

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	Comparative genomics and signatures of selection in North Atlantic eels. <i>Marine Genomics</i> , 2022, 62, 100933.	0.4	5
2	CO2 induced seawater acidification impacts survival and development of European eel embryos. <i>PLoS ONE</i> , 2022, 17, e0267228.	1.1	2
3	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
4	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
5	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
6	Performance thresholds of hatchery produced European eel larvae reared at different salinity regimes. <i>Aquaculture</i> , 2021, 539, 736651.	1.7	16
7	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
8	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
9	Comparative evaluation of genomic inbreeding parameters in seven commercial and autochthonous pig breeds. <i>Animal</i> , 2020, 14, 910-920.	1.3	36
10	Identification of a major locus determining a pigmentation defect in cultivated gilthead seabream (<i>Sparus aurata</i>). <i>PLoS ONE</i> , 2020, 15, e0236438.	0.6	6
11	Runs of homozygosity islands in Italian cosmopolitan and autochthonous pig breeds identify selection signatures in the porcine genome. <i>Livestock Science</i> , 2020, 240, 104219.	0.6	21
12	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
13	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
14	Differential impacts of carp and salmon pituitary extracts on induced oogenesis, egg quality, molecular ontogeny and embryonic developmental competence in European eel. <i>PLoS ONE</i> , 2020, 15, e0235617.	1.1	19
15	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
16	Taxonomic identification of Madagascar's free-ranging 'forest cats'. <i>Conservation Genetics</i> , 2020, 21, 443-451.	0.8	5
17	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
18	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

#	ARTICLE	IF	CITATIONS
19	Title is missing!. , 2020, 15, e0236438.		0
20	Title is missing!. , 2020, 15, e0236438.		0
21	Title is missing!. , 2020, 15, e0236438.		0
22	Title is missing!. , 2020, 15, e0236438.		0
23	Genome-wide association analyses for several exterior traits in the autochthonous Casertana pig breed. <i>Livestock Science</i> , 2019, 230, 103842.	0.6	12
24	Marker discovery and associations with \hat{I}^2 -carotene content in Indian dairy cattle and buffalo breeds. <i>Journal of Dairy Science</i> , 2019, 102, 10039-10055.	1.4	3
25	A next generation sequencing approach for targeted <i>Varroa destructor</i> (Acari: Varroidae) mitochondrial DNA analysis based on honey derived environmental DNA. <i>Journal of Invertebrate Pathology</i> , 2019, 161, 47-53.	1.5	15
26	Evaluation of SNP Genotyping in Alpacas Using the Bovine HD Genotyping Beadchip. <i>Frontiers in Genetics</i> , 2019, 10, 361.	1.1	11
27	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
28	Natural Selection Footprints Among African Chicken Breeds and Village Ecotypes. <i>Frontiers in Genetics</i> , 2019, 10, 376.	1.1	32
29	Detection of Co-expressed Pathway Modules Associated With Mineral Concentration and Meat Quality in Nelore Cattle. <i>Frontiers in Genetics</i> , 2019, 10, 210.	1.1	27
30	Few mitochondrial <sc>DNA</sc> sequences are inserted into the turkey (<i>Meleagris</i> Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 307 Td <i>Animal Genetics</i> , 2018, 49, 259-264.	0.6	5
31	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
32	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
33	Taking advantage from phenotype variability in a local animal genetic resource: identification of genomic regions associated with the hairless phenotype in Casertana pigs. <i>Animal Genetics</i> , 2018, 49, 321-325.	0.6	17
34	Genomic investigation of porcine periweaning failure to thrive syndrome (PFTS). <i>Veterinary Record</i> , 2018, 183, 95-95.	0.2	4
35	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
36	Preselection statistics and Random Forest classification identify population informative single nucleotide polymorphisms in cosmopolitan and autochthonous cattle breeds. <i>Animal</i> , 2018, 12, 12-19.	1.3	25

