

Francesca Bertolini

List of Publications by Year in descending order

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Version: 2024-02-01

80
papers

1,724
citations

279487

23
h-index

344852

36
g-index

83
all docs

83
docs citations

83
times ranked

1961
citing authors

#	ARTICLE	IF	CITATIONS
1	Signatures of selection and environmental adaptation across the goat genome post-domestication. <i>Genetics Selection Evolution</i> , 2018, 50, 57.	1.2	114
2	Genome-wide SNP profiling of worldwide goat populations reveals strong partitioning of diversity and highlights post-domestication migration routes. <i>Genetics Selection Evolution</i> , 2018, 50, 58.	1.2	87
3	Genome-wide patterns of homozygosity provide clues about the population history and adaptation of goats. <i>Genetics Selection Evolution</i> , 2018, 50, 59.	1.2	76
4	AdaptMap: exploring goat diversity and adaptation. <i>Genetics Selection Evolution</i> , 2018, 50, 61.	1.2	70
5	A Next Generation Semiconductor Based Sequencing Approach for the Identification of Meat Species in DNA Mixtures. <i>PLoS ONE</i> , 2015, 10, e0121701.	1.1	58
6	Genome-wide association studies for 30 haematological and blood clinical-biochemical traits in Large White pigs reveal genomic regions affecting intermediate phenotypes. <i>Scientific Reports</i> , 2019, 9, 7003.	1.6	55
7	Evidence of selection signatures that shape the Persian cat breed. <i>Mammalian Genome</i> , 2016, 27, 144-155.	1.0	50
8	Application of next generation semiconductor based sequencing to detect the botanical composition of monofloral, polyfloral and honeydew honey. <i>Food Control</i> , 2018, 86, 342-349.	2.8	47
9	Shotgun metagenomics of honey DNA: Evaluation of a methodological approach to describe a multi-kingdom honey bee derived environmental DNA signature. <i>PLoS ONE</i> , 2018, 13, e0205575.	1.1	46
10	Detection of Selection Signatures Among Brazilian, Sri Lankan, and Egyptian Chicken Populations Under Different Environmental Conditions. <i>Frontiers in Genetics</i> , 2018, 9, 737.	1.1	46
11	The Valdostana goat: a genome-wide investigation of the distinctiveness of its selective sweep regions. <i>Mammalian Genome</i> , 2017, 28, 114-128.	1.0	43
12	Application of next generation semiconductor based sequencing for species identification in dairy products. <i>Food Chemistry</i> , 2018, 246, 90-98.	4.2	42
13	Combined use of principal component analysis and random forests identify population-informative single nucleotide polymorphisms: application in cattle breeds. <i>Journal of Animal Breeding and Genetics</i> , 2015, 132, 346-356.	0.8	38
14	A machine learning approach for the identification of population-informative markers from high-throughput genotyping data: application to several pig breeds. <i>Animal</i> , 2020, 14, 223-232.	1.3	37
15	Comparative evaluation of genomic inbreeding parameters in seven commercial and autochthonous pig breeds. <i>Animal</i> , 2020, 14, 910-920.	1.3	36
16	The albinism of the feral Asinara white donkeys (<i>Equus asinus</i>) is determined by a missense mutation in a highly conserved position of the tyrosinase (<i>TYR</i>) gene deduced protein. <i>Animal Genetics</i> , 2016, 47, 120-124.	0.6	34
17	Patterns of homozygosity in insular and continental goat breeds. <i>Genetics Selection Evolution</i> , 2018, 50, 56.	1.2	33
18	Natural Selection Footprints Among African Chicken Breeds and Village Ecotypes. <i>Frontiers in Genetics</i> , 2019, 10, 376.	1.1	32

