

Luca Fontanesi

List of Publications by Year in descending order

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Version: 2024-02-01

251
papers

5,635
citations

81743

39
h-index

133063

59
g-index

256
all docs

256
docs citations

256
times ranked

4558
citing authors

#	ARTICLE	IF	CITATIONS
1	Entomological authentication of honey based on a DNA method that distinguishes <i>Apis mellifera</i> mitochondrial C mitotypes: Application to honey produced by <i>A. m. ligustica</i> and <i>A. m. carnica</i> . <i>Food Control</i> , 2022, 134, 108713.	2.8	9
2	Genomic diversity and signatures of selection in meat and fancy rabbit breeds based on high-density marker data. <i>Genetics Selection Evolution</i> , 2022, 54, 3.	1.2	8
3	Exploiting single-marker and haplotype-based genome-wide association studies to identify QTL for the number of teats in Italian Duroc pigs. <i>Livestock Science</i> , 2022, 257, 104849.	0.6	2
4	Mining livestock genome datasets for an unconventional characterization of animal DNA viromes. <i>Genomics</i> , 2022, 114, 110312.	1.3	7
5	One Health and Cattle Genetic Resources: Mining More than 500 Cattle Genomes to Identify Variants in Candidate Genes Potentially Affecting Coronavirus Infections. <i>Animals</i> , 2022, 12, 838.	1.0	1
6	Comparative analysis of inbreeding parameters and runs of homozygosity islands in 2 Italian autochthonous cattle breeds mainly raised in the Parmigiano-Reggiano cheese production region. <i>Journal of Dairy Science</i> , 2022, 105, 2408-2425.	1.4	8
7	Honey Environmental DNA Can Be Used to Detect and Monitor Honey Bee Pests: Development of Methods Useful to Identify <i>Aethina tumida</i> and <i>Galleria mellonella</i> Infestations. <i>Veterinary Sciences</i> , 2022, 9, 213.	0.6	3
8	Admixture and breed traceability in European indigenous pig breeds and wild boar using genome-wide SNP data. <i>Scientific Reports</i> , 2022, 12, 7346.	1.6	11
9	Nuclear mitochondrial DNA sequences in the rabbit genome. <i>Mitochondrion</i> , 2022, 66, 1-6.	1.6	2
10	Association between candidate gene markers and harness racing traits in Italian trotter horses. <i>Livestock Science</i> , 2021, 244, 104351.	0.6	2
11	A genome-wide association study for the number of teats in European rabbits (<i>Oryctolagus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.6	10
12	Genetics and molecular genetics of morphological and physiological traits and inherited disorders in the European rabbit.. , 2021, , 120-162.		2
13	Rabbit Genetic Resources Can Provide Several Animal Models to Explain at the Genetic Level the Diversity of Morphological and Physiological Relevant Traits. <i>Applied Sciences (Switzerland)</i> , 2021, 11, 373.	1.3	8
14	Describing variability in the tyrosinase (<i>TYR</i>) gene, the <i>albino</i> coat colour locus, in domestic and wild European rabbits. <i>Italian Journal of Animal Science</i> , 2021, 20, 181-187.	0.8	7
15	Redefinition of the Mora Romagnola Pig Breed Herd Book Standard Based on DNA Markers Useful to Authenticate Its "Mono-Breed" Products: An Example of Sustainable Conservation of a Livestock Genetic Resource. <i>Animals</i> , 2021, 11, 526.	1.0	14
16	Describing variability in pig genes involved in coronavirus infections for a One Health perspective in conservation of animal genetic resources. <i>Scientific Reports</i> , 2021, 11, 3359.	1.6	9
17	Runs of homozygosity provide a genome landscape picture of inbreeding and genetic history of European autochthonous and commercial pig breeds. <i>Animal Genetics</i> , 2021, 52, 155-170.	0.6	26
18	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

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19	Muscle Transcriptome Analysis Reveals Molecular Pathways Related to Oxidative Phosphorylation, Antioxidant Defense, Fatness and Growth in Mangalitsa and Moravka Pigs. <i>Animals</i> , 2021, 11, 844.	1.0	7
20	Single-marker and haplotype-based genome-wide association studies for the number of teats in two heavy pig breeds. <i>Animal Genetics</i> , 2021, 52, 440-450.	0.6	10
21	Exploiting within-breed variability in the autochthonous Reggiana breed identified several candidate genes affecting pigmentation-related traits, stature and udder defects in cattle. <i>Animal Genetics</i> , 2021, 52, 579-597.	0.6	5
22	Distribution of the Main <i>Apis mellifera</i> Mitochondrial DNA Lineages in Italy Assessed Using an Environmental DNA Approach. <i>Insects</i> , 2021, 12, 620.	1.0	10
23	Analysis of honey environmental DNA indicates that the honey bee (<i>Apis mellifera</i> L.) trypanosome parasite <i>Lotmaria passim</i> is widespread in the apiaries of the North of Italy. <i>Journal of Invertebrate Pathology</i> , 2021, 184, 107628.	1.5	14
24	Application of Next Generation Semiconductor-Based Sequencing for the Identification of <i>Apis mellifera</i> Complementary Sex Determiner (<i>csd</i>) Alleles from Honey DNA. <i>Insects</i> , 2021, 12, 868.	1.0	3
25	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
26	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
27	Genomic regions influencing intramuscular fat in divergently selected rabbit lines. <i>Animal Genetics</i> , 2020, 51, 58-69.	0.6	21
28	A genomewide association study in divergently selected lines in rabbits reveals novel genomic regions associated with litter size traits. <i>Journal of Animal Breeding and Genetics</i> , 2020, 137, 123-138.	0.8	12
29	Comparative evaluation of genomic inbreeding parameters in seven commercial and autochthonous pig breeds. <i>Animal</i> , 2020, 14, 910-920.	1.3	36
30	Targeted metabolomic profiles of piglet plasma reveal physiological changes over the suckling period. <i>Livestock Science</i> , 2020, 231, 103890.	0.6	4
31	Microscopic ossicle analyses and the complete mitochondrial genome sequence of <i>Holothuria (Roweothuria) polii</i> (Echinodermata; Holothuroidea) provide new information to support the phylogenetic positioning of this sea cucumber species. <i>Marine Genomics</i> , 2020, 51, 100735.	0.4	7
32	Identification of a major locus determining a pigmentation defect in cultivated gilthead seabream (<i>Sparus aurata</i>). <i>Genetics</i> , 2020, 216, 1000000.	0.6	6
33	A comparative genome landscape of mitochondrial DNA insertions into two cattle nuclear genome versions. <i>Animal Genetics</i> , 2020, 51, 149-151.	0.6	2
34	Effects of 17 performance, carcass and raw ham quality parameters on ham weight loss at first salting in heavy pigs, a meat quality indicator for the production of high quality dry-cured hams. <i>Meat Science</i> , 2020, 162, 108012.	2.7	8
35	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
36	Known loci in the <i>KIT</i> and <i>TYR</i> genes do not explain the depigmented white coat colour of Austro-Hungarian Baroque donkey. <i>Italian Journal of Animal Science</i> , 2020, 19, 739-743.	0.8	1

