

JosÃ© M YÃ¡ez

List of Publications by Year in descending order

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Version: 2024-02-01

86
papers

3,410
citations

147726

31
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175177

52
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112
all docs

112
docs citations

112
times ranked

1796
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-Wide Association Study (GWAS) for Growth Rate and Age at Sexual Maturation in Atlantic Salmon (<i>Salmo salar</i>). PLoS ONE, 2015, 10, e0119730.	1.1	177
2	Genomic predictions can accelerate selection for resistance against <i>Piscirickettsia salmonis</i> in Atlantic salmon (<i>Salmo salar</i>). BMC Genomics, 2017, 18, 121.	1.2	140
3	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
4	The use of genomic information increases the accuracy of breeding value predictions for sea louse (<i>Caligus rogercresseyi</i>) resistance in Atlantic salmon (<i>Salmo salar</i>). Genetics Selection Evolution, 2017, 49, 15.	1.2	129
5	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
6	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
7	Genetics and genomics of disease resistance in salmonid species. Frontiers in Genetics, 2014, 5, 415.	1.1	120
8	Genome-wide association analysis reveals loci associated with resistance against <i>Piscirickettsia salmonis</i> in two Atlantic salmon (<i>Salmo salar</i> L.) chromosomes. BMC Genomics, 2015, 16, 854.	1.2	120
9	Genetic co-variation between resistance against both <i>Caligus rogercresseyi</i> and <i>Piscirickettsia salmonis</i> , and body weight in Atlantic salmon (<i>Salmo salar</i>). Aquaculture, 2014, 433, 295-298.	1.7	103
10	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
11	Genome wide association study for resistance to <i>Caligus rogercresseyi</i> in Atlantic salmon (<i>Salmo salar</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5	1.7	95
12	Genomics in aquaculture to better understand species biology and accelerate genetic progress. Frontiers in Genetics, 2015, 6, 128.	1.1	82
13	Quantitative genetic variation of resistance against <i>Piscirickettsia salmonis</i> in Atlantic salmon (<i>Salmo salar</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 5	1.7	78
14	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
15	High-throughput transcriptome analysis of ISAV-infected Atlantic salmon <i>Salmo salar</i> unravels divergent immune responses associated to head-kidney, liver and gills tissues. Fish and Shellfish Immunology, 2015, 45, 367-377.	1.6	73
16	Bayesian genome-wide association analysis for body weight in farmed Atlantic salmon (<i>Salmo salar</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	0.6	70
17	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
18	Negative genetic correlation between resistance against <i>Piscirickettsia salmonis</i> and harvest weight in coho salmon (<i>Oncorhynchus kisutch</i>). Aquaculture, 2016, 459, 8-13.	1.7	63

