

# Paolo Ajmone Marsan

## List of Publications by Citations

**Source:** <https://exaly.com/author-pdf/8696345/paolo-ajmone-marsan-publications-by-citations.pdf>

**Version:** 2024-04-26

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

162  
papers

6,020  
citations

39  
h-index

73  
g-index

168  
ext. papers

7,466  
ext. citations

4.3  
avg, IF

5.09  
L-index

#	Paper	IF	Citations
162	Genome-wide survey of SNP variation uncovers the genetic structure of cattle breeds. <i>Science</i> , <b>2009</b> , 324, 528-32	33.3	612
161	Comparative analysis of genetic similarity among maize inbred lines detected by RFLPs, RAPDs, SSRs, and AFLPs. <i>Theoretical and Applied Genetics</i> , <b>1998</b> , 97, 1248-1255	6	363
160	Revealing the history of sheep domestication using retrovirus integrations. <i>Science</i> , <b>2009</b> , 324, 532-6	33.3	292
159	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> , <b>2008</b> , 105, 17659-64	11.5	199
158	Mitochondrial genomes of extinct aurochs survive in domestic cattle. <i>Current Biology</i> , <b>2008</b> , 18, R157-8	6.3	181
157	Are cattle, sheep, and goats endangered species?. <i>Molecular Ecology</i> , <b>2008</b> , 17, 275-84	5.7	168
156	Geographical partitioning of goat diversity in Europe and the Middle East. <i>Animal Genetics</i> , <b>2006</b> , 37, 327-34	2.5	145
155	Genetic diversity and its relationship to hybrid performance in maize as revealed by RFLP and AFLP markers. <i>Theoretical and Applied Genetics</i> , <b>1998</b> , 96, 219-227	6	140
154	On the origin of cattle: How aurochs became cattle and colonized the world. <i>Evolutionary Anthropology</i> , <b>2010</b> , 19, 148-157	4.7	139
153	The multifaceted origin of taurine cattle reflected by the mitochondrial genome. <i>PLoS ONE</i> , <b>2009</b> , 4, e5753	3.7	123
152	AFLP markers in a molecular linkage map of maize: codominant scoring and linkage group distribution. <i>Theoretical and Applied Genetics</i> , <b>1999</b> , 99, 425-31	6	118
151	AFLP markers for DNA fingerprinting in cattle. <i>Animal Genetics</i> , <b>1997</b> , 28, 418-26	2.5	116
150	Convergent genomic signatures of domestication in sheep and goats. <i>Nature Communications</i> , <b>2018</b> , 9, 813	17.4	112
149	Analysis of runs of homozygosity and their relationship with inbreeding in five cattle breeds farmed in Italy. <i>Animal Genetics</i> , <b>2015</b> , 46, 110-21	2.5	110
148	Genetic diversity in widespread species is not congruent with species richness in alpine plant communities. <i>Ecology Letters</i> , <b>2012</b> , 15, 1439-48	10	108
147	Adaptations to climate-mediated selective pressures in sheep. <i>Molecular Biology and Evolution</i> , <b>2014</b> , 31, 3324-43	8.3	104
146	Identification of selection signatures in cattle breeds selected for dairy production. <i>Genetics</i> , <b>2010</b> , 185, 1451-61	4	93