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37	Honey as a Source of Environmental DNA for the Detection and Monitoring of Honey Bee Pathogens and Parasites. <i>Veterinary Sciences</i> , 2020, 7, 113.	0.6	21
38	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
39	Shotgun sequencing of honey DNA can describe honey bee derived environmental signatures and the honey bee hologenome complexity. <i>Scientific Reports</i> , 2020, 10, 9279.	1.6	41
40	Genome-wide detection of copy number variants in European autochthonous and commercial pig breeds by whole-genome sequencing of DNA pools identified breed-characterising copy number states. <i>Animal Genetics</i> , 2020, 51, 541-556.	0.6	18
41	Haplotype-based genome-wide association studies reveal new loci for haematological and clinical-biochemical parameters in Large White pigs. <i>Animal Genetics</i> , 2020, 51, 601-606.	0.6	9
42	Genome-wide association analyses for coat colour patterns in the autochthonous Nero Siciliano pig breed. <i>Livestock Science</i> , 2020, 236, 104015.	0.6	6
43	Whole-genome sequencing of European autochthonous and commercial pig breeds allows the detection of signatures of selection for adaptation of genetic resources to different breeding and production systems. <i>Genetics Selection Evolution</i> , 2020, 52, 33.	1.2	45
44	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
45	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
46	Comparative population genomic analyses of the reconstructed local breed "Nero di Parma" with other commercial and autochthonous Italian pig breeds. <i>Livestock Science</i> , 2020, 235, 104014.	0.6	2
47	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
48	Environmental impacts of pig production systems using European local breeds: The contribution of carbon sequestration and emissions from grazing. <i>Journal of Cleaner Production</i> , 2019, 237, 117843.	4.6	23
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	Genomic diversity, linkage disequilibrium and selection signatures in European local pig breeds assessed with a high density SNP chip. <i>Scientific Reports</i> , 2019, 9, 13546.	1.6	78
51	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
52	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
53	Genetic markers associated with resistance to infectious diseases have no effects on production traits and haematological parameters in Italian Large White pigs. <i>Livestock Science</i> , 2019, 223, 32-38.	0.6	8
54	Signatures of de-domestication in autochthonous pig breeds and of domestication in wild boar populations from <i>MC1R</i> and <i>NR6A1</i> allele distribution. <i>Animal Genetics</i> , 2019, 50, 166-171.	0.6	26

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55	Dose-response of different dietary leucine levels on growth performance and amino acid metabolism in piglets differing for amino adipate-semialdehyde synthase genotypes. <i>Scientific Reports</i> , 2019, 9, 18496.	1.6	8
56	Few mitochondrial DNA sequences are inserted into the turkey (<i>Meleagris</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 707 Td <i>Animal Genetics</i> , 2018, 49, 259-264.	0.6	5
57	Authentication of honey based on a DNA method to differentiate <i>Apis mellifera</i> subspecies: Application to Sicilian honey bee (<i>A. m. siciliana</i>) and Iberian honey bee (<i>A. m. iberiensis</i>) honeys. <i>Food Control</i> , 2018, 91, 294-301.	2.8	33
58	Teat number parameters in Italian Large White pigs: Phenotypic analysis and association with <i>VERTN</i> (VRTN) gene allele variants. <i>Livestock Science</i> , 2018, 210, 68-72.	0.6	16
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	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
61	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
62	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
63	Genome-wide identification of runs of homozygosity islands and associated genes in local dairy cattle breeds. <i>Animal</i> , 2018, 12, 2480-2488.	1.3	65
64	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
65	Effects of single nucleotide polymorphisms and haplotypes of the protein kinase AMP-activated non-catalytic subunit gamma 3 (PRKAG3) gene on production, meat quality and carcass traits in Italian Large White pigs. <i>Meat Science</i> , 2018, 136, 44-49.	2.7	9
66	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
67	Application of next generation semiconductor based sequencing for species identification in dairy products. <i>Food Chemistry</i> , 2018, 246, 90-98.	4.2	42
68	Potential sensitivity of pork production situations aiming at high-quality products to the use of entire male pigs as an alternative to surgical castrates. <i>Animal</i> , 2018, 12, 1287-1295.	1.3	15
69	Diversity across major and candidate genes in European local pig breeds. <i>PLoS ONE</i> , 2018, 13, e0207475.	1.1	69
70	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
71	A comparative analysis of label-free liquid chromatography-mass spectrometry liver proteomic profiles highlights metabolic differences between pig breeds. <i>PLoS ONE</i> , 2018, 13, e0199649.	1.1	13
72	New Insights into the Melanophilin (MLPH) Gene Affecting Coat Color Dilution in Rabbits. <i>Genes</i> , 2018, 9, 430.	1.0	20

