Ali Esmailizadeh

List of Publications by Year in descending order

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257450 330143 1,834 89 24 citations h-index papers

37 g-index 102 102 102 1875 docs citations times ranked citing authors all docs

#	Article	IF	Citations
1	863 genomes reveal the origin and domestication of chicken. Cell Research, 2020, 30, 693-701.	12.0	144
2	Whole-genome resequencing of wild and domestic sheep identifies genes associated with morphological and agronomic traits. Nature Communications, 2020, 11, 2815.	12.8	142
3	The origin of domestication genes in goats. Science Advances, 2020, 6, eaaz5216.	10.3	86
4	Whole genomes and transcriptomes reveal adaptation and domestication of pistachio. Genome Biology, 2019, 20, 79.	8.8	81
5	Effects of the myostatin F94L substitution on beef traits1. Journal of Animal Science, 2008, 86, 1038-1046.	0.5	70
6	AdaptMap: exploring goat diversity and adaptation. Genetics Selection Evolution, 2018, 50, 61.	3.0	70
7	Convergent genomic signatures of high-altitude adaptation among domestic mammals. National Science Review, 2020, 7, 952-963.	9.5	52
8	Quantitative genetic analysis of growth traits and Kleiber ratios in Sanjabi sheep. Small Ruminant Research, 2010, 93, 88-93.	1.2	50
9	Whole-Genome Resequencing of Worldwide Wild and Domestic Sheep Elucidates Genetic Diversity, Introgression, and Agronomically Important Loci. Molecular Biology and Evolution, 2022, 39, .	8.9	50
10	Paternal Origins and Migratory Episodes of Domestic Sheep. Current Biology, 2020, 30, 4085-4095.e6.	3.9	49
11	Historical Introgression from Wild Relatives Enhanced Climatic Adaptation and Resistance to Pneumonia in Sheep. Molecular Biology and Evolution, 2021, 38, 838-855.	8.9	44
12	Local and global patterns of admixture and population structure in Iranian native cattle. BMC Genetics, 2016, 17, 108.	2.7	42
13	Pedigree analysis of Iran-Black sheep and inbreeding effects on growth and reproduction traits. Small Ruminant Research, 2014, 116, 14-20.	1.2	40
14	Estimates of phenotypic and genetic parameters for reproductive traits in Kermani sheep. Small Ruminant Research, 2010, 88, 27-31.	1.2	38
15	Whole-genome sequence analysis unveils different origins of European and Asiatic mouflon and domestication-related genes in sheep. Communications Biology, 2021, 4, 1307.	4.4	38
16	Identification of point mutations in exon 2 of GDF9 gene in Kermani sheep. Polish Journal of Veterinary Sciences, 2016, 19, 281-289.	0.2	37
17	Out of Southern East Asia of the Brown Rat Revealed by Large-Scale Genome Sequencing. Molecular Biology and Evolution, 2018, 35, 149-158.	8.9	36
18	Using microsatellite markers to analyze genetic diversity in 14 sheep types in Iran. Archives Animal Breeding, 2017, 60, 183-189.	1.4	34