145	Molecular tools and analytical approaches for the characterization of farm animal genetic diversity. <i>Animal Genetics</i> , <b>2012</b> , 43, 483-502	2.5	82
144	Chromosome-level assembly of the water buffalo genome surpasses human and goat genomes in sequence contiguity. <i>Nature Communications</i> , <b>2019</b> , 10, 260	17.4	75
143	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> , <b>2010</b> , 5, e15760	3.7	67
142	Double muscling in Marchigiana beef breed is caused by a stop codon in the third exon of myostatin gene. <i>Mammalian Genome</i> , <b>2003</b> , 14, 392-5	3.2	67
141	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> , <b>2003</b> , 66, 103-9	2.5	65
140	The mystery of Etruscan origins: novel clues from <i>Bos taurus</i> mitochondrial DNA. <i>Proceedings of the Royal Society B: Biological Sciences</i> , <b>2007</b> , 274, 1175-9	4.4	61
139	Origin and spread of <i>Bos taurus</i> : new clues from mitochondrial genomes belonging to haplogroup T1. <i>PLoS ONE</i> , <b>2012</b> , 7, e38601	3.7	58
138	Establishment and characterization of two new pig cell lines for use in virological diagnostic laboratories. <i>Journal of Virological Methods</i> , <b>2003</b> , 107, 205-12	2.6	55
137	Genome-wide analysis of Italian sheep diversity reveals a strong geographic pattern and cryptic relationships between breeds. <i>Animal Genetics</i> , <b>2014</b> , 45, 256-66	2.5	53
136	Genetic diversity of maize inbred lines within and among heterotic groups revealed by RFLPs. <i>Theoretical and Applied Genetics</i> , <b>1992</b> , 84, 17-25	6	52
135	Genome wide analysis of fertility and production traits in Italian Holstein cattle. <i>PLoS ONE</i> , <b>2013</b> , 8, e80249	3.9	52
134	Genetic diversity of Italian goat breeds assessed with a medium-density SNP chip. <i>Genetics Selection Evolution</i> , <b>2015</b> , 47, 62	4.9	51
133	Prospects and challenges for the conservation of farm animal genomic resources, 2015-2025. <i>Frontiers in Genetics</i> , <b>2015</b> , 6, 314	4.5	50
132	Landscape genomics and biased FST approaches reveal single nucleotide polymorphisms under selection in goat breeds of North-East Mediterranean. <i>BMC Genetics</i> , <b>2009</b> , 10, 7	2.6	46
131	An improved protocol for the production of AFLP markers in complex genomes by means of capillary electrophoresis. <i>Journal of Animal Breeding and Genetics</i> , <b>2005</b> , 122, 62-8	2.9	46
130	Whole mitochondrial genomes unveil the impact of domestication on goat matrilineal variability. <i>BMC Genomics</i> , <b>2015</b> , 16, 1115	4.5	45
129	Assessing genetic diversity in Italian goat populations using AFLP markers. <i>Animal Genetics</i> , <b>2001</b> , 32, 281-8	2.5	45
128	Design and validation of a 90K SNP genotyping assay for the water buffalo ( <i>Bubalus bubalis</i> ). <i>PLoS ONE</i> , <b>2017</b> , 12, e0185220	3.7	44

