

Luca Fontanesi

List of Publications by Year in descending order

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251
papers

5,635
citations

81743

39
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133063

59
g-index

256
all docs

256
docs citations

256
times ranked

4558
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 1 | Rabbit genome analysis reveals a polygenic basis for phenotypic change during domestication. <i>Science</i> , 2014, 345, 1074-1079. | 6.0 | 343 |
| 2 | 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 |
| 3 | Copy Number Variation and Missense Mutations of the Agouti Signaling Protein (<i>ASIP</i>) Gene in Goat Breeds with Different Coat Colors. <i>Cytogenetic and Genome Research</i> , 2009, 126, 333-347. | 0.6 | 125 |
| 4 | 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 |
| 5 | A first comparative map of copy number variations in the sheep genome. <i>Genomics</i> , 2011, 97, 158-165. | 1.3 | 103 |
| 6 | 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. <i>BMC Genetics</i> , 2009, 10, 47. | 2.7 | 85 |
| 7 | 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 |
| 8 | 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 |
| 9 | 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 |
| 10 | 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 |
| 11 | Quantitative Trait Loci Affecting Milk Yield and Protein Percentage in a Three-Country Brown Swiss Population. <i>Journal of Dairy Science</i> , 2008, 91, 767-783. | 1.4 | 73 |
| 12 | 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 |
| 13 | Diversity across major and candidate genes in European local pig breeds. <i>PLoS ONE</i> , 2018, 13, e0207475. | 1.1 | 69 |
| 14 | 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 |
| 15 | 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 |
| 16 | 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 |
| 17 | The porcine <i>fat mass and obesity associated</i> (<i>FTO</i>) gene is associated with fat deposition in Italian Duroc pigs. <i>Animal Genetics</i> , 2009, 40, 90-93. | 0.6 | 65 |
| 18 | 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 |

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|----|--|-----|-----------|
| 19 | 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 |
| 20 | A genomewide association study for average daily gain in Italian Large White pigs ¹ . <i>Journal of Animal Science</i> , 2014, 92, 1385-1394. | 0.2 | 64 |
| 21 | 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 |
| 22 | Analysis of expressed sequence tags of porcine skeletal muscle. <i>Gene</i> , 1999, 233, 181-188. | 1.0 | 60 |
| 23 | Analysis of melanocortin 1 receptor (<i>MC1R</i>) gene polymorphisms in some cattle breeds: their usefulness and application for breed traceability and authentication of Parmigiano Reggiano cheese. <i>Italian Journal of Animal Science</i> , 2007, 6, 257-272. | 0.8 | 59 |
| 24 | 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 |
| 25 | 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 |
| 26 | Genomic selection in pigs: state of the art and perspectives. <i>Italian Journal of Animal Science</i> , 2016, 15, 211-232. | 0.8 | 56 |
| 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 | Single nucleotide polymorphisms in several porcine cathepsin genes are associated with growth, carcass, and production traits in Italian Large White pigs ¹ . <i>Journal of Animal Science</i> , 2008, 86, 3300-3314. | 0.2 | 54 |
| 29 | Investigation of candidate genes for glycolytic potential of porcine skeletal muscle: Association with meat quality and production traits in Italian Large White pigs. <i>Meat Science</i> , 2008, 80, 780-787. | 2.7 | 52 |
| 30 | 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 |
| 31 | 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 |
| 32 | Conservation status and historical relatedness of Italian cattle breeds. <i>Genetics Selection Evolution</i> , 2018, 50, 35. | 1.2 | 50 |
| 33 | 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 |
| 34 | 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 |
| 35 | 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 |
| 36 | Confirmed association between a single nucleotide polymorphism in the <i>FTO</i> gene and obesity-related traits in heavy pigs. <i>Molecular Biology Reports</i> , 2010, 37, 461-466. | 1.0 | 46 |

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|----|--|-----|-----------|
| 37 | 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 |
| 38 | 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 |
| 39 | The insulin-like growth factor 2 (IGF2) gene intron3-g.3072G>A polymorphism is not the only <i>Sus scrofa</i> 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 |
| 40 | Application of next generation semiconductor based sequencing for species identification in dairy products. <i>Food Chemistry</i> , 2018, 246, 90-98. | 4.2 | 42 |
| 41 | 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 |
| 42 | 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 |
| 43 | High frequency percussive ventilation (HFPV). Principles and technique. <i>Minerva Anestesiologica</i> , 2003, 69, 841-8, 848-51. | 0.6 | 39 |
| 44 | 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 |
| 45 | 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 |
| 46 | 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 |
| 47 | 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 |
| 48 | 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 |
| 49 | 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 |
| 50 | 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. <i>Molecular Reproduction and Development</i> , 2008, 75, 1662-1668. | 1.0 | 36 |
| 51 | Comparative evaluation of genomic inbreeding parameters in seven commercial and autochthonous pig breeds. <i>Animal</i> , 2020, 14, 910-920. | 1.3 | 36 |
| 52 | Genetic authentication and traceability of food products of animal origin: new developments and perspectives. <i>Italian Journal of Animal Science</i> , 2009, 8, 9-18. | 0.8 | 35 |
| 53 | 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 |
| 54 | 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 |