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73	Conservation status and historical relatedness of Italian cattle breeds. <i>Genetics Selection Evolution</i> , 2018, 50, 35.	1.2	50
74	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
75	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
76	A genome-wide association study for a proxy of intermuscular fat level in the Italian Large White breed identifies genomic regions affecting an important quality parameter for dry-cured hams. <i>Animal Genetics</i> , 2017, 48, 459-465.	0.6	12
77	Wild opportunities with dedomestication genetics of rabbits. <i>Restoration Ecology</i> , 2017, 25, 330-332.	1.4	2
78	Meat Authenticity and Traceability. , 2017, , 585-633.		4
79	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
80	Genome-wide association study for ham weight loss at first salting in Italian Large White pigs: towards the genetic dissection of a key trait for dry-cured ham production. <i>Animal Genetics</i> , 2017, 48, 103-107.	0.6	18
81	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
82	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
83	Exploring gastric bacterial community in young pigs. <i>PLoS ONE</i> , 2017, 12, e0173029.	1.1	8
84	P8002 A genomic landscape of mitochondrial DNA insertions in the nuclear pig genome. <i>Journal of Animal Science</i> , 2016, 94, 181-182.	0.2	0
85	P1021 A next generation, semiconductor-based target re-sequencing DNA pool-seq approach for the identification of SNPs and association studies: Application to bitter taste receptor genes in different pig populations. <i>Journal of Animal Science</i> , 2016, 94, 24-25.	0.2	0
86	P5018 Genome-wide association studies for dry-cured ham quality traits in Italian Large White and Italian Duroc pigs. <i>Journal of Animal Science</i> , 2016, 94, 124-124.	0.2	0
87	P4038 Whole genome semiconductor based sequencing of farmed European sea bass (<i>dicentrarchus</i>) Tj ETQq1 1 0.784314 rgBT /Over genetic stocks. <i>Journal of Animal Science</i> , 2016, 94, 97-97.	0.2	0
88	P4025 Random forest based approaches identify breed-informative SNPs matching selection signature regions in the pig genome. <i>Journal of Animal Science</i> , 2016, 94, 91-91.	0.2	0
89	Identification of a Bitter-Taste Receptor Gene Repertoire in Different Lagomorphs Species. <i>Frontiers in Genetics</i> , 2016, 7, 55.	1.1	0
90	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

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91	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
92	Metabolomics and livestock genomics: Insights into a phenotyping frontier and its applications in animal breeding. <i>Animal Frontiers</i> , 2016, 6, 73-79.	0.8	57
93	Metabolomics evidences plasma and serum biomarkers differentiating two heavy pig breeds. <i>Animal</i> , 2016, 10, 1741-1748.	1.3	24
94	Genomic selection in pigs: state of the art and perspectives. <i>Italian Journal of Animal Science</i> , 2016, 15, 211-232.	0.8	56
95	Genomic inbreeding estimation in small populations: evaluation of runs of homozygosity in three local dairy cattle breeds. <i>Animal</i> , 2016, 10, 746-754.	1.3	129
96	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
97	Novel Y chromosome short tandem repeats in <i>Sus scrofa</i> and their variation in European wild boar and domestic pig populations. <i>Animal Genetics</i> , 2016, 47, 682-690.	0.6	6
98	Merging Metabolomics, Genetics, and Genomics in Livestock to Dissect Complex Production Traits. , 2016, , 43-62.		4
99	P3012 Deconstructing the pig genome-metabolome functional interactions. <i>Journal of Animal Science</i> , 2016, 94, 57-58.	0.2	2
100	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
101	LaGomiCsâ€”Lagomorph Genomics Consortium: An International Collaborative Effort for Sequencing the Genomes of an Entire Mammalian Order. <i>Journal of Heredity</i> , 2016, 107, 295-308.	1.0	19
102	Identification of Polymorphisms in the Rabbit Growth Hormone Receptor (<i>GHR</i>) Gene and Association with Finishing Weight in a Commercial Meat Rabbit Line. <i>Animal Biotechnology</i> , 2016, 27, 77-83.	0.7	8
103	Authentication of â€œmono-breedâ€ pork products: Identification of a coat colour gene marker in Cinta Senese pigs useful to this purpose. <i>Livestock Science</i> , 2016, 184, 71-77.	0.6	28
104	Genomic selection in a pig population including information from slaughtered full sibs of boars within a sib-testing program. <i>Animal</i> , 2015, 9, 750-759.	1.3	4
105	Combined use of principal component analysis and random forests identify populationâ€informative single nucleotide polymorphisms: application in cattle breeds. <i>Journal of Animal Breeding and Genetics</i> , 2015, 132, 346-356.	0.8	38
106	Identification and Validation of Copy Number Variants in Italian Brown Swiss Dairy Cattle Using Illumina Bovine SNP50 Beadchip [®] . <i>Italian Journal of Animal Science</i> , 2015, 14, 3900.	0.8	11
107	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
108	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