127	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> , <b>2001</b> , 102, 230-243	6	42
126	Differentiation of European cattle by AFLP fingerprinting. <i>Animal Genetics</i> , <b>2007</b> , 38, 60-6	2.5	41
125	Genome-wide SNP profiling of worldwide goat populations reveals strong partitioning of diversity and highlights post-domestication migration routes. <i>Genetics Selection Evolution</i> , <b>2018</b> , 50, 58	4.9	41
124	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> , <b>2018</b> , 101, 11004-11019	4.0	40
123	Traceability of four European Protected Geographic Indication (PGI) beef products using Single Nucleotide Polymorphisms (SNP) and Bayesian statistics. <i>Meat Science</i> , <b>2008</b> , 80, 1212-7	6.4	39
122	Sustainable ruminant production to help feed the planet. <i>Italian Journal of Animal Science</i> , <b>2017</b> , 16, 1402-1411	3.7	36
121	New Insights on Water Buffalo Genomic Diversity and Post-Domestication Migration Routes From Medium Density SNP Chip Data. <i>Frontiers in Genetics</i> , <b>2018</b> , 9, 53	4.5	36
120	Gut response induced by weaning in piglet features marked changes in immune and inflammatory response. <i>Functional and Integrative Genomics</i> , <b>2014</b> , 14, 657-71	3.8	36
119	Meta-Analysis of Mitochondrial DNA Reveals Several Population Bottlenecks during Worldwide Migrations of Cattle. <i>Diversity</i> , <b>2014</b> , 6, 178-187	2.5	36
118	Assessing SNP markers for assigning individuals to cattle populations. <i>Animal Genetics</i> , <b>2009</b> , 40, 18-26	2.5	36
117	A candidate gene association study for nine economically important traits in Italian Holstein cattle. <i>Animal Genetics</i> , <b>2014</b> , 45, 576-80	2.5	35
116	Conservation status and historical relatedness of Italian cattle breeds. <i>Genetics Selection Evolution</i> , <b>2018</b> , 50, 35	4.9	34
115	Distribution and Functionality of Copy Number Variation across European Cattle Populations. <i>Frontiers in Genetics</i> , <b>2017</b> , 8, 108	4.5	34
114	Massive screening of copy number population-scale variation in <i>Bos taurus</i> genome. <i>BMC Genomics</i> , <b>2013</b> , 14, 124	4.5	33
113	Internal controls for quantitative polymerase chain reaction of swine mammary glands during pregnancy and lactation. <i>Journal of Dairy Science</i> , <b>2008</b> , 91, 3057-66	4	33
112	A PLAG1 mutation contributed to stature recovery in modern cattle. <i>Scientific Reports</i> , <b>2017</b> , 7, 17140	4.9	32
111	The characterization of goat genetic diversity: Towards a genomic approach. <i>Small Ruminant Research</i> , <b>2014</b> , 121, 58-72	1.7	31
110	Genetic distances within and across cattle breeds as indicated by biallelic AFLP markers. <i>Animal Genetics</i> , <b>2002</b> , 33, 280-6	2.5	30

109	Revisiting demographic processes in cattle with genome-wide population genetic analysis. <i>Frontiers in Genetics</i> , <b>2015</b> , 6, 191	4.5	29
108	The b-32 protein from maize endosperm: characterization of genomic sequences encoding two alternative central domains. <i>Plant Molecular Biology</i> , <b>1990</b> , 14, 1031-40	4.6	29
107	Inbreeding and purging at the genomic Level: the Chillingham cattle reveal extensive, non-random SNP heterozygosity. <i>Animal Genetics</i> , <b>2016</b> , 47, 19-27	2.5	28
106	Relative extended haplotype homozygosity signals across breeds reveal dairy and beef specific signatures of selection. <i>Genetics Selection Evolution</i> , <b>2015</b> , 47, 25	4.9	27
105	Genome assembly and transcriptome resource for river buffalo, <i>Bubalus bubalis</i> (2n = 50). <i>GigaScience</i> , <b>2017</b> , 6, 1-6	7.6	27
104	Standard and Light-Cycler PCR methods for animal DNA species detection in animal feedstuffs. <i>Innovative Food Science and Emerging Technologies</i> , <b>2008</b> , 9, 18-23	6.8	27
103	Derivation and genome-wide association study of a principal component-based measure of heat tolerance in dairy cattle. <i>Journal of Dairy Science</i> , <b>2017</b> , 100, 4683-4697	4	26
102	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> , <b>2020</b> , 52, 25	4.9	25
101	BITE: an R package for biodiversity analyses		25
100	Signatures of selection in five Italian cattle breeds detected by a 54K SNP panel. <i>Molecular Biology Reports</i> , <b>2014</b> , 41, 957-65	2.8	24
99	Detecting population structure and recent demographic history in endangered livestock breeds: the case of the Italian autochthonous donkeys. <i>Animal Genetics</i> , <b>2013</b> , 44, 69-78	2.5	24
98	Breed assignment of Italian cattle using biallelic AFLP markers. <i>Animal Genetics</i> , <b>2007</b> , 38, 147-53	2.5	24
97	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> , <b>2009</b> , 40, 486-91	2.5	23
96	A second generation radiation hybrid map to aid the assembly of the bovine genome sequence. <i>BMC Genomics</i> , <b>2006</b> , 7, 283	4.5	23
95	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> , <b>2014</b> , 46, 27	4.9	22
94	Characterization of 37 breed-specific single-nucleotide polymorphisms in sheep. <i>Journal of Heredity</i> , <b>2006</b> , 97, 531-4	2.4	22
93	Signatures of selection? Patterns of microsatellite diversity on a chromosome containing a selected locus. <i>Heredity</i> , <b>2003</b> , 90, 350-8	3.6	22
92	Mitochondrial DNA variants of Podolian cattle breeds testify for a dual maternal origin. <i>PLoS ONE</i> , <b>2018</b> , 13, e0192567	3.7	21

