Genetic (co)variation between resistance to Aeromonas hydrophila and growth in tambaqui (Colossoma macropomum). Aquaculture, 2020, 523, 735225.	1.7	16
28	Changed Patterns of Genomic Variation Following Recent Domestication: Selection Sweeps in Farmed Atlantic Salmon. Frontiers in Genetics, 2020, 11, 264.	1.1	15
29	Mate selection provides similar genetic progress and average inbreeding than optimum contribution selection in the long-term. Aquaculture, 2020, 526, 735376.	1.7	3
30	Genetic (co)variation in skin pigmentation patterns and growth in rainbow trout. Animal, 2019, 13, 675-682.	1.3	12
31	Comparative Genomic Analysis of Three Salmonid Species Identifies Functional Candidate Genes Involved in Resistance to the Intracellular Bacterium Piscirickettsia salmonis. Frontiers in Genetics, 2019, 10, 665.	1.1	20
32	Genome-Wide Association Study and Cost-Efficient Genomic Predictions for Growth and Fillet Yield in Nile Tilapia (<i>Oreochromis niloticus</i>). G3: Genes, Genomes, Genetics, 2019, 9, 2597-2607.	0.8	64
33	Multiple Selection Signatures in Farmed Atlantic Salmon Adapted to Different Environments Across Hemispheres. Frontiers in Genetics, 2019, 10, 901.	1.1	41
34	Genome-Wide Patterns of Population Structure and Linkage Disequilibrium in Farmed Nile Tilapia (Oreochromis niloticus). Frontiers in Genetics, 2019, 10, 745.	1.1	27
35	Genetic parameters for resistance to Aeromonas hydrophila in the Neotropical fish pacu (Piaractus) Tj ETQq1 1 0.784314 rgBT /Overlock	1.7	21
36	Whole Genome Linkage Disequilibrium and Effective Population Size in a Coho Salmon (Oncorhynchus) Tj ETQq0 0.0 rgBT /Overlock 10	1.1	41

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37	Novel insights into the genetic relationship between growth and disease resistance in an aquaculture strain of Coho salmon (Oncorhynchus kisutch). Aquaculture, 2019, 511, 734207.	1.7	9
38	Genetic parameters for Piscirickettsia salmonis resistance, sea lice (Caligus rogercresseyi) susceptibility and harvest weight in rainbow trout (Oncorhynchus mykiss). Aquaculture, 2019, 510, 276-282.	1.7	29
39	Advances in genetic improvement for salmon and trout aquaculture: the Chilean situation and prospects. Reviews in Aquaculture, 2019, 11, 340-353.	4.6	49
40	Discovery and Functional Annotation of Quantitative Trait Loci Affecting Resistance to Sea Lice in Atlantic Salmon. Frontiers in Genetics, 2019, 10, 56.	1.1	59
41	Genome-Wide Association Analysis for Resistance to Infectious Pancreatic Necrosis Virus Identifies Candidate Genes Involved in Viral Replication and Immune Response in Rainbow Trout (<i>Oncorhynchus mykiss</i>). G3: Genes, Genomes, Genetics, 2019, 9, 2897-2904.	0.8	29
42	Fine Mapping Using Whole-Genome Sequencing Confirms Anti-Müllerian Hormone as a Major Gene for Sex Determination in Farmed Nile Tilapia (<i>Oreochromis niloticus</i> L.). G3: Genes, Genomes, Genetics, 2019, 9, 3213-3223.	0.8	45
43	Single-Step Genome-Wide Association Study for Resistance to <i>Piscirickettsia salmonis</i> in Rainbow Trout (<i>Oncorhynchus mykiss</i>). G3: Genes, Genomes, Genetics, 2019, 9, 3833-3841.	0.8	28
44	Comparing genomic signatures of domestication in two Atlantic salmon (<i>Salmo salar</i> L.) populations with different geographical origins. Evolutionary Applications, 2019, 12, 137-156.	1.5	58
45	Accuracy of genomic predictions using different imputation error rates in aquaculture breeding programs: A simulation study. Aquaculture, 2019, 503, 225-230.	1.7	21
46	Genome-wide association analysis for body weight identifies candidate genes related to development and metabolism in rainbow trout (Oncorhynchus mykiss). Molecular Genetics and Genomics, 2019, 294, 563-571.	1.0	43