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109	Comparison of three patterns of feed supplementation with live <i>Saccharomyces cerevisiae</i> yeast on postweaning diarrhea, health status, and blood metabolic profile of susceptible weaning pigs orally challenged with <i>Escherichia coli</i> F4ac1. <i>Journal of Animal Science</i> , 2015, 93, 2225-2233.	0.2	35
110	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
111	Association of 20 candidate gene markers with milk production and composition traits in sires of Reggiana breed, a local dairy cattle population. <i>Livestock Science</i> , 2015, 176, 14-21.	0.6	16
112	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
113	A retrospective analysis of allele frequency changes of major genes during 20 years of selection in the Italian Large White pig breed. <i>Journal of Animal Breeding and Genetics</i> , 2015, 132, 239-246.	0.8	20
114	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
115	A genomewide association study for average daily gain in Italian Large White pigs. <i>Journal of Animal Science</i> , 2014, 92, 1385-1394.	0.2	64
116	A frameshift mutation in the <i>melanophilin</i> gene causes the dilute coat colour in rabbit (<i>Oryctolagus cuniculus</i>) breeds. <i>Animal Genetics</i> , 2014, 45, 248-255.	0.6	32
117	Investigation of a Short Interspersed Nuclear Element Polymorphic Site in the Porcine <i>Vertnin</i> Gene: Allele Frequencies and Association Study With Meat Quality, Carcass and Production Traits in Italian Large White pigs. <i>Italian Journal of Animal Science</i> , 2014, 13, 3090.	0.8	12
118	Association of myostatin (MSTN) gene polymorphisms with morphological traits in the Italian Heavy Draft Horse breed. <i>Livestock Science</i> , 2014, 160, 29-36.	0.6	19
119	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
120	A premature stop codon in the <i>TYRP1</i> gene is associated with brown coat colour in the European rabbit (<i>Oryctolagus cuniculus</i>). <i>Animal Genetics</i> , 2014, 45, 600-603.	0.6	30
121	The genome-wide structure of two economically important indigenous Sicilian cattle breeds. <i>Journal of Animal Science</i> , 2014, 92, 4833-4842.	0.2	31
122	Rabbit genome analysis reveals a polygenic basis for phenotypic change during domestication. <i>Science</i> , 2014, 345, 1074-1079.	6.0	343
123	Differentiation of meat from European wild boars and domestic pigs using polymorphisms in the MC1R and NR6A1 genes. <i>Meat Science</i> , 2014, 98, 781-784.	2.7	38
124	Copy number variants in Italian Large White pigs detected using high-density single nucleotide polymorphisms and their association with back fat thickness. <i>Animal Genetics</i> , 2014, 45, 745-749.	0.6	27
125	A candidate gene association study for nine economically important traits in Italian Holstein cattle. <i>Animal Genetics</i> , 2014, 45, 576-580.	0.6	49
126	Analysis of the 227 bp short interspersed nuclear element (SINE) insertion of the promoter of the myostatin (MSTN) gene in different horse breeds. <i>Veterinaria Italiana</i> , 2014, 50, 193-7.	0.5	8

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127	The KIT Gene Is Associated with the English Spotting Coat Color Locus and Congenital Megacolon in Checkered Giant Rabbits (<i>Oryctolagus cuniculus</i>). <i>PLoS ONE</i> , 2014, 9, e93750.	1.1	41
128	The Rabbit as an Experimental and Production Animal: From Genomics to Proteomics. <i>Current Protein and Peptide Science</i> , 2014, 15, 134-145.	0.7	26
129	Nucleotide variability and haplotype heterogeneity at the porcine <i>FTO</i> gene. <i>Animal Genetics</i> , 2013, 44, 96-100.	0.6	8
130	Association study between single nucleotide polymorphisms in candidate genes and reproduction traits in Italian Large White sows. <i>Livestock Science</i> , 2013, 155, 172-179.	0.6	1
131	Association between melanocortin 4 receptor (MC4R) gene haplotypes and carcass and production traits in Italian Large White pigs evaluated with a selective genotyping approach. <i>Livestock Science</i> , 2013, 157, 48-56.	0.6	17
132	Analysis of Association Between a Microsatellite at Intron 1 of the Insulin-Like Growth Factor 1 (IGF1) Gene and Fat Deposition, Meat Production and Quality Traits in Italian Large White and Italian Duroc Pigs. <i>Italian Journal of Animal Science</i> , 2013, 12, e72.	0.8	2
133	SUS-BAR: a database of pig proteins with statistically validated structural and functional annotation. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat065-bat065.	1.4	4
134	The TBC1D1 Gene. <i>Vitamins and Hormones</i> , 2013, 91, 77-95.	0.7	15
135	A Missense Mutation in the Rabbit Melanocortin 4 Receptor (MC4R) Gene is Associated with Finishing Weight in a Meat Rabbit Line. <i>Animal Biotechnology</i> , 2013, 24, 268-277.	0.7	18
136	Mapping and Annotating Obesity-Related Genes in Pig And Human Genomes. <i>Protein and Peptide Letters</i> , 2013, 21, 840-846.	0.4	2
137	Investigation of the premelanosome protein (PMEL) or (SILV) gene and identification of polymorphism excluding it as the determinant of the dilute locus in domestic rabbits (<i>Oryctolagus cuniculus</i>). <i>Archives Animal Breeding</i> , 2013, 56, 42-49.	0.5	1
138	Analysis of Association Between the <i>MUC4</i> g.8227C>G Polymorphism and Production Traits in Italian Heavy Pigs Using a Selective Genotyping Approach. <i>Animal Biotechnology</i> , 2012, 23, 147-155.	0.7	22
139	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
140	Exploring copy number variation in the rabbit (<i>Oryctolagus cuniculus</i>) genome by array comparative genome hybridization. <i>Genomics</i> , 2012, 100, 245-251.	1.3	19
141	A genome wide association study for backfat thickness in Italian Large White pigs highlights new regions affecting fat deposition including neuronal genes. <i>BMC Genomics</i> , 2012, 13, 583.	1.2	80
142	Identification and association analysis of several hundred single nucleotide polymorphisms within candidate genes for back fat thickness in Italian Large White pigs using a selective genotyping approach. <i>Journal of Animal Science</i> , 2012, 90, 2450-2464.	0.2	65
143	A single nucleotide polymorphism in the rabbit growth hormone (GH1) gene is associated with market weight in a commercial rabbit population. <i>Livestock Science</i> , 2012, 147, 84-88.	0.6	19
144	Analysis of polymorphisms in the agouti signalling protein (ASIP) and melanocortin 1 receptor (MC1R) genes and association with coat colours in two Pramenka sheep types. <i>Small Ruminant Research</i> , 2012, 105, 89-96.	0.6	18

