

Paolo Ajmone Marsan

List of Publications by Year in Descending Order

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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	The βcasein (CSN2) A2 allelic variant alters milk protein profile and slightly worsens coagulation properties in Holstein cows.. <i>Journal of Dairy Science</i> , 2022 ,	4	3
161	Water Buffalo Genomic Diversity 2022 , 33-55		
160	Runs of homozygosity in the Italian goat breeds: impact of management practices in low-input systems.. <i>Genetics Selection Evolution</i> , 2021 , 53, 92	4.9	1
159	Genome-wide diversity of Pagliarola sheep residual population and its conservation implication. <i>Italian Journal of Animal Science</i> , 2021 , 20, 1695-1705	2.2	0
158	Genetic Regulation of Biomarkers as Stress Proxies in Dairy Cows. <i>Genes</i> , 2021 , 12,	4.2	2
157	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	4	4
156	Methylome Patterns of Cattle Adaptation to Heat Stress. <i>Frontiers in Genetics</i> , 2021 , 12, 633132	4.5	3
155	The climatic and genetic heritage of Italian goat breeds with genomic SNP data. <i>Scientific Reports</i> , 2021 , 11, 10986	4.9	2
154	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	4.9	6
153	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> , 2021 , 138, 389-402	2.9	1
152	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	4.9	4
151	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	4.9	2
150	The Quest for Genes Involved in Adaptation to Climate Change in Ruminant Livestock. <i>Animals</i> , 2021 , 11,	3.1	3
149	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	4.9	1
148	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	4.9	25
147	Reproductive biotechnology and critically endangered species: Merging in vitro gametogenesis with inner cell mass transfer. <i>Theriogenology</i> , 2020 , 155, 176-184	2.8	3
146	Untargeted metabolomic profiling of accessory sex gland fluid from Morada Nova rams. <i>Molecular Reproduction and Development</i> , 2020 , 87, 409-418	2.6	1

145	Identification of Ancestry Informative Marker (AIM) Panels to Assess Hybridisation between Feral and Domestic Sheep. <i>Animals</i> , 2020 , 10,	3.1	3
144	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 ²⁻⁵		1
143	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> , 2020 , 60, 3705-3723	11.5	11
142	Adaptive introgression from indicine cattle into white cattle breeds from Central Italy. <i>Scientific Reports</i> , 2020 , 10, 1279	4.9	20
141	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	3.8	12
140	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,	4.2	6
139	Unsupervised detection of ancestry tracks with the GHap r package. <i>Methods in Ecology and Evolution</i> , 2020 , 11, 1448-1454	7.7	2
138	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	3.7	2
137	Deciphering the patterns of genetic admixture and diversity in southern European cattle using genome-wide SNPs. <i>Evolutionary Applications</i> , 2019 , 12, 951-963	4.8	14
136	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	4.5	20
135	Chromosome-level assembly of the water buffalo genome surpasses human and goat genomes in sequence contiguity. <i>Nature Communications</i> , 2019 , 10, 260	17.4	75
134	Convergent genomic signatures of domestication in sheep and goats. <i>Nature Communications</i> , 2018 , 9, 813	17.4	112
133	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	4.5	14
132	Missense mutations of NCPAG gene affect calving ease in Piedmontese cattle: preliminary evidences. <i>Italian Journal of Animal Science</i> , 2018 , 17, 301-305	2.2	
131	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	4.5	15
130	Conservation status and historical relatedness of Italian cattle breeds. <i>Genetics Selection Evolution</i> , 2018 , 50, 35	4.9	34
129	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	4.5	36
128	Mitochondrial DNA variants of Podolian cattle breeds testify for a dual maternal origin. <i>PLoS ONE</i> , 2018 , 13, e0192567	3.7	21

