

Ali Esmailizadeh

List of Publications by Year in descending order

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Version: 2024-02-01

89
papers

1,834
citations

257450

24
h-index

330143

37
g-index

102
all docs

102
docs citations

102
times ranked

1875
citing authors

#	ARTICLE	IF	CITATIONS
1	Detection of candidate genes affecting milk production traits in sheep using whole-genome sequencing analysis. <i>Veterinary Medicine and Science</i> , 2022, 8, 1197-1204.	1.6	9
2	Transcriptome resequencing data for rock pigeon (<i>Columba livia</i>). <i>BMC Research Notes</i> , 2022, 15, 121.	1.4	0
3	Genic and non-genic SNP contributions to additive and dominance genetic effects in purebred and crossbred pig traits. <i>Scientific Reports</i> , 2022, 12, 3795.	3.3	1
4	Genetic diversity and signatures of selection for heat tolerance and immune response in Iranian native chickens. <i>BMC Genomics</i> , 2022, 23, 224.	2.8	10
5	Whole-Genome Resequencing of Worldwide Wild and Domestic Sheep Elucidates Genetic Diversity, Introgression, and Agronomically Important Loci. <i>Molecular Biology and Evolution</i> , 2022, 39, .	8.9	50
6	Correction: Genetic diversity and signatures of selection for heat tolerance and immune response in Iranian native chickens. <i>BMC Genomics</i> , 2022, 23, .	2.8	2
7	A Search for Eurasian Sheep Relationships: Genomic Assessment of the Autochthonous Sheep Breeds in Russia and the Persian Plateau. <i>Diversity</i> , 2022, 14, 445.	1.7	1
8	Historical Introgression from Wild Relatives Enhanced Climatic Adaptation and Resistance to Pneumonia in Sheep. <i>Molecular Biology and Evolution</i> , 2021, 38, 838-855.	8.9	44
9	Genomes reveal selective sweeps in kiang and donkey for high-altitude adaptation. <i>Zoological Research</i> , 2021, 42, 450-460.	2.1	9
10	Genome-Wide Detection of Copy Number Variations and Their Association With Distinct Phenotypes in the World's Sheep. <i>Frontiers in Genetics</i> , 2021, 12, 670582.	2.3	11
11	The pattern of runs of homozygosity and genomic inbreeding in world-wide sheep populations. <i>Genomics</i> , 2021, 113, 1407-1415.	2.9	26
12	Genomic Analyses Unveil Helmeted Guinea Fowl (<i>Numida meleagris</i>) Domestication in West Africa. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	6
13	Large-scale genomic analysis reveals the genetic cost of chicken domestication. <i>BMC Biology</i> , 2021, 19, 118.	3.8	22
14	Whole genome resequencing data sets of different species from <i>Pistacia</i> genus. <i>BMC Research Notes</i> , 2021, 14, 290.	1.4	1
15	Gene network analysis to determine the effect of hypoxia-associated genes on brain damages and tumorigenesis using an avian model. <i>Journal of Genetic Engineering and Biotechnology</i> , 2021, 19, 100.	3.3	2
16	Whole genome resequencing data for rock pigeon (<i>Columba livia</i>). <i>BMC Research Notes</i> , 2021, 14, 305.	1.4	1
17	A genome-wide scan to identify signatures of selection in two Iranian indigenous chicken ecotypes. <i>Genetics Selection Evolution</i> , 2021, 53, 72.	3.0	20
18	Genome-wide DNA arrays profiling unravels the genetic structure of Iranian sheep and pattern of admixture with worldwide coarse-wool sheep breeds. <i>Genomics</i> , 2021, 113, 3501-3511.	2.9	2