#	ARTICLE	IF	CITATIONS
145	Haplotype variability in the bovine <i>MITF</i> gene and association with piebaldism in Holstein and Simmental cattle breeds. <i>Animal Genetics</i> , 2012, 43, 250-256.	0.6	33
146	Association between a polymorphism in the <i>IGF2</i> gene and finishing weight in a commercial rabbit population. <i>Animal Genetics</i> , 2012, 43, 651-652.	0.6	9
147	A whole genome scan for QTL affecting milk protein percentage in Italian Holstein cattle, applying selective milk DNA pooling and multiple marker mapping in a daughter design. <i>Animal Genetics</i> , 2012, 43, 72-86.	0.6	14
148	Confirmation of the association between a single nucleotide polymorphism in the porcine <i>LDHA</i> gene and average daily gain and correlated traits in Italian Large White pigs. <i>Animal Genetics</i> , 2012, 43, 649-650.	0.6	10
149	Association between polymorphisms in cathepsin and cystatin genes with meat production and carcass traits in Italian Duroc pigs: confirmation of the effects of a cathepsin L (CTSL) gene marker. <i>Molecular Biology Reports</i> , 2012, 39, 109-115.	1.0	9
150	Association Analysis Between DNA Markers and Number of Functional Teats in Italian Large White Pigs. , 2012, , 181-185.		2
151	Identification and analysis of single nucleotide polymorphisms in the myosin VA (MYO5A) gene and its exclusion as the causative gene of the dilute coat colour locus in rabbit. <i>World Rabbit Science</i> , 2012, 20, .	0.1	7
152	A melanocortin 1 receptor (<i>MC1R</i>) gene polymorphism is useful for authentication of Massese sheep dairy products. <i>Journal of Dairy Research</i> , 2011, 78, 122-128.	0.7	21
153	Molecular and Pathological Characterization of a Non-Aganglionic Congenital Megacolon in the Rabbit. <i>Gastroenterology</i> , 2011, 140, S-601.	0.6	1
154	Microarray gene expression analysis of porcine skeletal muscle sampled at several post mortem time points. <i>Meat Science</i> , 2011, 88, 604-609.	2.7	5
155	A first comparative map of copy number variations in the sheep genome. <i>Genomics</i> , 2011, 97, 158-165.	1.3	103
156	Coat colours in the Massese sheep breed are associated with mutations in the agouti signalling protein (ASIP) and melanocortin 1 receptor (MC1R) genes. <i>Animal</i> , 2011, 5, 8-17.	1.3	68
157	Identification of polymorphisms in the rabbit (<i>Oryctolagus cuniculus</i>) <i>myostatin</i> (<i>MSTN</i>) gene and association analysis with finishing weight in a commercial rabbit population. <i>Animal Genetics</i> , 2011, 42, 339-339.	0.6	21
158	The porcine TBC1D1 gene: mapping, SNP identification, and association study with meat, carcass and production traits in Italian heavy pigs. <i>Molecular Biology Reports</i> , 2011, 38, 1425-1431.	1.0	31
159	A selective genotyping approach identifies single nucleotide polymorphisms in porcine chromosome 2 genes associated with production and carcass traits in Italian heavy pigs. <i>Italian Journal of Animal Science</i> , 2011, 10, e15.	0.8	14
160	<i>ESR1</i> and <i>ESR2</i> gene markers are not associated with number of piglets born alive in Italian Large White sows. <i>Italian Journal of Animal Science</i> , 2011, 10, e35.	0.8	9
161	Confirmed association between a single nucleotide polymorphism in the FTO gene and obesity-related traits in heavy pigs. <i>Molecular Biology Reports</i> , 2010, 37, 461-466.	1.0	46
162	A single nucleotide polymorphism in the porcine cathepsin K (CTSK) gene is associated with back fat thickness and production traits in Italian Duroc pigs. <i>Molecular Biology Reports</i> , 2010, 37, 491-495.	1.0	25