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19	The genome-wide structure of two economically important indigenous Sicilian cattle breeds1. Journal of Animal Science, 2014, 92, 4833-4842.	0.2	31
20	Entomological signatures in honey: an environmental DNA metabarcoding approach can disclose information on plant-sucking insects in agricultural and forest landscapes. Scientific Reports, 2018, 8, 9996.	1.6	31
21	Copy number variants in Italian Large White pigs detected using high-density single nucleotide polymorphisms and their association with back fat thickness. Animal Genetics, 2014, 45, 745-749.	0.6	27
22	Detection of Co-expressed Pathway Modules Associated With Mineral Concentration and Meat Quality in Nelore Cattle. Frontiers in Genetics, 2019, 10, 210.	1.1	27
23	Preselection statistics and Random Forest classification identify population informative single nucleotide polymorphisms in cosmopolitan and autochthonous cattle breeds. Animal, 2018, 12, 12-19.	1.3	25
24	Genome-wide association studies of inflammatory bowel disease in German shepherd dogs. PLoS ONE, 2018, 13, e0200685.	1.1	25
25	Novel screening assay for antioxidant protection against peroxy radical-induced loss of protein function. Journal of Pharmaceutical Sciences, 2007, 96, 2931-2944.	1.6	23
26	Innovative treatments for severe refractory asthma: how to choose the right option for the right patient?. Journal of Asthma and Allergy, 2017, Volume10, 237-247.	1.5	23
27	Analysis of Association Between the <i>MUC4</i> G.8227C>G Polymorphism and Production Traits in Italian Heavy Pigs Using a Selective Genotyping Approach. Animal Biotechnology, 2012, 23, 147-155.	0.7	22
28	Severe refractory asthma: current treatment options and ongoing research. Drugs in Context, 2018, 7, 1-15.	1.0	22
29	Precision Medicine in Targeted Therapies for Severe Asthma: Is There Any Place for "Omics" Technology?. BioMed Research International, 2018, 2018, 1-15.	0.9	21
30	Runs of homozygosity islands in Italian cosmopolitan and autochthonous pig breeds identify selection signatures in the porcine genome. Livestock Science, 2020, 240, 104219.	0.6	21
31	Differential impacts of carp and salmon pituitary extracts on induced oogenesis, egg quality, molecular ontogeny and embryonic developmental competence in European eel. PLoS ONE, 2020, 15, e0235617.	1.1	19
32	Next Generation Semiconductor Based Sequencing of the Donkey (<i>Equus asinus</i>) Genome Provided Comparative Sequence Data against the Horse Genome and a Few Millions of Single Nucleotide Polymorphisms. PLoS ONE, 2015, 10, e0131925.	1.1	18
33	Deconstructing the pig sex metabolome: Targeted metabolomics in heavy pigs revealed sexual dimorphisms in plasma biomarkers and metabolic pathways1. Journal of Animal Science, 2015, 93, 5681-5693.	0.2	17
34	A genomic landscape of mitochondrial DNA insertions in the pig nuclear genome provides evolutionary signatures of interspecies admixture. DNA Research, 2017, 24, 487-498.	1.5	17
35	Taking advantage from phenotype variability in a local animal genetic resource: identification of genomic regions associated with the hairless phenotype in Casertana pigs. Animal Genetics, 2018, 49, 321-325.	0.6	17
36	Genomic Analysis Suggests KITLG is Responsible for a Roan Pattern in two Pakistani Goat Breeds. Journal of Heredity, 2018, 109, 315-319.	1.0	17

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37	Twenty years of artificial directional selection have shaped the genome of the Italian Large White pig breed. <i>Animal Genetics</i> , 2016, 47, 181-191.	0.6	16
38	Genome-wide association studies for seven production traits highlight genomic regions useful to dissect dry-cured ham quality and production traits in Duroc heavy pigs. <i>Animal</i> , 2018, 12, 1777-1784.	1.3	16
39	Application of next generation semiconductor based sequencing for species identification and analysis of within-species mitotypes useful for authentication of meat derived products. <i>Food Control</i> , 2018, 91, 58-67.	2.8	16
40	Performance thresholds of hatchery produced European eel larvae reared at different salinity regimes. <i>Aquaculture</i> , 2021, 539, 736651.	1.7	16
41	Polymorphisms in an obesity-related gene (PCSK1) are associated with fat deposition and production traits in Italian heavy pigs. <i>Animal</i> , 2012, 6, 1913-1924.	1.3	15
42	The TBC1D1 Gene. <i>Vitamins and Hormones</i> , 2013, 91, 77-95.	0.7	15
43	A next generation sequencing approach for targeted Varroa destructor (Acari: Varroidae) mitochondrial DNA analysis based on honey derived environmental DNA. <i>Journal of Invertebrate Pathology</i> , 2019, 161, 47-53.	1.5	15
44	High-throughput SNP discovery in the rabbit (<i>Oryctolagus cuniculus</i>) genome by next-generation semiconductor based sequencing. <i>Animal Genetics</i> , 2014, 45, 304-307.	0.6	14
45	Next generation semiconductor based sequencing of bitter taste receptor genes in different pig populations and association analysis using a selective DNA pool-seq approach. <i>Animal Genetics</i> , 2017, 48, 97-102.	0.6	14
46	Genome-wide association study for the level of serum electrolytes in Italian Large White pigs. <i>Animal Genetics</i> , 2016, 47, 597-602.	0.6	13
47	Genomic investigation of piglet resilience following porcine epidemic diarrhea outbreaks. <i>Animal Genetics</i> , 2017, 48, 228-232.	0.6	13
48	Reduced Representation Libraries from DNA Pools Analysed with Next Generation Semiconductor Based-Sequencing to Identify SNPs in Extreme and Divergent Pigs for Back Fat Thickness. <i>International Journal of Genomics</i> , 2015, 2015, 1-8.	0.8	12
49	Genome-wide association analyses for several exterior traits in the autochthonous Casertana pig breed. <i>Livestock Science</i> , 2019, 230, 103842.	0.6	12
50	Comparative selection signature analyses identify genomic footprints in Reggiana cattle, the traditional breed of the Parmigiano-Reggiano cheese production system. <i>Animal</i> , 2020, 14, 921-932.	1.3	12
51	Next Generation Semiconductor Based-Sequencing of a Nutrigenetics Target Gene (GPR120) and Association with Growth Rate in Italian Large White Pigs. <i>Animal Biotechnology</i> , 2015, 26, 92-97.	0.7	11
52	Whole genome semiconductor based sequencing of farmed European sea bass (<i>Dicentrarchus labrax</i>) Mediterranean genetic stocks using a DNA pooling approach. <i>Marine Genomics</i> , 2016, 28, 63-70.	0.4	11
53	Evaluation of SNP Genotyping in Alpacas Using the Bovine HD Genotyping Beadchip. <i>Frontiers in Genetics</i> , 2019, 10, 361.	1.1	11
54	The porcine tribbles homolog 3 (TRIB3) gene: Identification of a missense mutation and association analysis with meat quality and production traits in Italian heavy pigs. <i>Meat Science</i> , 2010, 86, 808-813.	2.7	10

