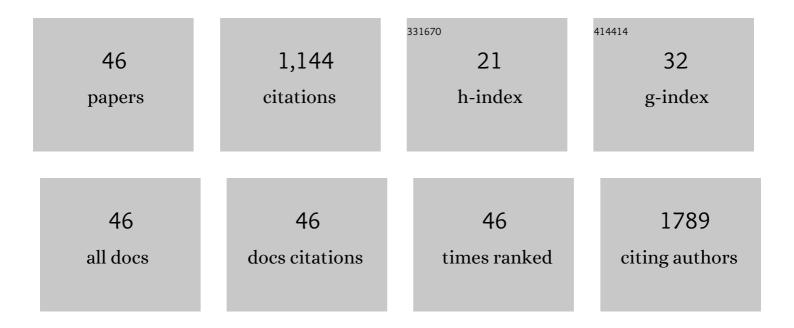
Mikel Iriondo

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1357879/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Discovery of SNP markers of red shrimp Aristeus antennatus for population structure in Western Mediterranean Sea. Conservation Genetics Resources, 2021, 13, 21-25.	0.8	2
2	Application of highâ€throughput single nucleotide polymorphism genotyping for assessing the origin of <scp><i>Engraulis encrasicolus</i></scp> eggs. Aquatic Conservation: Marine and Freshwater Ecosystems, 2020, 30, 1313-1324.	2.0	6
3	Genetic population structure of anchovy (Engraulis encrasicolus) in North-western Europe and variability in the seasonal distribution of the stocks. Fisheries Research, 2020, 229, 105619.	1.7	14
4	Genetic structure of Iranian indigenous sheep breeds: insights for conservation. Tropical Animal Health and Production, 2020, 52, 2283-2290.	1.4	9
5	Association between combinations of genetic polymorphisms and epidemiopathogenic forms of bovine paratuberculosis. Heliyon, 2018, 4, e00535.	3.2	16
6	Genomic selection signatures in sheep from the Western Pyrenees. Genetics Selection Evolution, 2018, 50, 9.	3.0	35
7	Development of gene-associated single nucleotide polymorphisms for Japanese anchovy Engraulis japonicus through cross-species amplification. Fisheries Science, 2018, 84, 1-7.	1.6	3
8	Reduced Single Nucleotide Polymorphism Panels for Assigning Atlantic Albacore and Bay of Biscay Anchovy Individuals to Their Geographic Origin: Toward Sustainable Fishery Management. Journal of Agricultural and Food Chemistry, 2017, 65, 4351-4358.	5.2	5
9	Evidence for gene-gene epistatic interactions between susceptibility genes for Mycobacterium avium subsp. paratuberculosis infection in cattle. Livestock Science, 2017, 195, 63-66.	1.6	9
10	Insights on the drivers of genetic divergence in the European anchovy. Scientific Reports, 2017, 7, 4180.	3.3	17
11	Genetic association study of systemic lupus erythematosus and disease subphenotypes in European populations. Clinical Rheumatology, 2016, 35, 1161-1168.	2.2	16
12	No loss of genetic diversity in the exploited and recently collapsed population of Bay of Biscay anchovy (Engraulis encrasicolus, L.). Marine Biology, 2016, 163, 1.	1.5	14
13	Transcriptome analysis deciphers evolutionary mechanisms underlying genetic differentiation between coastal and offshore anchovy populations in the Bay of Biscay. Marine Biology, 2016, 163, 1.	1.5	14
14	High resolution SNPs selection in Engraulis encrasicolus through Taqman OpenArray. Fisheries Research, 2016, 177, 31-38.	1.7	9
15	LDLR and PCSK9 Are Associated with the Presence of Antiphospholipid Antibodies and the Development of Thrombosis in aPLA Carriers. PLoS ONE, 2016, 11, e0146990.	2.5	24
16	Genetic variants associated with rheumatoid arthritis patients and serotypes in European populations. Clinical and Experimental Rheumatology, 2016, 34, 236-41.	0.8	6
17	Origin, evolution and conservation of the honey bees from La Palma Island (Canary Islands): molecular and morphological data. Journal of Apicultural Research, 2015, 54, 427-440.	1.5	9
18	New Nuclear SNP Markers Unravel the Genetic Structure and Effective Population Size of Albacore Tuna (Thunnus alalunga). PLoS ONE, 2015, 10, e0128247.	2.5	43