127	Oregano dietary supplementation modifies the liver transcriptome profile in broilers: RNASeq analysis. <i>Research in Veterinary Science</i> , 2018 , 117, 85-91	2.5	12
126	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	4.9	41
125	Association of Copy Number Variation at Intron 3 of With Navel Length in. <i>Frontiers in Genetics</i> , 2018 , 9, 627	4.5	9
124	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	4.5	16
123	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	4.0	40
122	Distribution of ncRNAs expression across hypothalamic-pituitary-gonadal axis in Capra hircus. <i>BMC Genomics</i> , 2018 , 19, 417	4.5	7
121	The Valdostana goat: a genome-wide investigation of the distinctiveness of its selective sweep regions. <i>Mammalian Genome</i> , 2017 , 28, 114-128	3.2	13
120	Sustainable ruminant production to help feed the planet. <i>Italian Journal of Animal Science</i> , 2017 , 16, 140-171	3.6	36
119	Potential neoplastic evolution of Vero cells: in vivo and in vitro characterization. <i>Cytotechnology</i> , 2017 , 69, 741-750	2.2	4
118	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	4	26
117	Mapping molecular diversity of indigenous goat genetic resources of Asia. <i>Small Ruminant Research</i> , 2017 , 148, 2-10	1.7	10
116	Johne's disease in cattle: an in vitro model to study early response to infection of Mycobacterium avium subsp. paratuberculosis using RNA-seq. <i>Molecular Immunology</i> , 2017 , 91, 259-271	4.3	14
115	Design and validation of a 90K SNP genotyping assay for the water buffalo (<i>Bubalus bubalis</i>). <i>PLoS ONE</i> , 2017 , 12, e0185220	3.7	44
114	Identification of additional loci associated with antibody response to Mycobacterium avium ssp. Paratuberculosis in cattle by GSEA-SNP analysis. <i>Mammalian Genome</i> , 2017 , 28, 520-527	3.2	8
113	A PLAG1 mutation contributed to stature recovery in modern cattle. <i>Scientific Reports</i> , 2017 , 7, 17140	4.9	32
112	Breed and adaptive response modulate bovine peripheral blood cells' transcriptome. <i>Journal of Animal Science and Biotechnology</i> , 2017 , 8, 11	6	3
111	Genome assembly and transcriptome resource for river buffalo, <i>Bubalus bubalis</i> (2n = 50). <i>GigaScience</i> , 2017 , 6, 1-6	7.6	27
110	Distribution and Functionality of Copy Number Variation across European Cattle Populations. <i>Frontiers in Genetics</i> , 2017 , 8, 108	4.5	34

