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List of Publications by Year in descending order

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Version: 2024-02-01

71
papers

1,648
citations

257450

24
h-index

345221

36
g-index

72
all docs

72
docs citations

72
times ranked

2696
citing authors

#	ARTICLE	IF	CITATIONS
1	Population Structure and Diversity in European Honey Bees (<i>Apis mellifera</i> L.) – An Empirical Comparison of Pool and Individual Whole-Genome Sequencing. <i>Genes</i> , 2022, 13, 182.	2.4	13
2	Recovering High-Quality Host Genomes from Gut Metagenomic Data through Genotype Imputation. <i>Genetics & Genomics Next</i> , 2022, 3, .	1.5	5
3	Discovery of SNP markers of red shrimp <i>Aristeus antennatus</i> for population structure in Western Mediterranean Sea. <i>Conservation Genetics Resources</i> , 2021, 13, 21-25.	0.8	2
4	Authoritative subspecies diagnosis tool for European honey bees based on ancestry informative SNPs. <i>BMC Genomics</i> , 2021, 22, 101.	2.8	34
5	Impact of dimethylpyrazole-based nitrification inhibitors on soil-borne bacteria. <i>Science of the Total Environment</i> , 2021, 792, 148374.	8.0	18
6	Transcriptomic dataset for <i>Sardina pilchardus</i> : Assembly, annotation, and expression of nine tissues. <i>Data in Brief</i> , 2021, 39, 107583.	1.0	1
7	Response of Horticultural Soil Microbiota to Different Fertilization Practices. <i>Plants</i> , 2020, 9, 1501.	3.5	12
8	EXFI: Exon and splice graph prediction without a reference genome. <i>Ecology and Evolution</i> , 2020, 10, 8880-8893.	1.9	0
9	Differences in honey bee bacterial diversity and composition in agricultural and pristine environments – a field study. <i>Apidologie</i> , 2020, 51, 1018-1037.	2.0	23
10	Digging into the Genomic Past of Swiss Honey Bees by Whole-Genome Sequencing Museum Specimens. <i>Genome Biology and Evolution</i> , 2020, 12, 2535-2551.	2.5	26
11	Application of high-throughput single nucleotide polymorphism genotyping for assessing the origin of <i>Engraulis encrasicolus</i> eggs. <i>Aquatic Conservation: Marine and Freshwater Ecosystems</i> , 2020, 30, 1313-1324.	2.0	6
12	Genetic population structure of anchovy (<i>Engraulis encrasicolus</i>) in North-western Europe and variability in the seasonal distribution of the stocks. <i>Fisheries Research</i> , 2020, 229, 105619.	1.7	14
13	Genetic structure of Iranian indigenous sheep breeds: insights for conservation. <i>Tropical Animal Health and Production</i> , 2020, 52, 2283-2290.	1.4	9
14	Unraveling DMPSA nitrification inhibitor impact on soil bacterial consortia under different tillage systems. <i>Agriculture, Ecosystems and Environment</i> , 2020, 301, 107029.	5.3	16
15	A novel transcriptome-derived SNPs array for tench (<i>Tinca tinca</i> L.). <i>PLoS ONE</i> , 2019, 14, e0213992.	2.5	3
16	Hygroregulation, a key ability for eusocial insects: Native Western European honeybees as a case study. <i>PLoS ONE</i> , 2019, 14, e0200048.	2.5	7
17	Spatial dynamics and mixing of bluefin tuna in the Atlantic Ocean and Mediterranean Sea revealed using next-generation sequencing. <i>Molecular Ecology Resources</i> , 2018, 18, 620-638.	4.8	34
18	Association between combinations of genetic polymorphisms and epidemiopathogenic forms of bovine paratuberculosis. <i>Heliyon</i> , 2018, 4, e00535.	3.2	16