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19	Exploring Genetic Factors Involved in Huntington Disease Age of Onset: E2F2 as a New Potential Modifier Gene. PLoS ONE, 2015, 10, e0131573.	2.5	11
20	Genetic structure of brown and Iberian hare populations in northern Iberia: Implications for conservation of genetic diversity. Journal of Wildlife Management, 2014, 78, 632-644.	1.8	2
21	Genetic Association Analysis of Paratuberculosis Forms in Holstein-Friesian Cattle. Veterinary Medicine International, 2014, 2014, 1-8.	1.5	26
22	Connectivity, neutral theories and the assessment of species vulnerability to global change in temperate estuaries. Estuarine, Coastal and Shelf Science, 2013, 131, 52-63.	2.1	28
23	Single nucleotide polymorphism discovery in albacore and Atlantic bluefin tuna provides insights into worldwide population structure. Animal Genetics, 2013, 44, 678-692.	1.7	47
24	Thrombotic Antiphospholipid Syndrome Shows Strong Haplotypic Association with SH2B3-ATXN2 Locus. PLoS ONE, 2013, 8, e67897.	2.5	18
25	Multiple SNP Markers Reveal Fine-Scale Population and Deep Phylogeographic Structure in European Anchovy (Engraulis encrasicolus L.). PLoS ONE, 2012, 7, e42201.	2.5	60
26	Permanent Genetic Resources added to Molecular Ecology Resources Database 1 October 2011 – 30 November 2011. Molecular Ecology Resources, 2012, 12, 374-376.	4.8	69
27	Singleâ€nucleotide polymorphisms in the bovine <scp><i>CD209</i></scp> candidate gene for susceptibility to infection by <i><scp>M</scp>ycobacterium avium</i> subsp. <i>paratuberculosis</i> . Animal Genetics, 2012, 43, 646-647.	1.7	7
28	Effects of a 10â€year conservation programme on the genetic diversity of the Pottoka pony – new clues regarding their origin. Journal of Animal Breeding and Genetics, 2012, 129, 234-243.	2.0	11
29	Worldwide genetic structure of albacore Thunnus alalunga revealed by microsatellite DNA markers. Marine Ecology - Progress Series, 2012, 471, 183-191.	1.9	29
30	Genetic variation of toll-like receptor genes and infection by Mycobacterium avium ssp. paratuberculosis in Holstein-Friesian cattle. Journal of Dairy Science, 2011, 94, 3635-3641.	3.4	38
31	Microsatellite based ovine parentage testing to identify the source responsible for the killing of an endangered species. Forensic Science International: Genetics, 2011, 5, 333-335.	3.1	8
32	Both geometric morphometric and microsatellite data consistently support the differentiation of the Apis mellifera M evolutionary branch. Apidologie, 2011, 42, 150-161.	2.0	79
33	High-density SNP genotyping detects homogeneity of Spanish and French Basques, and confirms their genomic distinctiveness from other European populations. Human Genetics, 2010, 128, 113-117.	3.8	43
34	Genetic association between bovine <i>NOD2</i> polymorphisms and infection by <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> in Holsteinâ€Friesian cattle. Animal Genetics, 2010, 41, 652-655.	1.7	39
35	Identification of single nucleotide polymorphisms in the bovine solute carrier family 11 member 1 (SLC11A1) gene and their association with infection by Mycobacterium avium subspecies paratuberculosis. Journal of Dairy Science, 2010, 93, 1713-1721.	3.4	52
36	SP110 as a novel susceptibility gene for Mycobacterium avium subspecies paratuberculosis infection in cattle. Journal of Dairy Science, 2010, 93, 5950-5958.	3.4	25

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37	Microsatellite variability in European anchovy (Engraulis encrasicolus) calls for further investigation of its genetic structure and biogeography. ICES Journal of Marine Science, 2009, 66, 2176-2182.	2.5	33
38	Identification of horse chestnut coat color genotype using SNaPshot®. BMC Research Notes, 2009, 2, 255.	1.4	3
39	Gene flow within the M evolutionary lineage ofApis mellifera: role of the Pyrenees, isolation by distance and post-glacial re-colonization routes in the western Europe. Apidologie, 2007, 38, 141-155.	2.0	70
40	The genetic distinctiveness of the three Iberian hare species: Lepus europaeus, L. granatensis, and L. castroviejoi. Mammalian Biology, 2006, 71, 52-59.	1.5	25
41	Genetic Diversity Within and Among Four South European Native Horse Breeds Based on Microsatellite DNA Analysis: Implications for Conservation. Journal of Heredity, 2005, 96, 670-678.	2.4	73
42	Tracking diversity and differentiation in six sheep breeds from the North Iberian Peninsula through DNA variation. Small Ruminant Research, 2004, 52, 195-202.	1.2	30
43	Analysis of the Genetic Structure of Endangered Bovine Breeds from the Western Pyrenees Using Dna Microsatellite Markers. Biochemical Genetics, 2004, 42, 99-108.	1.7	22
44	DNA polymorphisms detect ancient barriers to gene flow in Basques. American Journal of Physical Anthropology, 2003, 122, 73-84.	2.1	27
45	HLA-DQA1 in autochthonous Basques: Description of a genocline for the DQA1*0201 allele in Europe. International Journal of Legal Medicine, 1996, 109, 181-185.	2.2	9
46	Genetic typing with HUMTH01, HUMVWA31A and HUMFES/FPS short tandem repeat loci, D1S80 variable number tandem repeat locus and HLA-DQα of recent and from XII-XIII centuries spongy bone. Electrophoresis, 1995, 16, 1612-1616.	2.4	9