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19	Evidence of recent signatures of selection during domestication in an Atlantic salmon population. <i>Marine Genomics</i> , 2016, 26, 41-50.	0.4	62
20	Discovery and Functional Annotation of Quantitative Trait Loci Affecting Resistance to Sea Lice in Atlantic Salmon. <i>Frontiers in Genetics</i> , 2019, 10, 56.	1.1	59
21	Comparing genomic signatures of domestication in two Atlantic salmon (<i>Salmo salar</i> L.) populations with different geographical origins. <i>Evolutionary Applications</i> , 2019, 12, 137-156.	1.5	58
22	Accuracy of genotype imputation and genomic predictions in a two-generation farmed Atlantic salmon population using high-density and low-density SNP panels. <i>Aquaculture</i> , 2018, 491, 147-154.	1.7	56
23	Applications in the search for genomic selection signatures in fish. <i>Frontiers in Genetics</i> , 2014, 5, 458.	1.1	53
24	Gene Expression Response to Sea Lice in Atlantic Salmon Skin: RNA Sequencing Comparison Between Resistant and Susceptible Animals. <i>Frontiers in Genetics</i> , 2018, 9, 287.	1.1	50
25	Advances in genetic improvement for salmon and trout aquaculture: the Chilean situation and prospects. <i>Reviews in Aquaculture</i> , 2019, 11, 340-353.	4.6	49
26	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.). <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3213-3223.	0.8	45
27	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. <i>Microbial Drug Resistance</i> , 2016, 22, 432-444.	0.9	43
28	Genome-wide association analysis for body weight identifies candidate genes related to development and metabolism in rainbow trout (<i>Oncorhynchus mykiss</i>). <i>Molecular Genetics and Genomics</i> , 2019, 294, 563-571.	1.0	43
29	Multiple Selection Signatures in Farmed Atlantic Salmon Adapted to Different Environments Across Hemispheres. <i>Frontiers in Genetics</i> , 2019, 10, 901.	1.1	41
30	Whole Genome Linkage Disequilibrium and Effective Population Size in a Coho Salmon (<i>Oncorhynchus tshawytscha</i>) Overlock 10	1.1	41
31	Multi-trait GWAS using imputed high-density genotypes from whole-genome sequencing identifies genes associated with body traits in Nile tilapia. <i>BMC Genomics</i> , 2021, 22, 57.	1.2	39
32	Population Genomic Structure and Genome-Wide Linkage Disequilibrium in Farmed Atlantic Salmon (<i>Salmo salar</i> L.) Using Dense SNP Genotypes. <i>Frontiers in Genetics</i> , 2018, 9, 649.	1.1	38
33	Resistance against infectious pancreatic necrosis exhibits significant genetic variation and is not genetically correlated with harvest weight in rainbow trout (<i>Oncorhynchus mykiss</i>). <i>Aquaculture</i> , 2017, 479, 155-160.	1.7	34
34	Whole genome re-sequencing reveals recent signatures of selection in three strains of farmed Nile tilapia (<i>Oreochromis niloticus</i>). <i>Scientific Reports</i> , 2020, 10, 11514.	1.6	34
35	Genomics to accelerate genetic improvement in tilapia. <i>Animal Genetics</i> , 2020, 51, 658-674.	0.6	33
36	Increased accuracy of genomic predictions for growth under chronic thermal stress in rainbow trout by prioritizing variants from GWAS using imputed sequence data. <i>Evolutionary Applications</i> , 2022, 15, 537-552.	1.5	33

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37	Genetic parameters for <i>Piscirickettsia salmonis</i> resistance, sea lice (<i>Caligus rogercresseyi</i>) susceptibility and harvest weight in rainbow trout (<i>Oncorhynchus mykiss</i>). <i>Aquaculture</i> , 2019, 510, 276-282.	1.7	29
38	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>). <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2897-2904.	0.8	29
39	Single-Step Genome-Wide Association Study for Resistance to <i>Piscirickettsia salmonis</i> in Rainbow Trout (<i>Oncorhynchus mykiss</i>). <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3833-3841.	0.8	28
40	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 (<i>Salmo salar</i>). <i>Frontiers in Genetics</i> , 2019, 10, 1406.	1.1	28
41	Genome-Wide Patterns of Population Structure and Linkage Disequilibrium in Farmed Nile Tilapia (<i>Oreochromis niloticus</i>). <i>Frontiers in Genetics</i> , 2019, 10, 745.	1.1	27
42	Inbreeding and effective population size in a coho salmon (<i>Oncorhynchus kisutch</i>) breeding nucleus in Chile. <i>Aquaculture</i> , 2014, 420-421, S15-S19.	1.7	25
43	High-Throughput Single Nucleotide Polymorphism (SNP) Discovery and Validation Through Whole-Genome Resequencing in Nile Tilapia (<i>Oreochromis niloticus</i>). <i>Marine Biotechnology</i> , 2020, 22, 109-117.	1.1	25
44	Assessing footprints of selection in commercial Atlantic salmon populations using microsatellite data. <i>Animal Genetics</i> , 2013, 44, 223-226.	0.6	24
45	Correlated response of flesh color to selection for harvest weight in coho salmon (<i>Oncorhynchus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	1.7	24
46	Genetic parameters for resistance to <i>Aeromonas hydrophila</i> in the Neotropical fish pacu (<i>Piaractus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.7	21
47	Accuracy of genomic predictions using different imputation error rates in aquaculture breeding programs: A simulation study. <i>Aquaculture</i> , 2019, 503, 225-230.	1.7	21
48	Comparative Genomic Analysis of Three Salmonid Species Identifies Functional Candidate Genes Involved in Resistance to the Intracellular Bacterium <i>Piscirickettsia salmonis</i> . <i>Frontiers in Genetics</i> , 2019, 10, 665.	1.1	20
49	Evaluation of the growth and carcass quality of diallel crosses of four strains of Nile tilapia (<i>Oreochromis niloticus</i>). <i>Aquaculture</i> , 2016, 451, 213-222.	1.7	18
50	Opportunities and challenges of phenomics applied to livestock and aquaculture breeding in South America. <i>Animal Frontiers</i> , 2020, 10, 45-52.	0.8	18
51	Genetics of growth and survival under chronic heat stress and trade-offs with growth- and robustness-related traits in rainbow trout. <i>Aquaculture</i> , 2021, 531, 735685.	1.7	17
52	Genetic (co)variation between resistance to <i>Aeromonas hydrophila</i> and growth in tambaqui (<i>Colossoma macropomum</i>). <i>Aquaculture</i> , 2020, 523, 735225.	1.7	16
53	Changed Patterns of Genomic Variation Following Recent Domestication: Selection Sweeps in Farmed Atlantic Salmon. <i>Frontiers in Genetics</i> , 2020, 11, 264.	1.1	15
54	Investigating mechanisms underlying genetic resistance to Salmon Rickettsial Syndrome in Atlantic salmon using RNA sequencing. <i>BMC Genomics</i> , 2021, 22, 156.	1.2	15