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55	The MC4R c.893G>A mutation: A marker for growth and leanness associated with boar taint odour in Belgian pig breeds. <i>Meat Science</i> , 2015, 101, 1-4.	2.7	10
56	A viral metagenomic approach on a non-metagenomic experiment: Mining next generation sequencing datasets from pig DNA identified several porcine parvoviruses for a retrospective evaluation of viral infections. <i>PLoS ONE</i> , 2017, 12, e0179462.	1.1	9
57	Genome-wide association studies for the number of teats and teat asymmetry patterns in Large White pigs. <i>Animal Genetics</i> , 2020, 51, 595-600.	0.6	9
58	Towards precision medicine: The application of omics technologies in asthma management. <i>F1000Research</i> , 2018, 7, 423.	0.8	9
59	Looking at genetic structure and selection signatures of the Mexican chicken population using single nucleotide polymorphism markers. <i>Poultry Science</i> , 2018, 97, 791-802.	1.5	8
60	Exploring gastric bacterial community in young pigs. <i>PLoS ONE</i> , 2017, 12, e0173029.	1.1	8
61	Exploiting phenotype diversity in a local animal genetic resource: Identification of a single nucleotide polymorphism associated with the tail shape phenotype in the autochthonous Casertana pig breed. <i>Livestock Science</i> , 2018, 216, 148-152.	0.6	7
62	Identification of a major locus determining a pigmentation defect in cultivated gilthead seabream (<i>Sparus aurata</i>). <i>Journal of Heredity</i> , 2017, 108, 100-108.	0.6	6
63	Signatures of selection are present in the genome of two close autochthonous cattle breeds raised in the North of Italy and mainly distinguished for their coat colours. <i>Journal of Animal Breeding and Genetics</i> , 2021, , .	0.8	6
64	Few mitochondrial DNA sequences are inserted into the turkey (<i>Meleagris gallopavo</i>). <i>Animal Genetics</i> , 2018, 49, 259-264.	0.6	5
65	Taxonomic identification of Madagascar's free-ranging forest cats. <i>Conservation Genetics</i> , 2020, 21, 443-451.	0.8	5
66	Investigation of gut microbiome association with inflammatory bowel disease and depression: a machine learning approach. <i>F1000Research</i> , 0, 7, 702.	0.8	5
67	Comparative genomics and signatures of selection in North Atlantic eels. <i>Marine Genomics</i> , 2022, 62, 100933.	0.4	5
68	Genomic investigation of porcine periweaning failure to thrive syndrome (PFTS). <i>Veterinary Record</i> , 2018, 183, 95-95.	0.2	4
69	Marker discovery and associations with β -carotene content in Indian dairy cattle and buffalo breeds. <i>Journal of Dairy Science</i> , 2019, 102, 10039-10055.	1.4	3
70	Candidate gene markers associated with production, carcass and meat quality traits in Italian Large White pigs identified using a selective genotyping approach. <i>Livestock Science</i> , 2020, 240, 104145.	0.6	3
71	Genome-wide association studies for iris pigmentation and heterochromia patterns in Large White pigs. <i>Animal Genetics</i> , 2020, 51, 409-419.	0.6	3
72	Estimating breed composition for pigs: A case study focused on Mangalitsa pigs and two methods. <i>Livestock Science</i> , 2021, 244, 104398.	0.6	3

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73	A comparative whole genome sequencing analysis identified a candidate locus for lack of operculum in cultivated gilthead seabream (<i>Sparus aurata</i>). <i>Animal Genetics</i> , 2021, 52, 365-370.	0.6	3
74	Unravelling the changes during induced vitellogenesis in female European eel through RNA-Seq: What happens to the liver?. <i>PLoS ONE</i> , 2020, 15, e0236438.	1.1	2
75	CO2 induced seawater acidification impacts survival and development of European eel embryos. <i>PLoS ONE</i> , 2022, 17, e0267228.	1.1	2
76	Signatures of Selection and Genomic Diversity of Muskellunge (<i>Esox masquinongy</i>) from Two Populations in North America. <i>Genes</i> , 2021, 12, 1021.	1.0	0
77	Title is missing!. , 2020, 15, e0236438.		0
78	Title is missing!. , 2020, 15, e0236438.		0
79	Title is missing!. , 2020, 15, e0236438.		0
80	Title is missing!. , 2020, 15, e0236438.		0