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19	A directed search around caprine candidate loci provided evidence for microsatellites linkage to growth and cashmere yield in Rayini goats. Small Ruminant Research, 2009, 81, 146-151.	1.2	32
20	Association of bovine PPARGC1A and OPN genes with milk production and composition in Holstein cattle. Czech Journal of Animal Science, 2015, 60, 97-104.	1.3	32
21	Genetic analysis of ewe productivity traits in Moghani sheep. Small Ruminant Research, 2011, 96, 11-15.	1.2	30
22	A predictive assessment of genetic correlations between traits in chickens using markers. Genetics Selection Evolution, 2017, 49, 16.	3.0	30
23	Mutations in bone morphogenetic protein 15 and growth differentiation factor 9 genes are associated with increased litter size in fat-tailed sheep breeds. Veterinary Research Communications, 2011, 35, 157-167.	1.6	26
24	Polymorphism of the prolactin gene and its effect on fiber traits in goat. Russian Journal of Genetics, 2016, 52, 405-408.	0.6	26
25	The pattern of runs of homozygosity and genomic inbreeding in world-wide sheep populations. Genomics, 2021, 113, 1407-1415.	2.9	26
26	Quantitative trait loci for organ weights and adipose fat composition in Jersey and Limousin backâ€cross cattle finished on pasture or feedlot. Animal Genetics, 2010, 41, 589-596.	1.7	25
27	Genotyping of isolates of Clostridium perfringens from vaccinated and unvaccinated sheep. Small Ruminant Research, 2011, 95, 65-69.	1.2	24
28	Whole genome sequence analysis to detect signatures of positive selection for high fecundity in sheep. Reproduction in Domestic Animals, 2019, 54, 358-364.	1.4	23
29	Genomic and Phenotypic Analyses Reveal Mechanisms Underlying Homing Ability in Pigeon. Molecular Biology and Evolution, 2020, 37, 134-148.	8.9	23
30	Large-scale genomic analysis reveals the genetic cost of chicken domestication. BMC Biology, 2021, 19, 118.	3.8	22
31	Detection of breed-specific copy number variations in domestic chicken genome. Genome, 2018, 61, 7-14.	2.0	21
32	Quantitative trait loci for live animal and carcass composition traits in Jersey and Limousin backâ€cross cattle finished on pasture or feedlot. Animal Genetics, 2009, 40, 648-654.	1.7	20
33	A genome-wide scan to identify signatures of selection in two Iranian indigenous chicken ecotypes. Genetics Selection Evolution, 2021, 53, 72.	3.0	20
34	Whole-genome resequencing reveals selection signatures associated with milk production traits in African Kenana dairy zebu cattle. Genomics, 2020, 112, 880-885.	2.9	19
35	Prioritization for conservation of Iranian native cattle breeds based on genome-wide SNP data. Conservation Genetics, 2016, 17, 77-89.	1.5	16
36	Genetic mapping of quantitative trait loci affecting bodyweight on chromosome 1 in a commercial strain of Japanese quail. Animal Production Science, 2012, 52, 64.	1.3	15

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37	Maternal genomic variability of the wild boar (<i>Sus scrofa</i>) reveals the uniqueness of Eastâ€Caucasian and Central Italian populations. Ecology and Evolution, 2019, 9, 9467-9478.	1.9	15
38	Genetic diversity in Kermani sheep assessed from pedigree analysis. Small Ruminant Research, 2013, 114, 202-205.	1.2	14
39	Comparative population genomic analysis uncovers novel genomic footprints and genes associated with small body size in Chinese pony. BMC Genomics, 2020, 21, 496.	2.8	14
40	Quantitative trait loci underlying hatching weight and growth traits in an F2 intercross between two strains of Japanese quail. Animal Production Science, 2012, 52, 1012.	1.3	12
41	Quantitative Trait Loci Mapping Problem: An Extinction-Based Multi-Objective Evolutionary Algorithm Approach. Algorithms, 2013, 6, 546-564.	2.1	12
42	Identification of QTL for live weight and growth rate using DNA markers on chromosome 3 in an F2 population of Japanese quail. Molecular Biology Reports, 2014, 41, 1049-1057.	2.3	12
43	Genomic analysis reveals variant association with high altitude adaptation in native chickens. Scientific Reports, 2019, 9, 9224.	3.3	11
44	The evolutionary genetics of lactase persistence in seven ethnic groups across the Iranian plateau. Human Genomics, $2019,13,7.$	2.9	11
45	Genome-Wide Detection of Copy Number Variations and Their Association With Distinct Phenotypes in the World's Sheep. Frontiers in Genetics, 2021, 12, 670582.	2.3	11
46	Lambing season and fertility of fat-tailed ewes under an extensive production system are associated with liveweight and body condition around mating. Animal Production Science, 2009, 49, 1086.	1.3	11
47	Polymorphism of the Prolactin Gene and Its Effect on Fiber Traits in Goat. Russian Journal of Genetics, 2016, 52, 461-465.	0.4	11
48	Genetic mapping of quantitative trait loci for meat quality and muscle metabolic traits in cattle. Animal Genetics, 2011, 42, 592-599.	1.7	10
49	Comparative population genomics unveils candidate genes for athletic performance in Hanoverians. Genome, 2019, 62, 279-285.	2.0	10
50	Genetic diversity and signatures of selection for heat tolerance and immune response in Iranian native chickens. BMC Genomics, 2022, 23, 224.	2.8	10
51	Genetic structure of Iranian indigenous sheep breeds: insights for conservation. Tropical Animal Health and Production, 2020, 52, 2283-2290.	1.4	9
52	Genomes reveal selective sweeps in kiang and donkey for high-altitude adaptation. Zoological Research, 2021, 42, 450-460.	2.1	9
53	Potential dual expansion of domesticated donkeys revealed by worldwide analysis on mitochondrial sequences. Zoological Research, 2020, 41, 51-60.	2.1	9
54	Detection of candidate genes affecting milk production traits in sheep using wholeâ€genome sequencing analysis. Veterinary Medicine and Science, 2022, 8, 1197-1204.	1.6	9