47	Single-step genomic evaluation improves accuracy of breeding value predictions for resistance to infectious pancreatic necrosis virus in rainbow trout. Genomics, 2019, 111, 127-132.	1.3	74
48	Single-Nucleotide Polymorphisms (SNP) Mining and Their Effect on the Tridimensional Protein Structure Prediction in a Set of Immunity-Related Expressed Sequence Tags (EST) in Atlantic Salmon (Salmo salar). Frontiers in Genetics, 2019, 10, 1406.	1.1	28
49	Accuracy of genotype imputation and genomic predictions in a two-generation farmed Atlantic salmon population using high-density and low-density SNP panels. Aquaculture, 2018, 491, 147-154.	1.7	56
50	Genomic Predictions and Genome-Wide Association Study of Resistance Against <i>Piscirickettsia salmonis</i> in Coho Salmon (<i>Oncorhynchus kisutch</i>) Using ddRAD Sequencing. G3: Genes, Genomes, Genetics, 2018, 8, 1183-1194.	0.8	125
51	Genomic Prediction Accuracy for Resistance Against <i>Piscirickettsia salmonis</i> in Farmed Rainbow Trout. G3: Genes, Genomes, Genetics, 2018, 8, 719-726.	0.8	122
52	Population Genomic Structure and Genome-Wide Linkage Disequilibrium in Farmed Atlantic Salmon (Salmo salar L.) Using Dense SNP Genotypes. Frontiers in Genetics, 2018, 9, 649.	1.1	38
53	Determination of the Genetic Component of Fur-Chewing in Chinchillas (Chinchilla lanigera) and Its Economic Impact. Animals, 2018, 8, 144.	1.0	2
54	Gene Expression Response to Sea Lice in Atlantic Salmon Skin: RNA Sequencing Comparison Between Resistant and Susceptible Animals. Frontiers in Genetics, 2018, 9, 287.	1.1	50

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55	Mate selection allows changing the genetic variability of the progeny while optimizing genetic response and controlling inbreeding. Aquaculture, 2018, 495, 409-414.	1.7	8
56	Genome wide association study for resistance to Caligus rogercresseyi in Atlantic salmon (Salmo) Tj ETQq0 0 0 rgBT /Overlock_10 Tf 50	1.7	95
57	The use of genomic information increases the accuracy of breeding value predictions for sea louse (Caligus rogercresseyi) resistance in Atlantic salmon (Salmo salar). Genetics Selection Evolution, 2017, 49, 15.	1.2	129
58	Genomic predictions can accelerate selection for resistance against Piscirickettsia salmonis in Atlantic salmon (Salmo salar). BMC Genomics, 2017, 18, 121.	1.2	140
59	Mate selection in aquaculture breeding using differential evolution algorithm. Aquaculture Research, 2017, 48, 5490-5497.	0.9	13
60	Resistance against infectious pancreatic necrosis exhibits significant genetic variation and is not genetically correlated with harvest weight in rainbow trout (Oncorhynchus mykiss). Aquaculture, 2017, 479, 155-160.	1.7	34
61	Bayesian genome‐wide association analysis for body weight in farmed Atlantic salmon (<i>Salmo) Tj ETQq1 1 0.784314 rgBT /Overlock	0.6	70
62	Functional Annotation of All Salmonid Genomes (FAASG): an international initiative supporting future salmonid research, conservation and aquaculture. BMC Genomics, 2017, 18, 484.	1.2	99
63	Correlated response of flesh color to selection for harvest weight in coho salmon (Oncorhynchus) Tj ETQq1 1 0.784314 rgBT /Overlock	1.7	24
64	Level of agreement in the recognition of pain among equine practitioners in Chile. Veterinaria México OA, 2016, 3, .	0.2	1
65	Assessment of genetic variation for pathogen-specific mastitis resistance in Valle del Belice dairy sheep. BMC Veterinary Research, 2016, 12, 158.	0.7	10
66	Genomewide single nucleotide polymorphism discovery in Atlantic salmon (<i>Salmo salar</i>): validation in wild and farmed American and European populations. Molecular Ecology Resources, 2016, 16, 1002-1011.	2.2	134
