

# Paolo Ajmone Marsan

## List of Publications by Year in descending order

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162  
papers

8,533  
citations

50244

46  
h-index

54882

84  
g-index

168  
all docs

168  
docs citations

168  
times ranked

7636  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-Wide Survey of SNP Variation Uncovers the Genetic Structure of Cattle Breeds. <i>Science</i> , 2009, 324, 528-532.	6.0	746
2	Comparative analysis of genetic similarity among maize inbred lines detected by RFLPs, RAPDs, SSRs, and AFLPs. <i>Theoretical and Applied Genetics</i> , 1998, 97, 1248-1255.	1.8	432
3	Revealing the History of Sheep Domestication Using Retrovirus Integrations. <i>Science</i> , 2009, 324, 532-536.	6.0	402
4	The goat domestication process inferred from large-scale mitochondrial DNA analysis of wild and domestic individuals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 17659-17664.	3.3	279
5	Mitochondrial genomes of extinct aurochs survive in domestic cattle. <i>Current Biology</i> , 2008, 18, R157-R158.	1.8	231
6	Analysis of runs of homozygosity and their relationship with inbreeding in five cattle breeds farmed in Italy. <i>Animal Genetics</i> , 2015, 46, 110-121.	0.6	228
7	Convergent genomic signatures of domestication in sheep and goats. <i>Nature Communications</i> , 2018, 9, 813.	5.8	220
8	Are cattle, sheep, and goats endangered species?. <i>Molecular Ecology</i> , 2008, 17, 275-284.	2.0	217
9	On the origin of cattle: How aurochs became cattle and colonized the world. <i>Evolutionary Anthropology</i> , 2010, 19, 148-157.	1.7	182
10	Genetic diversity and its relationship to hybrid performance in maize as revealed by RFLP and AFLP markers. <i>Theoretical and Applied Genetics</i> , 1998, 96, 219-227.	1.8	173
11	Geographical partitioning of goat diversity in Europe and the Middle East. <i>Animal Genetics</i> , 2006, 37, 327-334.	0.6	172
12	Chromosome-level assembly of the water buffalo genome surpasses human and goat genomes in sequence contiguity. <i>Nature Communications</i> , 2019, 10, 260.	5.8	161
13	The Multifaceted Origin of Taurine Cattle Reflected by the Mitochondrial Genome. <i>PLoS ONE</i> , 2009, 4, e5753.	1.1	157
14	Adaptations to Climate-Mediated Selective Pressures in Sheep. <i>Molecular Biology and Evolution</i> , 2014, 31, 3324-3343.	3.5	149
15	AFLP markers for DNA fingerprinting in cattle. <i>Animal Genetics</i> , 1997, 28, 418-426.	0.6	147
16	Genetic diversity in widespread species is not congruent with species richness in alpine plant communities. <i>Ecology Letters</i> , 2012, 15, 1439-1448.	3.0	135
17	AFLP markers in a molecular linkage map of maize: codominant scoring and linkage group distribution. <i>Theoretical and Applied Genetics</i> , 1999, 99, 425-431.	1.8	125
18	Identification of Selection Signatures in Cattle Breeds Selected for Dairy Production. <i>Genetics</i> , 2010, 185, 1451-1461.	1.2	115