#	ARTICLE	IF	CITATIONS
163	Genetic structure of candidate genes for litter size in Italian Large White pigs. <i>Veterinary Research Communications</i> , 2010, 34, 203-206.	0.6	12
164	Sequence characterization of the melanocortin 1 receptor (MC1R) gene in sheep with different coat colours and identification of the putative e allele at the ovine Extension locus. <i>Small Ruminant Research</i> , 2010, 91, 200-207.	0.6	37
165	An initial comparative map of copy number variations in the goat (<i>Capra hircus</i>) genome. <i>BMC Genomics</i> , 2010, 11, 639.	1.2	120
166	A composite six bp in-frame deletion in the melanocortin 1 receptor (MC1R) gene is associated with the Japanese brindling coat colour in rabbits (<i>Oryctolagus cuniculus</i>). <i>BMC Genetics</i> , 2010, 11, 59.	2.7	28
167	Genetic heterogeneity at the bovine <i>KIT</i> gene in cattle breeds carrying different putative alleles at the <i>spotting</i> locus. <i>Animal Genetics</i> , 2010, 41, 295-303.	0.6	73
168	Genetic heterogeneity and selection signature at the <i>KIT</i> gene in pigs showing different coat colours and patterns. <i>Animal Genetics</i> , 2010, 41, 478-492.	0.6	62
169	Endothelin receptor B (<i>EDNRB</i>) is not the causative gene of the <i>English spotting</i> locus in the domestic rabbit (<i>Oryctolagus cuniculus</i>). <i>Animal Genetics</i> , 2010, 41, 669-670.	0.6	8
170	The insulin-like growth factor 2 (IGF2) gene intron3-g.3072G>A polymorphism is not the only Sus scrofa chromosome 2p mutation affecting meat production and carcass traits in pigs: Evidence from the effects of a cathepsin D (CTSD) gene polymorphism1. <i>Journal of Animal Science</i> , 2010, 88, 2235-2245.	0.2	44
171	Analysis of SNPs in the KIT gene of cattle with different coat colour patterns and perspectives to use these markers for breed traceability and authentication of beef and dairy products. <i>Italian Journal of Animal Science</i> , 2010, 9, .	0.8	25
172	<i>DGAT1</i> p.K232A polymorphism in dairy and dual purpose Italian cattle breeds. <i>Italian Journal of Animal Science</i> , 2010, 9, e16.	0.8	20
173	Analysis of Horse <i>Myostatin</i> Gene and Identification of Single Nucleotide Polymorphisms in Breeds of Different Morphological Types. <i>Journal of Biomedicine and Biotechnology</i> , 2010, 2010, 1-11.	3.0	51
174	Association between cathepsin L (CTSL) and cathepsin S (CTSS) polymorphisms and meat production and carcass traits in Italian Large White pigs. <i>Meat Science</i> , 2010, 85, 331-338.	2.7	21
175	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
176	Characterization of the rabbit agouti signaling protein (ASIP) gene: Transcripts and phylogenetic analyses and identification of the causative mutation of the nonagouti black coat colour. <i>Genomics</i> , 2010, 95, 166-175.	1.3	77
177	A genome scan for quantitative trait loci affecting milk somatic cell score in Israeli and Italian Holstein cows by means of selective DNA pooling with single- and multiple-marker mapping. <i>Journal of Dairy Science</i> , 2010, 93, 4913-4927.	1.4	24
178	Sequence Characterization of the <i>MC1R</i> Gene in Yak (<i>Poephagus grunniens</i>) Breeds with Different Coat Colors. <i>Journal of Biomedicine and Biotechnology</i> , 2009, 2009, 1-6.	3.0	22
179	Extensive Long-Range and Nonsyntenic Linkage Disequilibrium in Livestock Populations: Deconstruction of a Conundrum. <i>Genetics</i> , 2009, 181, 691-699.	1.2	16
180	HincII and PstI reveal polymorphisms at the porcine orosomucoid (ORM) locus. <i>Animal Genetics</i> , 2009, 25, 369-369.	0.6	1

#	ARTICLE	IF	CITATIONS
181	Missense and nonsense mutations in melanocortin 1 receptor (MC1R) gene of different goat breeds: association with red and black coat colour phenotypes but with unexpected evidences. BMC Genetics, 2009, 10, 47.	2.7	85
182	The porcine <i>fat</i> mass and obesity associated (<i>FTO</i>) gene is associated with fat deposition in Italian Duroc pigs. Animal Genetics, 2009, 40, 90-93.	0.6	65
183	GLYCOLYTIC POTENTIAL IN SEMIMEMBRANOSUS MUSCLE OF ITALIAN LARGE WHITE PIGS. Journal of Muscle Foods, 2009, 20, 392-400.	0.5	7
184	Copy Number Variation and Missense Mutations of the Agouti Signaling Protein (<i>ASIP</i>) Gene in Goat Breeds with Different Coat Colors. Cytogenetic and Genome Research, 2009, 126, 333-347.	0.6	125
185	Transcriptome analysis of skeletal muscle tissue to identify genes involved in pre-slaughter stress response in pigs. Italian Journal of Animal Science, 2009, 8, 69-71.	0.8	2
186	The FAGenomicH project: towards a whole candidate gene approach to identify markers associated with fatness and production traits in pigs and investigate the pig as a model for human obesity. Italian Journal of Animal Science, 2009, 8, 87-89.	0.8	0
187	Genetic authentication and traceability of food products of animal origin: new developments and perspectives. Italian Journal of Animal Science, 2009, 8, 9-18.	0.8	35
188	Differences of the porcine amelogenin X and Y chromosome genes (<i>AMELX</i> and <i>AMELY</i>) and their application for sex determination in pigs. Molecular Reproduction and Development, 2008, 75, 1662-1668.	1.0	36
189	High-Frequency Percussive Ventilation. , 2008, , 237-244.		0
190	Investigation of candidate genes for glycolytic potential of porcine skeletal muscle: Association with meat quality and production traits in Italian Large White pigs. Meat Science, 2008, 80, 780-787.	2.7	52
191	Evaluation of post mortem stability of porcine skeletal muscle RNA. Meat Science, 2008, 80, 1345-1351.	2.7	20
192	Quantitative Trait Loci Affecting Milk Yield and Protein Percentage in a Three-Country Brown Swiss Population. Journal of Dairy Science, 2008, 91, 767-783.	1.4	73
193	Sexing European rabbits (<i>Oryctolagus cuniculus</i>), European brown hares (<i>Lepus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tt 51 Molecular Ecology Resources, 2008, 8, 1294-1296.	2.2	12
194	Single nucleotide polymorphisms in several porcine cathepsin genes are associated with growth, carcass, and production traits in Italian Large White pigs1. Journal of Animal Science, 2008, 86, 3300-3314.	0.2	54
195	Analysis of melanocortin 1 receptor (<i>MC1R</i>) gene polymorphisms in some cattle breeds: their usefulness and application for breed traceability and authentication ofParmigiano Reggiano cheese. Italian Journal of Animal Science, 2007, 6, 257-272.	0.8	59
196	Analysis of the melanocortin receptor 1 (MC1R) gene in Sicilian goat breeds. Italian Journal of Animal Science, 2007, 6, 46-46.	0.8	0
197	Identification of mutations in the bovine KIT gene, a candidate for the Spotted locus in cattle. Italian Journal of Animal Science, 2007, 6, 218-218.	0.8	1
198	Investigation of the Agouti gene for the identification of useful markers for coat colour association studies in domestic rabbits. Italian Journal of Animal Science, 2007, 6, 138-138.	0.8	0