91	Revealing misassembled segments in the bovine reference genome by high resolution linkage disequilibrium scan. <i>BMC Genomics</i> , <b>2016</b> , 17, 705	4.5	21
90	Low levels of taurine introgression in the current Brazilian Nelore and Gir indicine cattle populations. <i>Genetics Selection Evolution</i> , <b>2015</b> , 47, 31	4.9	20
89	Adaptive introgression from indicine cattle into white cattle breeds from Central Italy. <i>Scientific Reports</i> , <b>2020</b> , 10, 1279	4.9	20
88	GHap: an R package for genome-wide haplotyping. <i>Bioinformatics</i> , <b>2016</b> , 32, 2861-2	7.2	20
87	Mitochondrial DNA of seven Italian sheep breeds shows faint signatures of domestication and suggests recent breed formation. <i>Mitochondrial DNA</i> , <b>2013</b> , 24, 577-83		20
86	Recent advance in DNA-based traceability and authentication of livestock meat PDO and PGI products. <i>Recent Patents on Food, Nutrition &amp; Agriculture</i> , <b>2013</b> , 5, 9-18	1.9	20
85	Geographical patterning of sixteen goat breeds from Italy, Albania and Greece assessed by Single Nucleotide Polymorphisms. <i>BMC Ecology</i> , <b>2009</b> , 9, 20	2.7	20
84	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> , <b>2019</b> , 20, 940	4.5	20
83	Spatial Trends of Genetic Variation of Domestic Ruminants in Europe. <i>Diversity</i> , <b>2010</b> , 2, 932-945	2.5	19
82	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> , <b>2006</b> , 833, 117-20 <sup>2</sup>	3.2	19
81	Revisiting AFLP fingerprinting for an unbiased assessment of genetic structure and differentiation of taurine and zebu cattle. <i>BMC Genetics</i> , <b>2014</b> , 15, 47	2.6	18
80	Searching new signals for production traits through gene-based association analysis in three Italian cattle breeds. <i>Animal Genetics</i> , <b>2015</b> , 46, 361-70	2.5	17
79	Genetic diversity of sheep breeds from Albania, Greece, and Italy assessed by mitochondrial DNA and nuclear polymorphisms (SNPs). <i>Scientific World Journal, The</i> , <b>2011</b> , 11, 1641-59	2.2	17
78	Characterization of single nucleotide polymorphisms in sheep and their variation as evidence of selection. <i>Animal Genetics</i> , <b>2006</b> , 37, 290-2	2.5	17
77	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> , <b>1992</b> , 60, 139-148	2.1	16
76	Pleiotropic Genes Affecting Carcass Traits in <i>Bos indicus</i> (Nellore) Cattle Are Modulators of Growth. <i>PLoS ONE</i> , <b>2016</b> , 11, e0158165	3.7	16
75	Combining Landscape Genomics and Ecological Modelling to Investigate Local Adaptation of Indigenous Ugandan Cattle to East Coast Fever. <i>Frontiers in Genetics</i> , <b>2018</b> , 9, 385	4.5	16
74	Integrative analysis of methylomic and transcriptomic data in fetal sheep muscle tissues in response to maternal diet during pregnancy. <i>BMC Genomics</i> , <b>2018</b> , 19, 123	4.5	15