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19	Molecular tools and analytical approaches for the characterization of farm animal genetic diversity. <i>Animal Genetics</i> , 2012, 43, 483-502.	0.6	104
20	Origin and Spread of <i>Bos taurus</i> : New Clues from Mitochondrial Genomes Belonging to Haplogroup T1. <i>PLoS ONE</i> , 2012, 7, e38601.	1.1	93
21	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
22	The Enigmatic Origin of Bovine mtDNA Haplogroup R: Sporadic Interbreeding or an Independent Event of <i>Bos primigenius</i> Domestication in Italy?. <i>PLoS ONE</i> , 2010, 5, e15760.	1.1	84
23	Genome-wide analysis of Italian sheep diversity reveals a strong geographic pattern and cryptic relationships between breeds. <i>Animal Genetics</i> , 2014, 45, 256-266.	0.6	84
24	Double muscling in Marchigiana beef breed is caused by a stop codon in the third exon of myostatin gene. <i>Mammalian Genome</i> , 2003, 14, 392-395.	1.0	82
25	New Insights on Water Buffalo Genomic Diversity and Post-Domestication Migration Routes From Medium Density SNP Chip Data. <i>Frontiers in Genetics</i> , 2018, 9, 53.	1.1	79
26	Design and validation of a 90K SNP genotyping assay for the water buffalo ( <i>Bubalus bubalis</i> ). <i>PLoS ONE</i> , 2017, 12, e0185220.	1.1	76
27	The mystery of Etruscan origins: novel clues from <i>Bos taurus</i> mitochondrial DNA. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2007, 274, 1175-1179.	1.2	74
28	Genetic diversity of Italian goat breeds assessed with a medium-density SNP chip. <i>Genetics Selection Evolution</i> , 2015, 47, 62.	1.2	72
29	Establishment and characterization of two new pig cell lines for use in virological diagnostic laboratories. <i>Journal of Virological Methods</i> , 2003, 107, 205-212.	1.0	67
30	A Competitive Polymerase Chain Reaction-Based Approach for the Identification and Semiquantification of Mitochondrial DNA in Differently Heat-Treated Bovine Meat and Bone Meal. <i>Journal of Food Protection</i> , 2003, 66, 103-109.	0.8	67
31	Distribution and Functionality of Copy Number Variation across European Cattle Populations. <i>Frontiers in Genetics</i> , 2017, 8, 108.	1.1	65
32	Genome Wide Analysis of Fertility and Production Traits in Italian Holstein Cattle. <i>PLoS ONE</i> , 2013, 8, e80219.	1.1	65
33	Prospects and challenges for the conservation of farm animal genomic resources, 2015-2025. <i>Frontiers in Genetics</i> , 2015, 6, 314.	1.1	64
34	Genetic diversity of maize inbred lines within and among heterotic groups revealed by RFLPs. <i>Theoretical and Applied Genetics</i> , 1992, 84, 17-25.	1.8	59
35	On the origin of European sheep as revealed by the diversity of the Balkan breeds and by optimizing population-genetic analysis tools. <i>Genetics Selection Evolution</i> , 2020, 52, 25.	1.2	58
36	Assessing genetic diversity in Italian goat populations using AFLP markers. <i>Animal Genetics</i> , 2001, 32, 281-288.	0.6	57

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37	Gut response induced by weaning in piglet features marked changes in immune and inflammatory response. <i>Functional and Integrative Genomics</i> , 2014, 14, 657-671.	1.4	56
38	Whole mitochondrial genomes unveil the impact of domestication on goat matrilineal variability. <i>BMC Genomics</i> , 2015, 16, 1115.	1.2	56
39	Sustainable ruminant production to help feed the planet. <i>Italian Journal of Animal Science</i> , 2017, 16, 140-171.	0.8	56
40	Genome assembly and transcriptome resource for river buffalo, <i>Bubalus bubalis</i> (2n = 50). <i>GigaScience</i> , 2017, 6, 1-6.	3.3	55
41	Genome-wide association study of milk fatty acid composition in Italian Simmental and Italian Holstein cows using single nucleotide polymorphism arrays. <i>Journal of Dairy Science</i> , 2018, 101, 11004-11019.	1.4	54
42	Combining Landscape Genomics and Ecological Modelling to Investigate Local Adaptation of Indigenous Ugandan Cattle to East Coast Fever. <i>Frontiers in Genetics</i> , 2018, 9, 385.	1.1	53
43	An improved protocol for the production of AFLPTM markers in complex genomes by means of capillary electrophoresis. <i>Journal of Animal Breeding and Genetics</i> , 2005, 122, 62-68.	0.8	52
44	Landscape genomics and biased FST approaches reveal single nucleotide polymorphisms under selection in goat breeds of North-East Mediterranean. <i>BMC Genetics</i> , 2009, 10, 7.	2.7	52
45	Assessing SNP markers for assigning individuals to cattle populations. <i>Animal Genetics</i> , 2009, 40, 18-26.	0.6	51
46	Meta-Analysis of Mitochondrial DNA Reveals Several Population Bottlenecks during Worldwide Migrations of Cattle. <i>Diversity</i> , 2014, 6, 178-187.	0.7	51
47	Conservation status and historical relatedness of Italian cattle breeds. <i>Genetics Selection Evolution</i> , 2018, 50, 35.	1.2	50
48	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
49	Relative extended haplotype homozygosity signals across breeds reveal dairy and beef specific signatures of selection. <i>Genetics Selection Evolution</i> , 2015, 47, 25.	1.2	49
50	Massive screening of copy number population-scale variation in <i>Bos taurus</i> genome. <i>BMC Genomics</i> , 2013, 14, 124.	1.2	48
51	Inbreeding and purging at the genomic Level: the Chillingham cattle reveal extensive, non-random <sc>SNP</sc> heterozygosity. <i>Animal Genetics</i> , 2016, 47, 19-27.	0.6	46
52	Identification of QTLs for grain yield and grain-related traits of maize ( <i>Zeamays L.</i> ) using an AFLP map, different testers, and cofactor analysis. <i>Theoretical and Applied Genetics</i> , 2001, 102, 230-243.	1.8	45
53	Revisiting demographic processes in cattle with genome-wide population genetic analysis. <i>Frontiers in Genetics</i> , 2015, 6, 191.	1.1	45
54	Differentiation of European cattle by AFLP fingerprinting. <i>Animal Genetics</i> , 2007, 38, 60-66.	0.6	44