#	ARTICLE	IF	CITATIONS
199	Bovine chromosome 20: milk production QTL and candidate gene analysis in the Italian Holstein-Friesian breed. <i>Italian Journal of Animal Science</i> , 2007, 6, 133-135.	0.8	8
200	Investigation of the DGAT1 K232A and VNTR mutations in dairy and dual purpose cattle breeds. <i>Italian Journal of Animal Science</i> , 2007, 6, 137-137.	0.8	1
201	Investigation of allele frequencies of the growth hormone receptor (GHR) F279Y mutation in dairy and dual purpose cattle breeds. <i>Italian Journal of Animal Science</i> , 2007, 6, 415-420.	0.8	12
202	Mutations in the bovine prolactin receptor (PRLR) gene: allele and haplotype frequencies in the Reggiana cattle breed. <i>Italian Journal of Animal Science</i> , 2007, 6, 207-207.	0.8	3
203	Nero Siciliano pig: analysis of coat colour affecting genes and perspectives for breed traceability. <i>Italian Journal of Animal Science</i> , 2007, 6, 105-105.	0.8	0
204	A new system for animal products traceability and authentication: use of DNA analysis of natural tracers and example of application to dry cured hams. <i>Italian Journal of Animal Science</i> , 2007, 6, 136-136.	0.8	3
205	Associations of functional candidate genes derived from gene expression profiles of prenatal porcine muscle tissue with meat quality and muscle deposition. <i>Animal Genetics</i> , 2007, 38, 474-484.	0.6	66
206	Analysis of the MC1R Gene in the Nero Siciliano Pig Breed and Usefulness of this Locus for Breed Traceability. <i>Veterinary Research Communications</i> , 2007, 31, 389-392.	0.6	24
207	Assessment of variability of genes associated with meat quality traits in Cinta Senese pigs. <i>Italian Journal of Animal Science</i> , 2007, 6, 101-101.	0.8	2
208	Transcriptome analysis of porcine skeletal muscle: differentially expressed genes in Italian Large White pigs with divergent values for glycolytic potential. <i>Italian Journal of Animal Science</i> , 2007, 6, 113-115.	0.8	1
209	Analysis of skeletal muscle tissue expression profiles in pig to identify genes involved in meat quality traits: effect of stress conditions before slaughtering in different pig breeds. <i>Italian Journal of Animal Science</i> , 2007, 6, 205-205.	0.8	1
210	Mutations in the melanocortin 1 receptor (MC1R) gene are associated with coat colours in the domestic rabbit (<i>Oryctolagus cuniculus</i>). <i>Animal Genetics</i> , 2006, 37, 489-493.	0.6	66
211	Mechanical loads modulate tidal volume and lung washout during high-frequency percussive ventilation. <i>Respiratory Physiology and Neurobiology</i> , 2006, 150, 44-51.	0.7	15
212	Investigation of SNPs in the ATP1A2, CA3 and DECR1 genes mapped to porcine chromosome 4: analysis in groups of pigs divergent for meat production and quality traits. <i>Italian Journal of Animal Science</i> , 2006, 5, 249-263.	0.8	6
213	The BovMAS Consortium: investigation of bovine chromosome 14 for quantitative trait loci affecting milk production and quality traits in the Italian Holstein Friesian breed. <i>Italian Journal of Animal Science</i> , 2005, 4, 16-18.	0.8	2
214	The BovMAS Consortium: identification of QTL for milk yield and milk protein percent on chromosome 14 in the Brown Swiss breed. <i>Italian Journal of Animal Science</i> , 2005, 4, 13-15.	0.8	2
215	A new approach in association study of single nucleotide polymorphism of genes for carcass and meat quality traits in commercial pigs. <i>Italian Journal of Animal Science</i> , 2004, 3, 177-189.	0.8	15
216	Linkage mapping of the porcine cathepsin F (CTSF) gene close to the QTL regions for meat and fat deposition traits on pig chromosome 2. <i>Animal Genetics</i> , 2004, 35, 155-157.	0.6	12