73	Allele frequencies and diversity parameters of 27 single nucleotide polymorphisms within and across goat breeds. <i>Molecular Ecology Notes</i> , <b>2006</b> , 6, 992-997		15
72	Safety risks for animals fed genetic modified (GM) plants. <i>Veterinary Research Communications</i> , <b>2005</b> , 29 Suppl 2, 13-8	2.9	15
71	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> , <b>2017</b> , 91, 259-271	4.3	14
70	Deciphering the patterns of genetic admixture and diversity in southern European cattle using genome-wide SNPs. <i>Evolutionary Applications</i> , <b>2019</b> , 12, 951-963	4.8	14
69	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> , <b>2018</b> , 19, 236	4.5	14
68	Tuscany autochthonous cattle breeds: an original genetic resource investigated by AFLP markers. <i>Journal of Animal Breeding and Genetics</i> , <b>2006</b> , 123, 10-6	2.9	14
67	The Valdostana goat: a genome-wide investigation of the distinctiveness of its selective sweep regions. <i>Mammalian Genome</i> , <b>2017</b> , 28, 114-128	3.2	13
66	Effect of microsatellite outliers on the genetic structure of eight Italian goat breeds. <i>Small Ruminant Research</i> , <b>2012</b> , 103, 99-107	1.7	13
65	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> , <b>2001</b> , 118, 173-180	2.9	13
64	Multilocus genotypic data reveal high genetic diversity and low population genetic structure of Iranian indigenous sheep. <i>Animal Genetics</i> , <b>2016</b> , 47, 463-70	2.5	13
63	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> , <b>2015</b> , 98, 8175-85	4	12
62	A method for single nucleotide polymorphism selection for parentage assessment in goats. <i>Journal of Dairy Science</i> , <b>2016</b> , 99, 3646-3653	4	12
61	Analysis of candidate SNPs affecting milk and functional traits in the dual-purpose Italian Simmental cattle. <i>Livestock Science</i> , <b>2015</b> , 173, 1-8	1.7	12
60	Assessing the spatial dependence of adaptive loci in 43 European and Western Asian goat breeds using AFLP markers. <i>PLoS ONE</i> , <b>2014</b> , 9, e86668	3.7	12
59	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> , <b>2012</b> , 95, 3390-400	4	12
58	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> , <b>2013</b> , 8, e59251	3.7	12
57	Oregano dietary supplementation modifies the liver transcriptome profile in broilers: RNASeq analysis. <i>Research in Veterinary Science</i> , <b>2018</b> , 117, 85-91	2.5	12
56	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> , <b>2020</b> , 20, 293-305	3.8	12