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55	Detection of selection signatures in farmed coho salmon (<i>Oncorhynchus kisutch</i>) using dense genome-wide information. <i>Scientific Reports</i> , 2021, 11, 9685.	1.6	15
56	Characterization of <i>Mycobacterium salmoniphilum</i> as causal agent of mycobacteriosis in Atlantic salmon, <i>Salmo salar</i> L., from a freshwater recirculation system. <i>Journal of Fish Diseases</i> , 2014, 37, 341-348.	0.9	14
57	From the viral perspective: Infectious salmon anemia virus (ISAV) transcriptome during the infective process in Atlantic salmon (<i>Salmo salar</i>). <i>Marine Genomics</i> , 2015, 20, 39-43.	0.4	14
58	Mate selection in aquaculture breeding using differential evolution algorithm. <i>Aquaculture Research</i> , 2017, 48, 5490-5497.	0.9	13
59	The CK1 gene family: expression patterning in zebrafish development. <i>Biological Research</i> , 2007, 40, 251-66.	1.5	12
60	Genetic (co)variation in skin pigmentation patterns and growth in rainbow trout. <i>Animal</i> , 2019, 13, 675-682.	1.3	12
61	Development of a multi-species SNP array for serrasalmid fish <i>Colossoma macropomum</i> and <i>Piaractus mesopotamicus</i> . <i>Scientific Reports</i> , 2021, 11, 19289.	1.6	12
62	The impact of genetic relationship between training and validation populations on genomic prediction accuracy in Atlantic salmon. <i>Aquaculture Reports</i> , 2022, 23, 101033.	0.7	12
63	Comparison of mortality and viral load in rainbow trout (<i>Oncorhynchus mykiss</i>) infected with infectious pancreatic necrosis virus (IPNV) genogroups 1 and 5. <i>Journal of Fish Diseases</i> , 2020, 43, 139-146.	0.9	11
64	Detection of selection signatures in the genome of a farmed population of anadromous rainbow trout (<i>Oncorhynchus mykiss</i>). <i>Genomics</i> , 2021, 113, 3395-3404.	1.3	11
65	Genomics applied to livestock and aquaculture breeding. <i>Evolutionary Applications</i> , 2022, 15, 517-522.	1.5	11
66	Assessment of genetic variation for pathogen-specific mastitis resistance in Valle del Belice dairy sheep. <i>BMC Veterinary Research</i> , 2016, 12, 158.	0.7	10
67	Estimates of Autozygosity Through Runs of Homozygosity in Farmed Coho Salmon. <i>Genes</i> , 2020, 11, 490.	1.0	10
68	Novel insights into the genetic relationship between growth and disease resistance in an aquaculture strain of Coho salmon (<i>Oncorhynchus kisutch</i>). <i>Aquaculture</i> , 2019, 511, 734207.	1.7	9
69	Genome-scale comparative analysis for host resistance against sea lice between Atlantic salmon and rainbow trout. <i>Scientific Reports</i> , 2021, 11, 13231.	1.6	9
70	Infectious pancreatic necrosis virus in salmonids: Molecular epidemiology and host response to infection. <i>Reviews in Aquaculture</i> , 2022, 14, 751-769.	4.6	9
71	Mate selection allows changing the genetic variability of the progeny while optimizing genetic response and controlling inbreeding. <i>Aquaculture</i> , 2018, 495, 409-414.	1.7	8
72	Development of a SNP linkage map and genome-wide association study for resistance to <i>Aeromonas hydrophila</i> in pacu (<i>Piaractus mesopotamicus</i>). <i>BMC Genomics</i> , 2020, 21, 672.	1.2	8