#	ARTICLE	IF	CITATIONS
217	Effects of mechanical load on flow, volume and pressure delivered by high-frequency percussive ventilation. <i>Respiratory Physiology and Neurobiology</i> , 2004, 142, 81-91.	0.7	32
218	Analysis of single nucleotide polymorphisms in major and candidate genes for production traits in Nero Siciliano pig breed. <i>Italian Journal of Animal Science</i> , 2004, 3, 19-29.	0.8	20
219	Linkage and QTL mapping for <i>Sus scrofa</i> chromosome 4. <i>Journal of Animal Breeding and Genetics</i> , 2003, 120, 28-37.	0.8	48
220	Linkage and QTL mapping for <i>Sus scrofa</i> chromosome 7. <i>Journal of Animal Breeding and Genetics</i> , 2003, 120, 56-65.	0.8	31
221	Linkage and QTL mapping for <i>Sus scrofa</i> chromosome 9. <i>Journal of Animal Breeding and Genetics</i> , 2003, 120, 74-81.	0.8	9
222	Characterization of a SINE indel polymorphism in the porcine AGL gene and assignment of the gene to chromosome 4q. <i>Animal Genetics</i> , 2003, 34, 146-148.	0.6	4
223	Identification of SNPs, mapping and analysis of allele frequencies in two candidate genes for meat production traits: the porcine myosin heavy chain 2B (MYH4) and the skeletal muscle myosin regulatory light chain 2 (HUMMLC2B). <i>Animal Genetics</i> , 2003, 34, 221-225.	0.6	38
224	Radiation hybrid mapping of three skeletal muscle genes (CKM, ECH1 and TNNT1) to porcine chromosome 6. <i>Animal Genetics</i> , 2003, 34, 302-303.	0.6	7
225	The porcine fast skeletal muscle troponin T3 (TNNT3) gene: identification of mutations and linkage mapping to chromosome 2. <i>Animal Genetics</i> , 2003, 34, 391-392.	0.6	4
226	Study of candidate genes for glycolytic potential of porcine skeletal muscle: identification and analysis of mutations, linkage and physical mapping and association with meat quality traits in pigs. <i>Cytogenetic and Genome Research</i> , 2003, 102, 145-151.	0.6	51
227	Mapping, identification of polymorphisms and analysis of allele frequencies in the porcine skeletal muscle myopalladin and titin genes. <i>Cytogenetic and Genome Research</i> , 2003, 102, 152-156.	0.6	10
228	The GENETPIG database: a tool for comparative mapping in pig (<i>Sus scrofa</i>). <i>Nucleic Acids Research</i> , 2003, 31, 138-141.	6.5	7
229	High frequency percussive ventilation (HFPV). Principles and technique. <i>Minerva Anestesiologica</i> , 2003, 69, 841-8, 848-51.	0.6	39
230	High frequency percussive ventilation (HFPV). Case reports. <i>Minerva Anestesiologica</i> , 2003, 69, 853-7, 858-60.	0.6	6
231	Isolation of porcine expressed sequence tags for the construction of a first genomic transcript map of the skeletal muscle in pig. <i>Animal Genetics</i> , 2002, 33, 3-18.	0.6	80
232	Investigation of candidate genes for meat quality in dry-cured ham production: the porcine cathepsin B (CTSB) and cystatin B (CSTB) genes. <i>Animal Genetics</i> , 2002, 33, 123-131.	0.6	36
233	A missense mutation in the porcine mitochondrial 2,4-dienoyl CoA reductase 1 (DECRI) gene and linkage mapping of this locus to chromosome 4. <i>Animal Genetics</i> , 2002, 33, 73-75.	0.6	9
234	The porcine sarcolipin (SLN) gene: identification of an SNP and linkage mapping to chromosome 9. <i>Animal Genetics</i> , 2001, 32, 109-110.	0.6	12

#	ARTICLE	IF	CITATIONS
235	Regional localization of the porcine cathepsin H (CTSH) and cathepsin L (CTSL) genes. <i>Animal Genetics</i> , 2001, 32, 321-323.	0.6	0
236	Regional localization of the porcine cathepsin H (CTSH) and cathepsin L (CTSL) genes. <i>Animal Genetics</i> , 2001, 32, 321-323.	0.6	10
237	Linkage mapping of the Î±-B-crystallin (CRYAB) gene to porcine chromosome 9. <i>Animal Genetics</i> , 2000, 31, 287-288.	0.6	1
238	Mapping of 14 expressed sequence tags (ESTs) from porcine skeletal muscle by somatic cell hybrid analysis. <i>Animal Genetics</i> , 2000, 31, 400-403.	0.6	21
239	Linkage assignment of the fast skeletal alkali myosin light polypeptide 1 (MYL1) gene to porcine chromosome 15. <i>Animal Genetics</i> , 2000, 31, 415-416.	0.6	5
240	Linkage assignments of the porcine ATP1A2, ATP1B1 and V-ATPase (CGI-11) genes to chromosome 4. <i>Animal Genetics</i> , 2000, 31, 416-418.	0.6	0
241	Linkage assignments of the porcine ATP1A2, ATP1B1 and V-ATPase (CGI-11) genes to chromosome 4. <i>Animal Genetics</i> , 2000, 31, 416-418.	0.6	9
242	The porcine Poly(rC)-Binding Protein 2 (PCBP2) gene maps to chromosome 5. <i>Animal Genetics</i> , 1999, 30, 165-166.	0.6	3
243	Mapping of the Na ⁺ , K ⁺ -ATPase subunit Î± 2 (ATP1A2) and muscle phosphofructokinase (PFKM) genes in pig by somatic cell hybrid analysis. <i>Animal Genetics</i> , 1999, 30, 57-60.	0.6	9
244	Analysis of expressed sequence tags of porcine skeletal muscle. <i>Gene</i> , 1999, 233, 181-188.	1.0	60
245	A probe containing ancient repetitive elements detects a new marker (S0521) on porcine chromosome 6. <i>Animal Genetics</i> , 1999, 30, 76-77.	0.6	0
246	Isolation and localization of the skeletal myosin heavy chain 2X gene on pig chromosome 12q1.4-q1.5. <i>Mammalian Genome</i> , 1998, 9, 412-413.	1.0	6
247	Evaluating Evolutionary Divergence with Microsatellites. <i>Journal of Molecular Evolution</i> , 1998, 46, 121-126.	0.8	27
248	Isolation and mapping of two porcine skeletal muscle myosin heavy chain isoforms. <i>Animal Genetics</i> , 1998, 29, 91-97.	0.6	13
249	The porcine proteasome subunit A4 (PSMA4) gene: isolation of a partial cDNA, linkage and physical mapping. <i>Animal Genetics</i> , 1998, 29, 385-388.	0.6	8
250	Livestock variation of linked microsatellite markers in diverse swine breeds. <i>Animal Biotechnology</i> , 1998, 9, 55-66.	0.7	9
251	Isolation and sequencing of porcine fast skeletal muscle alkali myosin light chain 3 cDNA. <i>Animal Biotechnology</i> , 1997, 8, 179-185.	0.7	7