55	Occurrence, biological properties and potential effects on human health of Ecasomorphin 7: Current knowledge and concerns. <i>Critical Reviews in Food Science and Nutrition</i> , <b>2020</b> , 60, 3705-3723	11.5	11
54	Mapping molecular diversity of indigenous goat genetic resources of Asia. <i>Small Ruminant Research</i> , <b>2017</b> , 148, 2-10	1.7	10
53	Analysis of stable events of transformation in wheat via PEG-mediated DNA uptake into protoplasts. <i>Plant Science</i> , <b>1993</b> , 93, 85-94	5.3	10
52	Use of canonical discriminant analysis to study signatures of selection in cattle. <i>Genetics Selection Evolution</i> , <b>2016</b> , 48, 58	4.9	9
51	Association of Copy Number Variation at Intron 3 of With Navel Length in. <i>Frontiers in Genetics</i> , <b>2018</b> , 9, 627	4.5	9
50	Association between single nucleotide polymorphisms (SNPs) and milk production traits in Italian Brown cattle. <i>Livestock Science</i> , <b>2013</b> , 157, 93-99	1.7	8
49	Identification of additional loci associated with antibody response to Mycobacterium avium ssp. Paratuberculosis in cattle by GSEA-SNP analysis. <i>Mammalian Genome</i> , <b>2017</b> , 28, 520-527	3.2	8
48	Application of AFLP technology to radiation hybrid mapping. <i>Chromosome Research</i> , <b>2004</b> , 12, 285-97	4.4	8
47	Transformation of Solanum integrifolium poir via Agrobacterium tumefaciens: Plant regeneration and progeny analysis. <i>Plant Cell Reports</i> , <b>1992</b> , 11, 11-5	5.1	8
46	Use of partial least squares regression to impute SNP genotypes in Italian cattle breeds. <i>Genetics Selection Evolution</i> , <b>2013</b> , 45, 15	4.9	7
45	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> , <b>2013</b> , 8, 465-74	4.3	7
44	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> , <b>2007</b> , 39, 41-49	1.9	7
43	Nanotechnologies applied to the analysis of the animal genome. <i>Veterinary Research Communications</i> , <b>2007</b> , 31 Suppl 1, 153-9	2.9	7
42	Synergies between assisted reproduction technologies and functional genomics. <i>Genetics Selection Evolution</i> , <b>2016</b> , 48, 53	4.9	7
41	Distribution of ncRNAs expression across hypothalamic-pituitary-gonadal axis in Capra hircus. <i>BMC Genomics</i> , <b>2018</b> , 19, 417	4.5	7
40	Imputation accuracy is robust to cattle reference genome updates. <i>Animal Genetics</i> , <b>2015</b> , 46, 69-72	2.5	6
39	The other side of comparative genomics: genes with no orthologs between the cow and other mammalian species. <i>BMC Genomics</i> , <b>2009</b> , 10, 604	4.5	6
38	Genome-Wide DNA Methylation and Gene Expression Profiles in Cows Subjected to Different Stress Level as Assessed by Cortisol in Milk. <i>Genes</i> , <b>2020</b> , 11,	4.2	6



37	On the origin and diversification of Podolian cattle breeds: testing scenarios of European colonization using genome-wide SNP data. <i>Genetics Selection Evolution</i> , <b>2021</b> , 53, 48	4.9	6
36	Genome wide scan for somatic cell counts in holstein bulls. <i>BMC Proceedings</i> , <b>2011</b> , 5 Suppl 4, S17	2.3	5
35	Potential neoplastic evolution of Vero cells: in vivo and in vitro characterization. <i>Cytotechnology</i> , <b>2017</b> , 69, 741-750	2.2	4
34	Detection of QTL for milk protein percentage in Italian Friesian cattle by AFLP markers and selective genotyping. <i>Journal of Dairy Research</i> , <b>2008</b> , 75, 430-8	1.6	4
33	Associations between differential somatic cell count and milk yield, quality, and technological characteristics in Holstein cows. <i>Journal of Dairy Science</i> , <b>2021</b> , 104, 4822-4836	4	4
32	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> , <b>2021</b> , 53, 20	4.9	4
31	Reproductive biotechnology and critically endangered species: Merging in vitro gametogenesis with inner cell mass transfer. <i>Theriogenology</i> , <b>2020</b> , 155, 176-184	2.8	3
30	Identification of Ancestry Informative Marker (AIM) Panels to Assess Hybridisation between Feral and Domestic Sheep. <i>Animals</i> , <b>2020</b> , 10,	3.1	3
29	Breed and adaptive response modulate bovine peripheral blood cells' transcriptome. <i>Journal of Animal Science and Biotechnology</i> , <b>2017</b> , 8, 11	6	3
28	Methylome Patterns of Cattle Adaptation to Heat Stress. <i>Frontiers in Genetics</i> , <b>2021</b> , 12, 633132	4.5	3
27	The Quest for Genes Involved in Adaptation to Climate Change in Ruminant Livestock. <i>Animals</i> , <b>2021</b> , 11,	3.1	3
26	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> , <b>2022</b> ,	4	3
25	Genome-Wide Epigenetic Characterization of Tissues from Three Germ Layers Isolated from Sheep Fetuses. <i>Frontiers in Genetics</i> , <b>2017</b> , 8, 115	4.5	2
24	Traceability of the PGI product Vitellone Bianco dell'Appennino Centrale by SNP markers. <i>Italian Journal of Animal Science</i> , <b>2007</b> , 6, 174-174	2.2	2
23	Pattern of ancient goat migration revealed by AFLP molecular markers. <i>Italian Journal of Animal Science</i> , <b>2005</b> , 4, 55-57	2.2	2
22	Construction and Use of Genetic Maps in Cereals <b>2002</b> , 347-369		2
21	Phylogeny and distribution of Y-chromosomal haplotypes in domestic, ancient and wild goats		2
20	Unsupervised detection of ancestry tracks with the GMap package. <i>Methods in Ecology and Evolution</i> , <b>2020</b> , 11, 1448-1454	7.7	2