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19	Detection of a novel single nucleotide polymorphism in IGF2 gene with a negative impact on egg production and body weight in Japanese quail (<i>Coturnix japonica</i>). <i>Journal of Genetic Engineering and Biotechnology</i> , 2021, 19, 170.	3.3	2
20	Whole-genome sequence analysis unveils different origins of European and Asiatic mouflon and domestication-related genes in sheep. <i>Communications Biology</i> , 2021, 4, 1307.	4.4	38
21	Whole-genome resequencing reveals selection signatures associated with milk production traits in African Kenana dairy zebu cattle. <i>Genomics</i> , 2020, 112, 880-885.	2.9	19
22	Genomic and Phenotypic Analyses Reveal Mechanisms Underlying Homing Ability in Pigeon. <i>Molecular Biology and Evolution</i> , 2020, 37, 134-148.	8.9	23
23	Convergent genomic signatures of high-altitude adaptation among domestic mammals. <i>National Science Review</i> , 2020, 7, 952-963.	9.5	52
24	Paternal Origins and Migratory Episodes of Domestic Sheep. <i>Current Biology</i> , 2020, 30, 4085-4095.e6.	3.9	49
25	Genome resequencing data for Iranian local dogs and wolves. <i>BMC Research Notes</i> , 2020, 13, 436.	1.4	0
26	Comparative population genomic analysis uncovers novel genomic footprints and genes associated with small body size in Chinese pony. <i>BMC Genomics</i> , 2020, 21, 496.	2.8	14
27	Mammary tissue transcriptomic analysis for construction of integrated regulatory networks involved in lactogenesis of <i>Ovis aries</i> . <i>Genomics</i> , 2020, 112, 4277-4287.	2.9	5
28	The origin of domestication genes in goats. <i>Science Advances</i> , 2020, 6, eaaz5216.	10.3	86
29	The lactase persistence allele "22018 G/A associated with body mass index in an Asian population. <i>Gene Reports</i> , 2020, 19, 100621.	0.8	1
30	Whole-genome resequencing of wild and domestic sheep identifies genes associated with morphological and agronomic traits. <i>Nature Communications</i> , 2020, 11, 2815.	12.8	142
31	Whole genome resequencing of the Iranian native dogs and wolves to unravel variome during dog domestication. <i>BMC Genomics</i> , 2020, 21, 207.	2.8	6
32	Genetic structure of Iranian indigenous sheep breeds: insights for conservation. <i>Tropical Animal Health and Production</i> , 2020, 52, 2283-2290.	1.4	9
33	863 genomes reveal the origin and domestication of chicken. <i>Cell Research</i> , 2020, 30, 693-701.	12.0	144
34	Whole-genome sequence analysis reveals candidate genomic footprints and genes associated with reproductive traits in Thoroughbred horse. <i>Reproduction in Domestic Animals</i> , 2020, 55, 200-208.	1.4	3
35	Performance of pedigree and various forms of marker-derived relationship coefficients in genomic prediction and their correlations. <i>Journal of Animal Breeding and Genetics</i> , 2020, 137, 423-437.	2.0	1
36	Potential dual expansion of domesticated donkeys revealed by worldwide analysis on mitochondrial sequences. <i>Zoological Research</i> , 2020, 41, 51-60.	2.1	9

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37	Polymorphism of DMRT3 Gene and Its Association with Body Measurements in Horse Breeds. Russian Journal of Genetics, 2020, 56, 1232-1240.	0.6	4
38	Maternal genomic variability of the wild boar (<i>Sus scrofa</i>) reveals the uniqueness of East-Caucasian and Central Italian populations. Ecology and Evolution, 2019, 9, 9467-9478.	1.9	15
39	Genomic analysis reveals variant association with high altitude adaptation in native chickens. Scientific Reports, 2019, 9, 9224.	3.3	11
40	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
41	Whole genomes and transcriptomes reveal adaptation and domestication of pistachio. Genome Biology, 2019, 20, 79.	8.8	81
42	The evolutionary genetics of lactase persistence in seven ethnic groups across the Iranian plateau. Human Genomics, 2019, 13, 7.	2.9	11
43	Comparative population genomics unveils candidate genes for athletic performance in Hanoverians. Genome, 2019, 62, 279-285.	2.0	10
44	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
45	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
46	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
47	Mitochondrial DNA sequence variation in Iranian native dogs. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2018, 29, 394-402.	0.7	1
48	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
49	Detection of breed-specific copy number variations in domestic chicken genome. Genome, 2018, 61, 7-14.	2.0	21
50	AdaptMap: exploring goat diversity and adaptation. Genetics Selection Evolution, 2018, 50, 61.	3.0	70
51	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
52	Mapping Quantitative Trait Affecting Live Weight on Chromosome 5 in Japanese Quail. Research on Animal Production, 2018, 9, 111-118.	0.0	1
53	A predictive assessment of genetic correlations between traits in chickens using markers. Genetics Selection Evolution, 2017, 49, 16.	3.0	30
54	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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55	A chromosome-wide QTL mapping on chromosome 2 to identify loci affecting live weight and carcass traits in F2 population of Japanese quail. <i>Czech Journal of Animal Science</i> , 2016, 61, 290-297.	1.3	5
56	Polymorphism of the prolactin gene and its effect on fiber traits in goat. <i>Russian Journal of Genetics</i> , 2016, 52, 405-408.	0.6	26
57	Local and global patterns of admixture and population structure in Iranian native cattle. <i>BMC Genetics</i> , 2016, 17, 108.	2.7	42
58	Identification of point mutations in exon 2 of GDF9 gene in Kermani sheep. <i>Polish Journal of Veterinary Sciences</i> , 2016, 19, 281-289.	0.2	37
59	A molecular genome scan to identify DNA segments associated with live weight in Japanese quail. <i>Molecular Biology Reports</i> , 2016, 43, 1267-1272.	2.3	4
60	Prioritization for conservation of Iranian native cattle breeds based on genome-wide SNP data. <i>Conservation Genetics</i> , 2016, 17, 77-89.	1.5	16
61	Genetic Variation of Goat Interferon Regulatory Factor 3 Gene and Its Implication in Goat Evolution. <i>PLoS ONE</i> , 2016, 11, e0161962.	2.5	2
62	Polymorphism of the Prolactin Gene and Its Effect on Fiber Traits in Goat. <i>Russian Journal of Genetics</i> , 2016, 52, 461-465.	0.4	11
63	Detection of chromosomal segments underlying scrotal circumference in ram lambs and age at onset of puberty in ewe lambs. <i>Animal Production Science</i> , 2015, 55, 1018.	1.3	1
64	Association of bovine PPARGC1A and OPN genes with milk production and composition in Holstein cattle. <i>Czech Journal of Animal Science</i> , 2015, 60, 97-104.	1.3	32
65	Pedigree analysis of Iran-Black sheep and inbreeding effects on growth and reproduction traits. <i>Small Ruminant Research</i> , 2014, 116, 14-20.	1.2	40
66	Identification of QTL for live weight and growth rate using DNA markers on chromosome 3 in an F2 population of Japanese quail. <i>Molecular Biology Reports</i> , 2014, 41, 1049-1057.	2.3	12
67	Genome scan analysis for genetic mapping of quantitative trait loci underlying birth weight and onset of puberty in doe kids (<i>Capra hircus</i>). <i>Animal Genetics</i> , 2014, 45, 849-854.	1.7	1
68	Genetic analysis of an F2 intercross between two strains of Japanese quail provided evidence for quantitative trait loci affecting carcass composition and internal organs. <i>Molecular Biology Reports</i> , 2014, 41, 4455-4462.	2.3	6
69	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. <i>Kahramanmaraş Sırtakırmam Üniversitesi Tarım Ve Doğa Dergisi</i> , 2014, 17, 41.		0
70	Genetic diversity in Kermani sheep assessed from pedigree analysis. <i>Small Ruminant Research</i> , 2013, 114, 202-205.	1.2	14
71	Quantitative Trait Loci Mapping Problem: An Extinction-Based Multi-Objective Evolutionary Algorithm Approach. <i>Algorithms</i> , 2013, 6, 546-564.	2.1	12
72	Genetic mapping of quantitative trait loci affecting bodyweight on chromosome 1 in a commercial strain of Japanese quail. <i>Animal Production Science</i> , 2012, 52, 64.	1.3	15