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55	A partial genome scan to identify quantitative trait loci affecting birthweight in Kermani sheep. Small Ruminant Research, 2010, 94, 73-78.	1.2	7
56	Canine transmissible venereal tumor genome reveals ancient introgression from coyotes to pre-contact dogs in North America. Cell Research, 2019, 29, 592-595.	12.0	7
57	Genetic analysis of an F2 intercross between two strains of Japanese quail provided evidence for quantitative trait loci affecting carcass composition and internal organs. Molecular Biology Reports, 2014, 41, 4455-4462.	2.3	6
58	Whole genome resequencing of the Iranian native dogs and wolves to unravel variome during dog domestication. BMC Genomics, 2020, 21, 207.	2.8	6
59	Genomic Analyses Unveil Helmeted Guinea Fowl (<i>Numida meleagris</i>) Domestication in West Africa. Genome Biology and Evolution, 2021, 13, .	2.5	6
60	Fattening performance of purebred and crossbred lambs from fat-tailed Kurdi ewes mated to four Iranian native ram breeds. Tropical Animal Health and Production, 2012, 44, 217-223.	1.4	5
61	A chromosome-wide QTL mapping on chromosome 2 to identify loci affecting live weight and carcass traits in F2 population of Japanese quail. Czech Journal of Animal Science, 2016, 61, 290-297.	1.3	5
62	Mapping of genome-wide copy number variations in the Iranian indigenous cattle using a dense SNP data set. Animal Production Science, 2018, 58, 1192.	1,3	5
63	Mammary tissue transcriptomic analysis for construction of integrated regulatory networks involved in lactogenesis of Ovis aries. Genomics, 2020, 112, 4277-4287.	2.9	5
64	A molecular genome scan to identify DNA segments associated with live weight in Japanese quail. Molecular Biology Reports, 2016, 43, 1267-1272.	2.3	4
65	Use of Random Regression Test-Day Model to Estimate Genetic Parameters of Milk Yield in Holstein Cows. Open Journal of Animal Sciences, 2018, 08, 27-38.	0.6	4
66	Polymorphism of DMRT3 Gene and Its Association with Body Measurements in Horse Breeds. Russian Journal of Genetics, 2020, 56, 1232-1240.	0.6	4
67	Supplementation with whole cottonseed changes milk composition and milk fatty acid profile in dairy cows. Animal Production Science, 2011, 51, 95.	1.3	3
68	Effects of pre-incubation upside-down positioning of eggs from breeder flocks with different ages on hatchability and chick quality. Animal Production Science, 2012, 52, 269.	1.3	3
69	Wholeâ€genome sequence analysis reveals candidate genomic footprints and genes associated with reproductive traits in Thoroughbred horse. Reproduction in Domestic Animals, 2020, 55, 200-208.	1.4	3
70	Gene network analysis to determine the effect of hypoxia-associated genes on brain damages and tumorigenesis using an avian model. Journal of Genetic Engineering and Biotechnology, 2021, 19, 100.	3.3	2
71	Genome-wide DNA arrays profiling unravels the genetic structure of Iranian sheep and pattern of admixture with worldwide coarse-wool sheep breeds. Genomics, 2021, 113, 3501-3511.	2.9	2
72	Genetic Variation of Goat Interferon Regulatory Factor 3 Gene and Its Implication in Goat Evolution. PLoS ONE, 2016, 11, e0161962.	2.5	2