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19	Accumulation of trace elements within <i>Vitis vinifera</i> L. varieties cultivated in Biscay (Basque Country) for txakoli production: a two-year case study. <i>Environmental Chemistry</i> , 2018, 15, 215.	1.5	0
20	Genomic selection signatures in sheep from the Western Pyrenees. <i>Genetics Selection Evolution</i> , 2018, 50, 9.	3.0	35
21	Development of gene-associated single nucleotide polymorphisms for Japanese anchovy <i>Engraulis japonicus</i> through cross-species amplification. <i>Fisheries Science</i> , 2018, 84, 1-7.	1.6	3
22	Reduced Single Nucleotide Polymorphism Panels for Assigning Atlantic Albacore and Bay of Biscay Anchovy Individuals to Their Geographic Origin: Toward Sustainable Fishery Management. <i>Journal of Agricultural and Food Chemistry</i> , 2017, 65, 4351-4358.	5.2	5
23	Detection of endocrine disrupting chemicals and evidence of their effects on the HPG axis of the European anchovy <i>Engraulis encrasicolus</i> . <i>Marine Environmental Research</i> , 2017, 127, 137-147.	2.5	10
24	Evidence for gene-gene epistatic interactions between susceptibility genes for <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> infection in cattle. <i>Livestock Science</i> , 2017, 195, 63-66.	1.6	9
25	Insights on the drivers of genetic divergence in the European anchovy. <i>Scientific Reports</i> , 2017, 7, 4180.	3.3	17
26	Unraveling the environmental and anthropogenic drivers of bacterial community changes in the Estuary of Bilbao and its tributaries. <i>PLoS ONE</i> , 2017, 12, e0178755.	2.5	34
27	18S V9 metabarcoding correctly depicts plankton estuarine community drivers. <i>Marine Ecology - Progress Series</i> , 2017, 584, 31-43.	1.9	20
28	Genetic association study of systemic lupus erythematosus and disease subphenotypes in European populations. <i>Clinical Rheumatology</i> , 2016, 35, 1161-1168.	2.2	16
29	18S rRNA V9 metabarcoding for diet characterization: a critical evaluation with two sympatric zooplanktivorous fish species. <i>Ecology and Evolution</i> , 2016, 6, 1809-1824.	1.9	91
30	No loss of genetic diversity in the exploited and recently collapsed population of Bay of Biscay anchovy (<i>Engraulis encrasicolus</i> , L.). <i>Marine Biology</i> , 2016, 163, 1.	1.5	14
31	Transcriptome analysis deciphers evolutionary mechanisms underlying genetic differentiation between coastal and offshore anchovy populations in the Bay of Biscay. <i>Marine Biology</i> , 2016, 163, 1.	1.5	14
32	Insights on the origin of invasive copepods colonizing Basque estuaries; a DNA barcoding approach. <i>Marine Biodiversity Records</i> , 2016, 9, .	1.2	14
33	<i>Clupeiformes</i> ™ Egg Envelope Proteins characterization: The case of <i>Engraulis encrasicolus</i> as a proxy for stock assessment through a novel molecular tool. <i>Molecular Phylogenetics and Evolution</i> , 2016, 100, 95-108.	2.7	2
34	Is metabarcoding suitable for estuarine plankton monitoring? A comparative study with microscopy. <i>Marine Biology</i> , 2016, 163, 1.	1.5	101
35	High resolution SNPs selection in <i>Engraulis encrasicolus</i> through Taqman OpenArray. <i>Fisheries Research</i> , 2016, 177, 31-38.	1.7	9
36	LDLR and PCSK9 Are Associated with the Presence of Antiphospholipid Antibodies and the Development of Thrombosis in aPLA Carriers. <i>PLoS ONE</i> , 2016, 11, e0146990.	2.5	24

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37	Serological and Genetic Evidence for Altered Complement System Functionality in Systemic Lupus Erythematosus: Findings of the GAPAID Consortium. <i>PLoS ONE</i> , 2016, 11, e0150685.	2.5	5
38	Genetic variants associated with rheumatoid arthritis patients and serotypes in European populations. <i>Clinical and Experimental Rheumatology</i> , 2016, 34, 236-41.	0.8	6
39	Origin, evolution and conservation of the honey bees from La Palma Island (Canary Islands): molecular and morphological data. <i>Journal of Apicultural Research</i> , 2015, 54, 427-440.	1.5	9
40	Genomic Resources Notes Accepted 1 June 2015 - 31 July 2015. <i>Molecular Ecology Resources</i> , 2015, 15, 1510-1512.	4.8	6
41	Macrozooplankton predation impact on anchovy (<i>Engraulis encrasicolus</i>) eggs mortality at the Bay of Biscay shelf break spawning centre. <i>ICES Journal of Marine Science</i> , 2015, 72, 1370-1379.	2.5	3
42	A real-time PCR assay to estimate invertebrate and fish predation on anchovy eggs in the Bay of Biscay. <i>Progress in Oceanography</i> , 2015, 131, 82-99.	3.2	13
43	New Nuclear SNP Markers Unravel the Genetic Structure and Effective Population Size of Albacore Tuna (<i>Thunnus alalunga</i>). <i>PLoS ONE</i> , 2015, 10, e0128247.	2.5	43
44	Influence of MTHFR C677T polymorphism on methotrexate monotherapy discontinuation in rheumatoid arthritis patients: results from the GAPAID European project. <i>Clinical and Experimental Rheumatology</i> , 2015, 33, 699-705.	0.8	8
45	Genetic structure of brown and Iberian hare populations in northern Iberia: Implications for conservation of genetic diversity. <i>Journal of Wildlife Management</i> , 2014, 78, 632-644.	1.8	2
46	Genetic Association Analysis of Paratuberculosis Forms in Holstein-Friesian Cattle. <i>Veterinary Medicine International</i> , 2014, 2014, 1-8.	1.5	26
47	Connectivity, neutral theories and the assessment of species vulnerability to global change in temperate estuaries. <i>Estuarine, Coastal and Shelf Science</i> , 2013, 131, 52-63.	2.1	28
48	Single nucleotide polymorphism discovery in albacore and Atlantic bluefin tuna provides insights into worldwide population structure. <i>Animal Genetics</i> , 2013, 44, 678-692.	1.7	47
49	Thrombotic Antiphospholipid Syndrome Shows Strong Haplotypic Association with SH2B3-ATXN2 Locus. <i>PLoS ONE</i> , 2013, 8, e67897.	2.5	18
50	SNP Discovery in European Anchovy (<i>Engraulis encrasicolus</i> , L) by High-Throughput Transcriptome and Genome Sequencing. <i>PLoS ONE</i> , 2013, 8, e70051.	2.5	38
51	Multiple SNP Markers Reveal Fine-Scale Population and Deep Phylogeographic Structure in European Anchovy (<i>Engraulis encrasicolus</i> L.). <i>PLoS ONE</i> , 2012, 7, e42201.	2.5	60
52	Permanent Genetic Resources added to Molecular Ecology Resources Database 1 October 2011 – 30 November 2011. <i>Molecular Ecology Resources</i> , 2012, 12, 374-376.	4.8	69
53	Single nucleotide polymorphisms in the bovine <i>CD209</i> candidate gene for susceptibility to infection by <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> . <i>Animal Genetics</i> , 2012, 43, 646-647.	1.7	7
54	Effects of a 10-year conservation programme on the genetic diversity of the Pottoka pony – new clues regarding their origin. <i>Journal of Animal Breeding and Genetics</i> , 2012, 129, 234-243.	2.0	11