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55	The characterization of goat genetic diversity: Towards a genomic approach. <i>Small Ruminant Research</i> , 2014, 121, 58-72.	0.6	44
56	Traceability of four European Protected Geographic Indication (PGI) beef products using Single Nucleotide Polymorphisms (SNP) and Bayesian statistics. <i>Meat Science</i> , 2008, 80, 1212-1217.	2.7	43
57	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
58	Derivation and genome-wide association study of a principal component-based measure of heat tolerance in dairy cattle. <i>Journal of Dairy Science</i> , 2017, 100, 4683-4697.	1.4	43
59	A PLAG1 mutation contributed to stature recovery in modern cattle. <i>Scientific Reports</i> , 2017, 7, 17140.	1.6	42
60	Revealing misassembled segments in the bovine reference genome by high resolution linkage disequilibrium scan. <i>BMC Genomics</i> , 2016, 17, 705.	1.2	41
61	Adaptive introgression from indicine cattle into white cattle breeds from Central Italy. <i>Scientific Reports</i> , 2020, 10, 1279.	1.6	40
62	Genetic distances within and across cattle breeds as indicated by biallelic AFLP markers. <i>Animal Genetics</i> , 2002, 33, 280-286.	0.6	39
63	Internal Controls for Quantitative Polymerase Chain Reaction of Swine Mammary Glands During Pregnancy and Lactation. <i>Journal of Dairy Science</i> , 2008, 91, 3057-3066.	1.4	39
64	Detecting population structure and recent demographic history in endangered livestock breeds: the case of the Italian autochthonous donkeys. <i>Animal Genetics</i> , 2013, 44, 69-78.	0.6	37
65	Investigation of the genetic diversity of domestic <i>Capra hircus</i> breeds reared within an early goat domestication area in Iran. <i>Genetics Selection Evolution</i> , 2014, 46, 27.	1.2	36
66	The b-32 protein from maize endosperm: characterization of genomic sequences encoding two alternative central domains. <i>Plant Molecular Biology</i> , 1990, 14, 1031-1040.	2.0	34
67	Standard and Light-Cycler PCR methods for animal DNA species detection in animal feedstuffs. <i>Innovative Food Science and Emerging Technologies</i> , 2008, 9, 18-23.	2.7	32
68	Integrative analysis of methylomic and transcriptomic data in fetal sheep muscle tissues in response to maternal diet during pregnancy. <i>BMC Genomics</i> , 2018, 19, 123.	1.2	32
69	Occurrence, biological properties and potential effects on human health of $\beta$ -casomorphin 7: Current knowledge and concerns. <i>Critical Reviews in Food Science and Nutrition</i> , 2020, 60, 3705-3723.	5.4	32
70	GHap: an R package for genome-wide haplotyping. <i>Bioinformatics</i> , 2016, 32, 2861-2862.	1.8	31
71	Mitochondrial DNA variants of Podolian cattle breeds testify for a dual maternal origin. <i>PLoS ONE</i> , 2018, 13, e0192567.	1.1	30
72	The $\beta$ -casein (CSN2) A2 allelic variant alters milk protein profile and slightly worsens coagulation properties in Holstein cows. <i>Journal of Dairy Science</i> , 2022, 105, 3794-3809.	1.4	30