19	Genetic Regulation of Biomarkers as Stress Proxies in Dairy Cows. <i>Genes</i> , <b>2021</b> , 12,	4.2	2
18	The climatic and genetic heritage of Italian goat breeds with genomic SNP data. <i>Scientific Reports</i> , <b>2021</b> , 11, 10986	4.9	2
17	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> , <b>2020</b> , 15, e0231162	3.7	2
16	Associations between ultrasound measurements and hematochemical parameters for the assessment of liver metabolic status in Holstein-Friesian cows. <i>Scientific Reports</i> , <b>2021</b> , 11, 16314	4.9	2
15	Untargeted metabolomic profiling of accessory sex gland fluid from Morada Nova rams. <i>Molecular Reproduction and Development</i> , <b>2020</b> , 87, 409-418	2.6	1
14	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> , <b>2020</b> , 61, 451-463 <sup>2.5</sup>		1
13	Maximum difference analysis: a new empirical method for genome-wide association studies. <i>Italian Journal of Animal Science</i> , <b>2016</b> , 15, 396-406	2.2	1
12	Assessment of AFLP marker behaviour in enriching STS radiation hybrid maps. <i>Animal Genetics</i> , <b>2008</b> , 39, 383-94	2.5	1
11	Runs of homozygosity in the Italian goat breeds: impact of management practices in low-input systems.. <i>Genetics Selection Evolution</i> , <b>2021</b> , 53, 92	4.9	1
10	Multiple adaptive solutions to face climatic constraints: novel insights in the debate over the role of convergence in local adaptation		1
9	Detecting footprints of selection in Ovis aries by a spatial analysis approach. <i>Italian Journal of Animal Science</i> , <b>2007</b> , 6, 171-173	2.2	1
8	Combining landscape genomics and ecological modelling to investigate local adaptation of indigenous Ugandan cattle to East Coast fever		1
7	Genomic prediction for latent variables related to milk fatty acid composition in Holstein, Simmental and Brown Swiss dairy cattle breeds. <i>Journal of Animal Breeding and Genetics</i> , <b>2021</b> , 138, 389-402 <sup>2.9</sup>		1
6	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> , <b>2021</b> , 104, 10934-10949 <sup>1</sup>		1
5	Food for Healthy Living and Active Ageing. <i>Studies in Health Technology and Informatics</i> , <b>2014</b> , 203, 32-43 <sup>3.5</sup>		1
4	Nutrition and Ageing. <i>Studies in Health Technology and Informatics</i> , <b>2014</b> , 203, 112-21	0.5	1
3	Genome-wide diversity of Pagliarola sheep residual population and its conservation implication. <i>Italian Journal of Animal Science</i> , <b>2021</b> , 20, 1695-1705	2.2	0
2	Missense mutations of NCPAG gene affect calving ease in Piedmontese cattle: preliminary evidences. <i>Italian Journal of Animal Science</i> , <b>2018</b> , 17, 301-305	2.2	

- 1 Water Buffalo Genomic Diversity **2022**, 33-55