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73	Microbiota composition and susceptibility to florfenicol and oxytetracycline of bacterial isolates from mussels (<i>Mytilus</i> spp.) reared on different years and distance from salmon farms. <i>Environmental Research</i> , 2022, 204, 112068.	3.7	8
74	Effect of triploidy in the expression of immune-related genes in coho salmon <i>Oncorhynchus kisutch</i> (Walbaum) infected with <i>Piscirickettsia salmonis</i> . <i>Aquaculture Research</i> , 2015, 46, 59-63.	0.9	7
75	Quantitative genetic variation for resistance to the parasite <i>Ichthyophthirius multifiliis</i> in the Neotropical fish tambaqui (<i>Colossoma macropomum</i>). <i>Aquaculture Reports</i> , 2020, 17, 100338.	0.7	7
76	Differential Transcriptomic Response of Rainbow Trout to Infection with Two Strains of IPNV. <i>Viruses</i> , 2022, 14, 21.	1.5	7
77	Application of a novel 50K SNP genotyping array to assess the genetic diversity and linkage disequilibrium in a farmed Pacific white shrimp (<i>Litopenaeus vannamei</i>) population. <i>Aquaculture Reports</i> , 2021, 20, 100691.	0.7	6
78	Accuracy of genotype imputation to whole genome sequencing level using different populations of Nile tilapia. <i>Aquaculture</i> , 2022, 551, 737947.	1.7	6
79	Linkage map for chromosome-level genome anchoring and genome-wide association study for resistance to <i>Aeromonas hydrophila</i> in <i>Colossoma macropomum</i> . <i>Aquaculture</i> , 2022, 560, 738462.	1.7	5
80	Characterization of new microsatellite markers derived from sequence databases for the emu (<i>Dromaius novaehollandiae</i>). <i>Molecular Ecology Resources</i> , 2008, 8, 1442-1444.	2.2	4
81	Pharmacological iron-chelation as an assisted nutritional immunity strategy against <i>Piscirickettsia salmonis</i> infection. <i>Veterinary Research</i> , 2020, 51, 134.	1.1	3
82	Mate selection provides similar genetic progress and average inbreeding than optimum contribution selection in the long-term. <i>Aquaculture</i> , 2020, 526, 735376.	1.7	3
83	Determination of the Genetic Component of Fur-Chewing in Chinchillas (<i>Chinchilla lanigera</i>) and Its Economic Impact. <i>Animals</i> , 2018, 8, 144.	1.0	2
84	Genotype-by-environment interaction for growth in seawater and freshwater in Atlantic salmon (<i>Salmo salar</i>). <i>Aquaculture</i> , 2022, 548, 737674.	1.7	2
85	Level of agreement in the recognition of pain among equine practitioners in Chile. <i>Veterinaria MÃ©xico OA</i> , 2016, 3, .	0.2	1
86	Concordancia entre mÃ©dicos veterinarios que trabajan en Chile en el reconocimiento del dolor en equinos. <i>Veterinaria Mexico</i> , 2016, 3, .	0.0	0