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List of Publications by Year
in descending order

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46 papers	1,144 citations	331259 21 h-index	414034 32 g-index
46 all docs	46 docs citations	46 times ranked	1789 citing authors

#	Article	IF	Citations
1	Both geometric morphometric and microsatellite data consistently support the differentiation of the Apis mellifera M evolutionary branch. Apidologie, 2011, 42, 150-161.	0.9	79
2	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.	1.0	73
3	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.	0.9	70
4	Permanent Genetic Resources added to Molecular Ecology Resources Database 1 October 2011 â€“ 30 November 2011. Molecular Ecology Resources, 2012, 12, 374-376.	2.2	69
5	Multiple SNP Markers Reveal Fine-Scale Population and Deep Phylogeographic Structure in European Anchovy (Engraulis encrasicolus L.). PLoS ONE, 2012, 7, e42201.	1.1	60
6	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.	1.4	52
7	Single nucleotide polymorphism discovery in albacore and Atlantic bluefin tuna provides insights into worldwide population structure. Animal Genetics, 2013, 44, 678-692.	0.6	47
8	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.	1.8	43
9	New Nuclear SNP Markers Unravel the Genetic Structure and Effective Population Size of Albacore Tuna (Thunnus alalunga). PLoS ONE, 2015, 10, e0128247.	1.1	43
10	Genetic association between bovine NOD2 polymorphisms and infection by Mycobacterium avium subsp. paratuberculosis in Holsteinâ€Friesian cattle. Animal Genetics, 2010, 41, 652-655.	0.6	39
11	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.	1.4	38
12	Genomic selection signatures in sheep from the Western Pyrenees. Genetics Selection Evolution, 2018, 50, 9.	1.2	35
13	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.	1.2	33
14	Tracking diversity and differentiation in six sheep breeds from the North Iberian Peninsula through DNA variation. Small Ruminant Research, 2004, 52, 195-202.	0.6	30
15	Worldwide genetic structure of albacore Thunnus alalunga revealed by microsatellite DNA markers. Marine Ecology - Progress Series, 2012, 471, 183-191.	0.9	29
16	Connectivity, neutral theories and the assessment of species vulnerability to global change in temperate estuaries. Estuarine, Coastal and Shelf Science, 2013, 131, 52-63.	0.9	28
17	DNA polymorphisms detect ancient barriers to gene flow in Basques. American Journal of Physical Anthropology, 2003, 122, 73-84.	2.1	27
18	Genetic Association Analysis of Paratuberculosis Forms in Holstein-Friesian Cattle. Veterinary Medicine International, 2014, 2014, 1-8.	0.6	26

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19	The genetic distinctiveness of the three Iberian hare species: Lepus europaeus, L. granatensis, and L. castroviejoi. Mammalian Biology, 2006, 71, 52-59.	0.8	25
20	SP110 as a novel susceptibility gene for Mycobacterium avium subspecies paratuberculosis infection in cattle. Journal of Dairy Science, 2010, 93, 5950-5958.	1.4	25
21	LDLR and PCSK9 Are Associated with the Presence of Antiphospholipid Antibodies and the Development of Thrombosis in aPLA Carriers. PLoS ONE, 2016, 11, e0146990.	1.1	24
22	Analysis of the Genetic Structure of Endangered Bovine Breeds from the Western Pyrenees Using Dna Microsatellite Markers. Biochemical Genetics, 2004, 42, 99-108.	0.8	22
23	Thrombotic Antiphospholipid Syndrome Shows Strong Haplotypic Association with SH2B3-ATXN2 Locus. PLoS ONE, 2013, 8, e67897.	1.1	18
24	Insights on the drivers of genetic divergence in the European anchovy. Scientific Reports, 2017, 7, 4180.	1.6	17
25	Genetic association study of systemic lupus erythematosus and disease subphenotypes in European populations. Clinical Rheumatology, 2016, 35, 1161-1168.	1.0	16
26	Association between combinations of genetic polymorphisms and epidemiopathogenic forms of bovine paratuberculosis. Heliyon, 2018, 4, e00535.	1.4	16
27	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.	0.7	14
28	Transcriptome analysis deciphers evolutionary mechanisms underlying genetic differentiation between coastal and offshore anchovy populations in the Bay of Biscay. Marine Biology, 2016, 163, 1.	0.7	14
29	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.	0.9	14
30	Effects of a 10â€year conservation programme on the genetic diversity of the Pottoka pony â€“ new clues regarding their origin. Journal of Animal Breeding and Genetics, 2012, 129, 234-243.	0.8	11
31	Exploring Genetic Factors Involved in Huntington Disease Age of Onset: E2F2 as a New Potential Modifier Gene. PLoS ONE, 2015, 10, e0131573.	1.1	11
32	Genetic typing with HUMTH01, HUMVWA31A and HUMFES/FPS short tandem repeat loci, D1S80 variable number tandem repeat locus and HLA-DQÎ± of recent and from XII-XIII centuries spongy bone. Electrophoresis, 1995, 16, 1612-1616.	1.3	9
33	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.	1.2	9
34	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.	0.7	9
35	High resolution SNPs selection in Engraulis encrasicolus through Taqman OpenArray. Fisheries Research, 2016, 177, 31-38.	0.9	9
36	Evidence for gene-gene epistatic interactions between susceptibility genes for Mycobacterium avium subsp. paratuberculosis infection in cattle. Livestock Science, 2017, 195, 63-66.	0.6	9

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37	Genetic structure of Iranian indigenous sheep breeds: insights for conservation. Tropical Animal Health and Production, 2020, 52, 2283-2290.	0.5	9
38	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.	1.6	8
39	Singleâ€nucleotide polymorphisms in the bovine<scp>CD209</scp> candidate gene for susceptibility to infection by <scp>M</scp>ycobacterium avium subsp. paratuberculosis. Animal Genetics, 2012, 43, 646-647.	0.6	7
40	Application of highâ€throughput single nucleotide polymorphism genotyping for assessing the origin of <scp>Engraulis encrasicolus</scp> eggs. Aquatic Conservation: Marine and Freshwater Ecosystems, 2020, 30, 1313-1324.	0.9	6
41	Genetic variants associated with rheumatoid arthritis patients and serotypes in European populations. Clinical and Experimental Rheumatology, 2016, 34, 236-41.	0.4	6
42	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.	2.4	5
43	Identification of horse chestnut coat color genotype using SNaPshotÂ®. BMC Research Notes, 2009, 2, 255.	0.6	3
44	Development of gene-associated single nucleotide polymorphisms for Japanese anchovy Engraulis japonicus through cross-species amplification. Fisheries Science, 2018, 84, 1-7.	0.7	3
45	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.	0.7	2
46	Discovery of SNP markers of red shrimp Aristeus antennatus for population structure in Western Mediterranean Sea. Conservation Genetics Resources, 2021, 13, 21-25.	0.4	2