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73	Detection of a novel single nucleotide polymorphism in IGF2 gene with a negative impact on egg production and body weight in Japanese quail (Coturnix japonica). Journal of Genetic Engineering and Biotechnology, 2021, 19, 170.	3.3	2
74	Correction: Genetic diversity and signatures of selection for heat tolerance and immune response in Iranian native chickens. BMC Genomics, 2022, 23, .	2.8	2
75	Effects of QTL parameters and marker density on efficiency of Haley–Knott regression interval mapping of QTL with complex traits and use of artificial neural network for prediction of the efficiency of HK method in livestock. Journal of Applied Animal Research, 2012, 40, 247-255.	1.2	1
76	Genomeâ€scan analysis for genetic mapping of quantitative trait loci underlying birth weight and onset of puberty in doe kids (<i><scp>C</scp>apra hircus</i>). Animal Genetics, 2014, 45, 849-854.	1.7	1
77	Detection of chromosomal segments underlying scrotal circumference in ram lambs and age at onset of puberty in ewe lambs. Animal Production Science, 2015, 55, 1018.	1.3	1
78	Mitochondrial DNA sequence variation in Iranian native dogs. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2018, 29, 394-402.	0.7	1
79	Importance of genotype by environment interaction on genetic analysis of milk yield in Iranian Holstein cows using a random regression model. Animal Production Science, 2019, 59, 1438.	1.3	1
80	The lactase persistence allele $\hat{a} \in 22018$ G/A associated with body mass index in an Asian population. Gene Reports, 2020, 19, 100621.	0.8	1
81	Performance of pedigree and various forms of markerâ€derived relationship coefficients in genomic prediction and their correlations. Journal of Animal Breeding and Genetics, 2020, 137, 423-437.	2.0	1
82	Whole genome resequencing data sets of different species from Pistacia genus. BMC Research Notes, 2021, 14, 290.	1.4	1
83	Whole genome resequencing data for rock pigeon (Columba livia). BMC Research Notes, 2021, 14, 305.	1.4	1
84	Mapping Quantitative Trait Affecting Live Weight on Chromosome 5 in Japanese Quail. Research on Animal Production, 2018, 9, 111-118.	0.0	1
85	Genic and non-genic SNP contributions to additive and dominance genetic effects in purebred and crossbred pig traits. Scientific Reports, 2022, 12, 3795.	3.3	1
86	A Search for Eurasian Sheep Relationships: Genomic Assessment of the Autochthonous Sheep Breeds in Russia and the Persian Plateau. Diversity, 2022, 14, 445.	1.7	1
87	Genome resequencing data for Iranian local dogs and wolves. BMC Research Notes, 2020, 13, 436.	1.4	O
88	The Effects of Chicken Box, Chick Paper Type and Flock Age on Sound Level and Leg Abnormalities in One-Day Old Chicks in the Hatchery. Kahramanmaraş Sütçü İmam Üniversitesi Tarım Ve Doğa Derg 17, 41.	gis o.2 014,	0
89	Transcriptome resequencing data for rock pigeon (Columba livia). BMC Research Notes, 2022, 15, 121.	1.4	O