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37	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
38	Application of next generation semiconductor based sequencing for species identification in dairy products. <i>Food Chemistry</i> , 2018, 246, 90-98.	4.2	42
39	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
40	Signatures of selection and environmental adaptation across the goat genome post-domestication. <i>Genetics Selection Evolution</i> , 2018, 50, 57.	1.2	114
41	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
42	Patterns of homozygosity in insular and continental goat breeds. <i>Genetics Selection Evolution</i> , 2018, 50, 56.	1.2	33
43	AdaptMap: exploring goat diversity and adaptation. <i>Genetics Selection Evolution</i> , 2018, 50, 61.	1.2	70
44	Severe refractory asthma: current treatment options and ongoing research. <i>Drugs in Context</i> , 2018, 7, 1-15.	1.0	22
45	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
46	Genome-wide association studies of inflammatory bowel disease in German shepherd dogs. <i>PLoS ONE</i> , 2018, 13, e0200685.	1.1	25
47	Precision Medicine in Targeted Therapies for Severe Asthma: Is There Any Place for "Omics" Technology?. <i>BioMed Research International</i> , 2018, 2018, 1-15.	0.9	21
48	Entomological signatures in honey: an environmental DNA metabarcoding approach can disclose information on plant-sucking insects in agricultural and forest landscapes. <i>Scientific Reports</i> , 2018, 8, 9996.	1.6	31
49	Genomic Analysis Suggests KITLG is Responsible for a Roan Pattern in two Pakistani Goat Breeds. <i>Journal of Heredity</i> , 2018, 109, 315-319.	1.0	17
50	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
51	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
52	Towards precision medicine: The application of omics technologies in asthma management. <i>F1000Research</i> , 2018, 7, 423.	0.8	9
53	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
54	A genomic landscape of mitochondrial DNA insertions in the pig nuclear genome provides evolutionary signatures of interspecies admixture. <i>DNA Research</i> , 2017, 24, 487-498.	1.5	17

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55	Genomic investigation of piglet resilience following porcine epidemic diarrhea outbreaks. <i>Animal Genetics</i> , 2017, 48, 228-232.	0.6	13
56	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
57	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
58	Innovative treatments for severe refractory asthma: how to choose the right option for the right patient?. <i>Journal of Asthma and Allergy</i> , 2017, Volume10, 237-247.	1.5	23
59	Exploring gastric bacterial community in young pigs. <i>PLoS ONE</i> , 2017, 12, e0173029.	1.1	8
60	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
61	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
62	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
63	Evidence of selection signatures that shape the Persian cat breed. <i>Mammalian Genome</i> , 2016, 27, 144-155.	1.0	50
64	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
65	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
66	Deconstructing the pig sex metabolome: Targeted metabolomics in heavy pigs revealed sexual dimorphisms in plasma biomarkers and metabolic pathways1. <i>Journal of Animal Science</i> , 2015, 93, 5681-5693.	0.2	17
67	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. <i>PLoS ONE</i> , 2015, 10, e0131925.	1.1	18
68	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
69	Next Generation Semiconductor Based-Sequencing of a Nutrigenetics Target Gene (<i>GPR120</i>) and Association with Growth Rate in Italian Large White Pigs. <i>Animal Biotechnology</i> , 2015, 26, 92-97.	0.7	11
70	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
71	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
72	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

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73	The genome-wide structure of two economically important indigenous Sicilian cattle breeds1. Journal of Animal Science, 2014, 92, 4833-4842.	0.2	31
74	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
75	The TBC1D1 Gene. Vitamins and Hormones, 2013, 91, 77-95.	0.7	15
76	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
77	Polymorphisms in an obesity-related gene (PCSK1) are associated with fat deposition and production traits in Italian heavy pigs. Animal, 2012, 6, 1913-1924.	1.3	15
78	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. Meat Science, 2010, 86, 808-813.	2.7	10
79	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
80	Investigation of gut microbiome association with inflammatory bowel disease and depression: a machine learning approach. F1000Research, 0, 7, 702.	0.8	5