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73	Breed assignment of Italian cattle using biallelic AFLP <sup>®</sup> markers. <i>Animal Genetics</i> , 2007, 38, 147-153.	0.6	29
74	Discovery, characterization and validation of single nucleotide polymorphisms within 206 bovine genes that may be considered as candidate genes for beef production and quality. <i>Animal Genetics</i> , 2009, 40, 486-491.	0.6	29
75	Low levels of taurine introgression in the current Brazilian Nelore and Gir indicine cattle populations. <i>Genetics Selection Evolution</i> , 2015, 47, 31.	1.2	29
76	Characterization of 37 Breed-Specific Single-Nucleotide Polymorphisms in Sheep. <i>Journal of Heredity</i> , 2006, 97, 531-534.	1.0	28
77	Genetic Diversity of Sheep Breeds from Albania, Greece, and Italy Assessed by Mitochondrial DNA and Nuclear Polymorphisms (SNPs). <i>Scientific World Journal</i> , The, 2011, 11, 1641-1659.	0.8	27
78	A second generation radiation hybrid map to aid the assembly of the bovine genome sequence. <i>BMC Genomics</i> , 2006, 7, 283.	1.2	26
79	Signatures of selection in five Italian cattle breeds detected by a 54K SNP panel. <i>Molecular Biology Reports</i> , 2014, 41, 957-965.	1.0	26
80	Epigenetic analysis of high and low motile sperm populations reveals methylation variation in satellite regions within the pericentromeric position and in genes functionally related to sperm DNA organization and maintenance in <i>Bos taurus</i> . <i>BMC Genomics</i> , 2019, 20, 940.	1.2	26
81	Mitochondrial DNA of seven Italian sheep breeds shows faint signatures of domestication and suggests recent breed formation. <i>Mitochondrial DNA</i> , 2013, 24, 577-583.	0.6	25
82	Signatures of selection? Patterns of microsatellite diversity on a chromosome containing a selected locus. <i>Heredity</i> , 2003, 90, 350-358.	1.2	24
83	Geographical patterning of sixteen goat breeds from Italy, Albania and Greece assessed by Single Nucleotide Polymorphisms. <i>BMC Ecology</i> , 2009, 9, 20.	3.0	24
84	Recent Advance in DNA-based Traceability and Authentication of Livestock Meat PDO and PGI Products. <i>Recent Patents on Food, Nutrition &amp; Agriculture</i> , 2013, 5, 9-18.	0.5	24
85	Assessment of population structure by single nucleotide polymorphisms (SNPs) in goat breeds. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2006, 833, 117-120.	1.2	23
86	Johne's disease in cattle: an in vitro model to study early response to infection of <i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> using RNA-seq. <i>Molecular Immunology</i> , 2017, 91, 259-271.	1.0	23
87	Association of Copy Number Variation at Intron 3 of HMG2 With Navel Length in <i>Bos indicus</i> . <i>Frontiers in Genetics</i> , 2018, 9, 627.	1.1	23
88	The climatic and genetic heritage of Italian goat breeds with genomic SNP data. <i>Scientific Reports</i> , 2021, 11, 10986.	1.6	23
89	Pleiotropic Genes Affecting Carcass Traits in <i>Bos indicus</i> (Nelore) Cattle Are Modulators of Growth. <i>PLoS ONE</i> , 2016, 11, e0158165.	1.1	23
90	Spatial Trends of Genetic Variation of Domestic Ruminants in Europe. <i>Diversity</i> , 2010, 2, 932-945.	0.7	22