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|----|--|-----|-----------|
| 55 | 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 |
| 56 | 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 |
| 57 | 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 |
| 58 | 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 |
| 59 | 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 |
| 60 | The porcine <i>TBC1D1</i> 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 |
| 61 | 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 |
| 62 | 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 |
| 63 | 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 |
| 64 | A composite six bp in-frame deletion in the melanocortin 1 receptor (<i>MC1R</i>) 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 |
| 65 | Authentication of "mono-breed" 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 |
| 66 | Evaluating Evolutionary Divergence with Microsatellites. <i>Journal of Molecular Evolution</i> , 1998, 46, 121-126. | 0.8 | 27 |
| 67 | 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 |
| 68 | Signatures of 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 |
| 69 | 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 |
| 70 | 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 |
| 71 | A single nucleotide polymorphism in the porcine cathepsin K (<i>CTSK</i>) 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 |
| 72 | Analysis of SNPs in the <i>KIT</i> 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 |

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|----|---|-----|-----------|
| 73 | 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 |
| 74 | 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 |
| 75 | 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 |
| 76 | Metabolomics evidences plasma and serum biomarkers differentiating two heavy pig breeds. <i>Animal</i> , 2016, 10, 1741-1748. | 1.3 | 24 |
| 77 | 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 |
| 78 | Sequence Characterization of the MC1R Gene in Yak (<i>Capra hircus</i>) Breeds with Different Coat Colors. <i>Journal of Biomedicine and Biotechnology</i> , 2009, 2009, 1-6. | 3.0 | 22 |
| 79 | Analysis of Association Between the MUC4 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 |
| 80 | 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 |
| 81 | 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 |
| 82 | A melanocortin 1 receptor (MC1R) gene polymorphism is useful for authentication of Massese sheep dairy products. <i>Journal of Dairy Research</i> , 2011, 78, 122-128. | 0.7 | 21 |
| 83 | Identification of polymorphisms in the rabbit (<i>Oryctolagus cuniculus</i>) myostatin (MSTN) gene and association analysis with finishing weight in a commercial rabbit population. <i>Animal Genetics</i> , 2011, 42, 339-339. | 0.6 | 21 |
| 84 | Genomic regions influencing intramuscular fat in divergently selected rabbit lines. <i>Animal Genetics</i> , 2020, 51, 58-69. | 0.6 | 21 |
| 85 | 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 |
| 86 | 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 |
| 87 | Evaluation of post mortem stability of porcine skeletal muscle RNA. <i>Meat Science</i> , 2008, 80, 1345-1351. | 2.7 | 20 |
| 88 | DGAT1 p.K232A polymorphism in dairy and dual purpose Italian cattle breeds. <i>Italian Journal of Animal Science</i> , 2010, 9, e16. | 0.8 | 20 |
| 89 | 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 |
| 90 | 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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|-----|--|-----|-----------|
| 91 | 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 |
| 92 | 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 |
| 93 | 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 |
| 94 | 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 |
| 95 | 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 |
| 96 | 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 |
| 97 | 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 |
| 98 | 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 |
| 99 | 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 |
| 100 | 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 |
| 101 | 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 |
| 102 | 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 |
| 103 | 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 |
| 104 | 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 |
| 105 | Extensive Long-Range and Nonsyntenic Linkage Disequilibrium in Livestock Populations: Deconstruction of a Conundrum. <i>Genetics</i> , 2009, 181, 691-699. | 1.2 | 16 |
| 106 | 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 |
| 107 | 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 |
| 108 | Teat number parameters in Italian Large White pigs: Phenotypic analysis and association with vertnin (VRTN) gene allele variants. <i>Livestock Science</i> , 2018, 210, 68-72. | 0.6 | 16 |

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|-----|---|-----|-----------|
| 109 | 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 |
| 110 | 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 |
| 111 | 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 |
| 112 | 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 |
| 113 | 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 |
| 114 | The TBC1D1 Gene. <i>Vitamins and Hormones</i> , 2013, 91, 77-95. | 0.7 | 15 |
| 115 | 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 |
| 116 | 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 |
| 117 | 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 |
| 118 | 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 |
| 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 | 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 |
| 121 | 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 |
| 122 | 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 |
| 123 | Isolation and mapping of two porcine skeletal muscle myosin heavy chain isoforms. <i>Animal Genetics</i> , 1998, 29, 91-97. | 0.6 | 13 |
| 124 | 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 |
| 125 | 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 |
| 126 | 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 |

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|-----|--|-----|-----------|
| 127 | 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 |
| 128 | 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 |
| 129 | Sexing European rabbits (<i>Oryctolagus cuniculus</i>), European brown hares (<i>Lepus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 6 Molecular Ecology Resources, 2008, 8, 1294-1296. | 2.2 | 12 |
| 130 | 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 |
| 131 | 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 |
| 132 | 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 |
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