67	Evidence of recent signatures of selection during domestication in an Atlantic salmon population. Marine Genomics, 2016, 26, 41-50.	0.4	62
68	Characterization of Antimicrobial Susceptibility and Its Association with Virulence Genes Related to Adherence, Invasion, and Cytotoxicity in <i>Campylobacter jejuni</i> and <i>Campylobacter coli</i> Isolates from Animals, Meat, and Humans. Microbial Drug Resistance, 2016, 22, 432-444.	0.9	43
69	Negative genetic correlation between resistance against Piscirickettsia salmonis and harvest weight in coho salmon (Oncorhynchus kisutch). Aquaculture, 2016, 459, 8-13.	1.7	63
70	Evaluation of the growth and carcass quality of diallel crosses of four strains of Nile tilapia (Oerochromis niloticus). Aquaculture, 2016, 451, 213-222.	1.7	18
71	Concordancia entre médicos veterinarios que trabajan en Chile en el reconocimiento del dolor en equinos. Veterinaria Mexico, 2016, 3, .	0.0	0
72	Genome-wide association analysis reveals loci associated with resistance against Piscirickettsia salmonis in two Atlantic salmon (Salmo salar L.) chromosomes. BMC Genomics, 2015, 16, 854.	1.2	120

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73	Genomics in aquaculture to better understand species biology and accelerate genetic progress. Frontiers in Genetics, 2015, 6, 128.	1.1	82
74	From the viral perspective: Infectious salmon anemia virus (ISAV) transcriptome during the infective process in Atlantic salmon (Salmo salar). Marine Genomics, 2015, 20, 39-43.	0.4	14
75	High-throughput transcriptome analysis of ISAV-infected Atlantic salmon Salmo salar unravels divergent immune responses associated to head-kidney, liver and gills tissues. Fish and Shellfish Immunology, 2015, 45, 367-377.	1.6	73
76	Effect of triploidy in the expression of immune-related genes in coho salmonOncorhynchus kisutch(Walbaum) infected withPiscirickettsia salmonis. Aquaculture Research, 2015, 46, 59-63.	0.9	7
77	Genome-Wide Association Study (GWAS) for Growth Rate and Age at Sexual Maturation in Atlantic Salmon (Salmo salar). PLoS ONE, 2015, 10, e0119730.	1.1	177
78	Genetics and genomics of disease resistance in salmonid species. Frontiers in Genetics, 2014, 5, 415.	1.1	120
79	Characterization of <i><scp>M</scp>ycobacterium salmoniphilum</i> as causal agent of mycobacteriosis in <scp>A</scp>tlantic salmon, <i><scp>S</scp>almo salar </i><scp>L</scp>., from a freshwater recirculation system. Journal of Fish Diseases, 2014, 37, 341-348.	0.9	14
80	Inbreeding and effective population size in a coho salmon (Oncorhynchus kisutch) breeding nucleus in Chile. Aquaculture, 2014, 420-421, S15-S19.	1.7	25
81	Genetic co-variation between resistance against both Caligus rogercresseyi and Piscirickettsia salmonis, and body weight in Atlantic salmon (Salmo salar). Aquaculture, 2014, 433, 295-298.	1.7	103
82	Applications in the search for genomic selection signatures in fish. Frontiers in Genetics, 2014, 5, 458.	1.1	53
83	Assessing footprints of selection in commercial <scp>A</scp>tlantic salmon populations using microsatellite data. Animal Genetics, 2013, 44, 223-226.	0.6	24
84	Quantitative genetic variation of resistance against Piscirickettsia salmonis in Atlantic salmon (Salmo) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	1.7	78
85	Characterization of new microsatellite markers derived from sequence databases for the emu (<i>Dromaius novaehollandiae</i>). Molecular Ecology Resources, 2008, 8, 1442-1444.	2.2	4
86	The CK1 gene family: expression patterning in zebrafish development. Biological Research, 2007, 40, 251-66.	1.5	12