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55	Worldwide genetic structure of albacore <i>Thunnus alalunga</i> revealed by microsatellite DNA markers. <i>Marine Ecology - Progress Series</i> , 2012, 471, 183-191.	1.9	29
56	Genetic variation of toll-like receptor genes and infection by <i>Mycobacterium avium</i> ssp. <i>paratuberculosis</i> in Holstein-Friesian cattle. <i>Journal of Dairy Science</i> , 2011, 94, 3635-3641.	3.4	38
57	Microsatellite based ovine parentage testing to identify the source responsible for the killing of an endangered species. <i>Forensic Science International: Genetics</i> , 2011, 5, 333-335.	3.1	8
58	Both geometric morphometric and microsatellite data consistently support the differentiation of the <i>Apis mellifera</i> M evolutionary branch. <i>Apidologie</i> , 2011, 42, 150-161.	2.0	79
59	High-density SNP genotyping detects homogeneity of Spanish and French Basques, and confirms their genomic distinctiveness from other European populations. <i>Human Genetics</i> , 2010, 128, 113-117.	3.8	43
60	Genetic association between bovine <i>NOD2</i> polymorphisms and infection by <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> in Holstein-Friesian cattle. <i>Animal Genetics</i> , 2010, 41, 652-655.	1.7	39
61	Identification of single nucleotide polymorphisms in the bovine solute carrier family 11 member 1 (<i>SLC11A1</i>) gene and their association with infection by <i>Mycobacterium avium</i> subspecies <i>paratuberculosis</i> . <i>Journal of Dairy Science</i> , 2010, 93, 1713-1721.	3.4	52
62	SP110 as a novel susceptibility gene for <i>Mycobacterium avium</i> subspecies <i>paratuberculosis</i> infection in cattle. <i>Journal of Dairy Science</i> , 2010, 93, 5950-5958.	3.4	25
63	Microsatellite variability in European anchovy (<i>Engraulis encrasicolus</i>) calls for further investigation of its genetic structure and biogeography. <i>ICES Journal of Marine Science</i> , 2009, 66, 2176-2182.	2.5	33
64	Identification of horse chestnut coat color genotype using SNaPshot®. <i>BMC Research Notes</i> , 2009, 2, 255.	1.4	3
65	Forensic analysis of dog (<i>Canis lupus familiaris</i>) mitochondrial DNA sequences: An inter-laboratory study of the GEP-ISFC working group. <i>Forensic Science International: Genetics</i> , 2009, 4, 49-54.	3.1	22
66	Innate immune gene expression in individual zebrafish after <i>Listonella anguillarum</i> inoculation. <i>Fish and Shellfish Immunology</i> , 2007, 23, 1285-1293.	3.6	69
67	Gene flow within the M evolutionary lineage of <i>Apis mellifera</i> : role of the Pyrenees, isolation by distance and post-glacial re-colonization routes in the western Europe. <i>Apidologie</i> , 2007, 38, 141-155.	2.0	70
68	The genetic distinctiveness of the three Iberian hare species: <i>Lepus europaeus</i> , <i>L. granatensis</i> , and <i>L. castroviejoi</i> . <i>Mammalian Biology</i> , 2006, 71, 52-59.	1.5	25
69	Tracking diversity and differentiation in six sheep breeds from the North Iberian Peninsula through DNA variation. <i>Small Ruminant Research</i> , 2004, 52, 195-202.	1.2	30
70	Analysis of the Genetic Structure of Endangered Bovine Breeds from the Western Pyrenees Using Dna Microsatellite Markers. <i>Biochemical Genetics</i> , 2004, 42, 99-108.	1.7	22
71	Allele distributions of two novel SNPs within the sheep <i>Cyp19</i> gene. <i>Journal of Animal Breeding and Genetics</i> , 2002, 119, 402-405.	2.0	4