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91	Revisiting AFLP fingerprinting for an unbiased assessment of genetic structure and differentiation of taurine and zebu cattle. <i>BMC Genetics</i> , 2014, 15, 47.	2.7	22
92	Deciphering the patterns of genetic admixture and diversity in southern European cattle using genome-wide SNPs. <i>Evolutionary Applications</i> , 2019, 12, 951-963.	1.5	22
93	Associations between differential somatic cell count and milk yield, quality, and technological characteristics in Holstein cows. <i>Journal of Dairy Science</i> , 2021, 104, 4822-4836.	1.4	22
94	Methylome Patterns of Cattle Adaptation to Heat Stress. <i>Frontiers in Genetics</i> , 2021, 12, 633132.	1.1	21
95	Cluster analysis of RFLP data from related maize inbred lines of the BSSS and LSC heterotic groups and comparison with pedigree data. <i>Euphytica</i> , 1992, 60, 139-148.	0.6	20
96	Diversity in five goat populations of the Lombardy Alps: comparison of estimates obtained from morphometric traits and molecular markers. <i>Journal of Animal Breeding and Genetics</i> , 2001, 118, 173-180.	0.8	20
97	Imputation accuracy is robust to cattle reference genome updates. <i>Animal Genetics</i> , 2015, 46, 69-72.	0.6	20
98	Searching new signals for production traits through gene-based association analysis in three Italian cattle breeds. <i>Animal Genetics</i> , 2015, 46, 361-370.	0.6	20
99	Evaluation of circulating leukocyte transcriptome and its relationship with immune function and blood markers in dairy cows during the transition period. <i>Functional and Integrative Genomics</i> , 2020, 20, 293-305.	1.4	20
100	Allele frequencies and diversity parameters of 27 single nucleotide polymorphisms within and across goat breeds. <i>Molecular Ecology Notes</i> , 2006, 6, 992-997.	1.7	19
101	Gene co-expression networks in liver and muscle transcriptome reveal sex-specific gene expression in lambs fed with a mix of essential oils. <i>BMC Genomics</i> , 2018, 19, 236.	1.2	19
102	Oregano dietary supplementation modifies the liver transcriptome profile in broilers: RNASeq analysis. <i>Research in Veterinary Science</i> , 2018, 117, 85-91.	0.9	19
103	Fine Mapping for Weaver Syndrome in Brown Swiss Cattle and the Identification of 41 Concordant Mutations across NRCAM, PNPLA8 and CTTNBP2. <i>PLoS ONE</i> , 2013, 8, e59251.	1.1	18
104	Multilocus genotypic data reveal high genetic diversity and low population genetic structure of Iranian indigenous sheep. <i>Animal Genetics</i> , 2016, 47, 463-470.	0.6	18
105	On the origin and diversification of Podolian cattle breeds: testing scenarios of European colonization using genome-wide SNP data. <i>Genetics Selection Evolution</i> , 2021, 53, 48.	1.2	18
106	The Quest for Genes Involved in Adaptation to Climate Change in Ruminant Livestock. <i>Animals</i> , 2021, 11, 2833.	1.0	18
107	Tuscany autochthonous cattle breeds: an original genetic resource investigated by AFLP markers. <i>Journal of Animal Breeding and Genetics</i> , 2006, 123, 10-16.	0.8	17
108	Characterization of single nucleotide polymorphisms in sheep and their variation as evidence of selection. <i>Animal Genetics</i> , 2006, 37, 290-292.	0.6	17