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73	Quantitative trait loci underlying hatching weight and growth traits in an F2 intercross between two strains of Japanese quail. <i>Animal Production Science</i> , 2012, 52, 1012.	1.3	12
74	Effects of pre-incubation upside-down positioning of eggs from breeder flocks with different ages on hatchability and chick quality. <i>Animal Production Science</i> , 2012, 52, 269.	1.3	3
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. <i>Journal of Applied Animal Research</i> , 2012, 40, 247-255.	1.2	1
76	Fattening performance of purebred and crossbred lambs from fat-tailed Kurdi ewes mated to four Iranian native ram breeds. <i>Tropical Animal Health and Production</i> , 2012, 44, 217-223.	1.4	5
77	Genetic mapping of quantitative trait loci for meat quality and muscle metabolic traits in cattle. <i>Animal Genetics</i> , 2011, 42, 592-599.	1.7	10
78	Genotyping of isolates of <i>Clostridium perfringens</i> from vaccinated and unvaccinated sheep. <i>Small Ruminant Research</i> , 2011, 95, 65-69.	1.2	24
79	Genetic analysis of ewe productivity traits in Moghani sheep. <i>Small Ruminant Research</i> , 2011, 96, 11-15.	1.2	30
80	Mutations in bone morphogenetic protein 15 and growth differentiation factor 9 genes are associated with increased litter size in fat-tailed sheep breeds. <i>Veterinary Research Communications</i> , 2011, 35, 157-167.	1.6	26
81	Supplementation with whole cottonseed changes milk composition and milk fatty acid profile in dairy cows. <i>Animal Production Science</i> , 2011, 51, 95.	1.3	3
82	Estimates of phenotypic and genetic parameters for reproductive traits in Kermani sheep. <i>Small Ruminant Research</i> , 2010, 88, 27-31.	1.2	38
83	Quantitative genetic analysis of growth traits and Kleiber ratios in Sanjabi sheep. <i>Small Ruminant Research</i> , 2010, 93, 88-93.	1.2	50
84	A partial genome scan to identify quantitative trait loci affecting birthweight in Kermani sheep. <i>Small Ruminant Research</i> , 2010, 94, 73-78.	1.2	7
85	Quantitative trait loci for organ weights and adipose fat composition in Jersey and Limousin backcross cattle finished on pasture or feedlot. <i>Animal Genetics</i> , 2010, 41, 589-596.	1.7	25
86	A directed search around caprine candidate loci provided evidence for microsatellites linkage to growth and cashmere yield in Rayini goats. <i>Small Ruminant Research</i> , 2009, 81, 146-151.	1.2	32
87	Quantitative trait loci for live animal and carcass composition traits in Jersey and Limousin backcross cattle finished on pasture or feedlot. <i>Animal Genetics</i> , 2009, 40, 648-654.	1.7	20
88	Lambing season and fertility of fat-tailed ewes under an extensive production system are associated with liveweight and body condition around mating. <i>Animal Production Science</i> , 2009, 49, 1086.	1.3	11
89	Effects of the myostatin F94L substitution on beef traits ¹ . <i>Journal of Animal Science</i> , 2008, 86, 1038-1046.	0.5	70