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109	The distribution of runs of homozygosity in the genome of river and swamp buffaloes reveals a history of adaptation, migration and crossbred events. <i>Genetics Selection Evolution</i> , 2021, 53, 20.	1.2	17
110	Safety Risks for Animals Fed Genetic Modified (GM) Plants. <i>Veterinary Research Communications</i> , 2005, 29, 13-18.	0.6	16
111	Effect of microsatellite outliers on the genetic structure of eight Italian goat breeds. <i>Small Ruminant Research</i> , 2012, 103, 99-107.	0.6	16
112	Genome-wide association analysis in Italian Simmental cows for lactation curve traits using a low-density (7K) SNP panel. <i>Journal of Dairy Science</i> , 2015, 98, 8175-8185.	1.4	16
113	Assessing The Spatial Dependence of Adaptive Loci in 43 European and Western Asian Goat Breeds Using AFLP Markers. <i>PLoS ONE</i> , 2014, 9, e86668.	1.1	15
114	Analysis of candidate SNPs affecting milk and functional traits in the dual-purpose Italian Simmental cattle. <i>Livestock Science</i> , 2015, 173, 1-8.	0.6	15
115	A method for single nucleotide polymorphism selection for parentage assessment in goats. <i>Journal of Dairy Science</i> , 2016, 99, 3646-3653.	1.4	15
116	Runs of homozygosity in the Italian goat breeds: impact of management practices in low-input systems. <i>Genetics Selection Evolution</i> , 2021, 53, 92.	1.2	15
117	Prediction of genomic breeding values for dairy traits in Italian Brown and Simmental bulls using a principal component approach. <i>Journal of Dairy Science</i> , 2012, 95, 3390-3400.	1.4	14
118	Use of canonical discriminant analysis to study signatures of selection in cattle. <i>Genetics Selection Evolution</i> , 2016, 48, 58.	1.2	14
119	Mapping molecular diversity of indigenous goat genetic resources of Asia. <i>Small Ruminant Research</i> , 2017, 148, 2-10.	0.6	14
120	Genetic parameters of differential somatic cell count, milk composition, and cheese-making traits measured and predicted using spectral data in Holstein cows. <i>Journal of Dairy Science</i> , 2021, 104, 10934-10949.	1.4	14
121	Identification of Ancestry Informative Marker (AIM) Panels to Assess Hybridisation between Feral and Domestic Sheep. <i>Animals</i> , 2020, 10, 582.	1.0	13
122	Associations between ultrasound measurements and hematochemical parameters for the assessment of liver metabolic status in Holstein-Friesian cows. <i>Scientific Reports</i> , 2021, 11, 16314.	1.6	13
123	Transformation of <i>Solanum integrifolium</i> poir via <i>Agrobacterium tumefaciens</i> : Plant regeneration and progeny analysis. <i>Plant Cell Reports</i> , 1992, 11, 11-5.	2.8	11
124	Analysis of stable events of transformation in wheat via PEG-mediated DNA uptake into protoplasts. <i>Plant Science</i> , 1993, 93, 85-94.	1.7	11
125	Application of AFLP® technology to radiation hybrid mapping. <i>Chromosome Research</i> , 2004, 12, 285-297.	1.0	11
126	Synergies between assisted reproduction technologies and functional genomics. <i>Genetics Selection Evolution</i> , 2016, 48, 53.	1.2	11



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127	Genome-Wide Epigenetic Characterization of Tissues from Three Germ Layers Isolated from Sheep Fetuses. <i>Frontiers in Genetics</i> , 2017, 8, 115.	1.1	11
128	Distribution of ncRNAs expression across hypothalamic-pituitary-gonadal axis in <i>Capra hircus</i> . <i>BMC Genomics</i> , 2018, 19, 417.	1.2	11
129	Genome-Wide DNA Methylation and Gene Expression Profiles in Cows Subjected to Different Stress Level as Assessed by Cortisol in Milk. <i>Genes</i> , 2020, 11, 850.	1.0	11
130	Nanotechnologies Applied to the Analysis of the Animal Genome. <i>Veterinary Research Communications</i> , 2007, 31, 153-159.	0.6	10
131	Association between single nucleotide polymorphisms (SNPs) and milk production traits in Italian Brown cattle. <i>Livestock Science</i> , 2013, 157, 93-99.	0.6	10
132	The nutrigenomic investigation of C57BL/6N mice fed a short-term high-fat diet highlights early changes in clock genes expression. <i>Genes and Nutrition</i> , 2013, 8, 465-474.	1.2	10
133	Identification of additional loci associated with antibody response to <i>Mycobacterium avium</i> ssp. <i>Paratuberculosis</i> in cattle by GSEA SNP analysis. <i>Mammalian Genome</i> , 2017, 28, 520-527.	1.0	10
134	The other side of comparative genomics: genes with no orthologs between the cow and other mammalian species. <i>BMC Genomics</i> , 2009, 10, 604.	1.2	8
135	Use of partial least squares regression to impute SNP genotypes in Italian Cattle breeds. <i>Genetics Selection Evolution</i> , 2013, 45, 15.	1.2	8
136	Potential neoplastic evolution of Vero cells: in vivo and in vitro characterization. <i>Cytotechnology</i> , 2017, 69, 741-750.	0.7	8
137	A genetically unique Chinese cattle population shows evidence of common ancestry with wild species when analysed with a reduced ascertainment bias SNP panel. <i>PLoS ONE</i> , 2020, 15, e0231162.	1.1	8
138	Application of amplified fragment length polymorphism markers to assess molecular polymorphisms in gynogenetic haploid embryos of turbot ( <i>Scophthalmus maximus</i> ). <i>Aquaculture Research</i> , 2008, 39, 41-49.	0.9	7
139	Genome wide scan for somatic cell counts in holstein bulls. <i>BMC Proceedings</i> , 2011, 5, S17.	1.8	7
140	Reproductive biotechnology and critically endangered species: Merging in vitro gametogenesis with inner cell mass transfer. <i>Theriogenology</i> , 2020, 155, 176-184.	0.9	7
141	Genome-wide diversity of Pagliarola sheep residual population and its conservation implication. <i>Italian Journal of Animal Science</i> , 2021, 20, 1695-1705.	0.8	7
142	The SNP-Based Profiling of Montecristo Feral Goat Populations Reveals a History of Isolation, Bottlenecks, and the Effects of Management. <i>Genes</i> , 2022, 13, 213.	1.0	7
143	Detection of QTL for milk protein percentage in Italian Friesian cattle by AFLP markers and selective genotyping. <i>Journal of Dairy Research</i> , 2008, 75, 430-438.	0.7	6
144	Unsupervised detection of ancestry tracks with the GHap package. <i>Methods in Ecology and Evolution</i> , 2020, 11, 1448-1454.	2.2	6

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145	Breed and adaptive response modulate bovine peripheral blood cellsâ€™ transcriptome. <i>Journal of Animal Science and Biotechnology</i> , 2017, 8, 11.	2.1	5
146	Associations between Milk Fatty Acid Profile and Body Condition Score, Ultrasound Hepatic Measurements and Blood Metabolites in Holstein Cows. <i>Animals</i> , 2022, 12, 1202.	1.0	5
147	Editorial: Haplotype Analysis Applied to Livestock Genomics. <i>Frontiers in Genetics</i> , 2021, 12, 660478.	1.1	4
148	Pattern of ancient goat migration revealed by AFLP molecular markers. <i>Italian Journal of Animal Science</i> , 2005, 4, 55-57.	0.8	3
149	Untargeted metabolomic profiling of accessory sex gland fluid from Morada Nova rams. <i>Molecular Reproduction and Development</i> , 2020, 87, 409-418.	1.0	3
150	Use of multivariate factor analysis of detailed milk fatty acid profile to perform a genome-wide association study in Italian Simmental and Italian Holstein. <i>Journal of Applied Genetics</i> , 2020, 61, 451-463.	1.0	3
151	Genetic Regulation of Biomarkers as Stress Proxies in Dairy Cows. <i>Genes</i> , 2021, 12, 534.	1.0	3
152	One-Day Molecular Detection of Salmonella and Campylobacter in Chicken Meat: A Pilot Study. <i>Foods</i> , 2021, 10, 1132.	1.9	3
153	Traceability of the PGI product "Vitellone Bianco dell'Appennino Centrale" by SNP markers. <i>Italian Journal of Animal Science</i> , 2007, 6, 174-174.	0.8	2
154	Assessment of AFLP marker behaviour in enriching STS radiation hybrid maps. <i>Animal Genetics</i> , 2008, 39, 383-394.	0.6	2
155	Construction and Use of Genetic Maps in Cereals. , 2002, , 347-369.		2
156	Nutrition and Ageing. <i>Studies in Health Technology and Informatics</i> , 2014, 203, 112-21.	0.2	2
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