109	Genome-Wide Epigenetic Characterization of Tissues from Three Germ Layers Isolated from Sheep Fetuses. <i>Frontiers in Genetics</i> , 2017 , 8, 115	4.5	2
108	Maximum difference analysis: a new empirical method for genome-wide association studies. <i>Italian Journal of Animal Science</i> , 2016 , 15, 396-406	2.2	1
107	GHap: an R package for genome-wide haplotyping. <i>Bioinformatics</i> , 2016 , 32, 2861-2	7.2	20
106	A method for single nucleotide polymorphism selection for parentage assessment in goats. <i>Journal of Dairy Science</i> , 2016 , 99, 3646-3653	4	12
105	Pleiotropic Genes Affecting Carcass Traits in Bos indicus (Nellore) Cattle Are Modulators of Growth. <i>PLoS ONE</i> , 2016 , 11, e0158165	3.7	16
104	Revealing misassembled segments in the bovine reference genome by high resolution linkage disequilibrium scan. <i>BMC Genomics</i> , 2016 , 17, 705	4.5	21
103	Multilocus genotypic data reveal high genetic diversity and low population genetic structure of Iranian indigenous sheep. <i>Animal Genetics</i> , 2016 , 47, 463-70	2.5	13
102	Synergies between assisted reproduction technologies and functional genomics. <i>Genetics Selection Evolution</i> , 2016 , 48, 53	4.9	7
101	Use of canonical discriminant analysis to study signatures of selection in cattle. <i>Genetics Selection Evolution</i> , 2016 , 48, 58	4.9	9
100	Inbreeding and purging at the genomic Level: the Chillingham cattle reveal extensive, non-random SNP heterozygosity. <i>Animal Genetics</i> , 2016 , 47, 19-27	2.5	28
99	Low levels of taurine introgression in the current Brazilian Nelore and Gir indicine cattle populations. <i>Genetics Selection Evolution</i> , 2015 , 47, 31	4.9	20
98	Relative extended haplotype homozygosity signals across breeds reveal dairy and beef specific signatures of selection. <i>Genetics Selection Evolution</i> , 2015 , 47, 25	4.9	27
97	Genetic diversity of Italian goat breeds assessed with a medium-density SNP chip. <i>Genetics Selection Evolution</i> , 2015 , 47, 62	4.9	51
96	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, 8175-85	4	12
95	Analysis of runs of homozygosity and their relationship with inbreeding in five cattle breeds farmed in Italy. <i>Animal Genetics</i> , 2015 , 46, 110-21	2.5	110
94	Whole mitochondrial genomes unveil the impact of domestication on goat matrilineal variability. <i>BMC Genomics</i> , 2015 , 16, 1115	4.5	45
93	Imputation accuracy is robust to cattle reference genome updates. <i>Animal Genetics</i> , 2015 , 46, 69-72	2.5	6
92	Searching new signals for production traits through gene-based association analysis in three Italian cattle breeds. <i>Animal Genetics</i> , 2015 , 46, 361-70	2.5	17

91	Revisiting demographic processes in cattle with genome-wide population genetic analysis. <i>Frontiers in Genetics</i> , 2015 , 6, 191	4.5	29
90	Prospects and challenges for the conservation of farm animal genomic resources, 2015-2025. <i>Frontiers in Genetics</i> , 2015 , 6, 314	4.5	50
89	Analysis of candidate SNPs affecting milk and functional traits in the dual-purpose Italian Simmental cattle. <i>Livestock Science</i> , 2015 , 173, 1-8	1.7	12
88	Signatures of selection in five Italian cattle breeds detected by a 54K SNP panel. <i>Molecular Biology Reports</i> , 2014 , 41, 957-65	2.8	24
87	Genome-wide analysis of Italian sheep diversity reveals a strong geographic pattern and cryptic relationships between breeds. <i>Animal Genetics</i> , 2014 , 45, 256-66	2.5	53
86	The characterization of goat genetic diversity: Towards a genomic approach. <i>Small Ruminant Research</i> , 2014 , 121, 58-72	1.7	31
85	Gut response induced by weaning in piglet features marked changes in immune and inflammatory response. <i>Functional and Integrative Genomics</i> , 2014 , 14, 657-71	3.8	36
84	Revisiting AFLP fingerprinting for an unbiased assessment of genetic structure and differentiation of taurine and zebu cattle. <i>BMC Genetics</i> , 2014 , 15, 47	2.6	18
83	A candidate gene association study for nine economically important traits in Italian Holstein cattle. <i>Animal Genetics</i> , 2014 , 45, 576-80	2.5	35
82	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	3.7	12
81	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	4.9	22
80	Meta-Analysis of Mitochondrial DNA Reveals Several Population Bottlenecks during Worldwide Migrations of Cattle. <i>Diversity</i> , 2014 , 6, 178-187	2.5	36
79	Adaptations to climate-mediated selective pressures in sheep. <i>Molecular Biology and Evolution</i> , 2014 , 31, 3324-43	8.3	104
78	Food for Healthy Living and Active Ageing. <i>Studies in Health Technology and Informatics</i> , 2014 , 203, 32-43	0.5	1
77	Nutrition and Ageing. <i>Studies in Health Technology and Informatics</i> , 2014 , 203, 112-21	0.5	1
76	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	2.5	24
75	Use of partial least squares regression to impute SNP genotypes in Italian cattle breeds. <i>Genetics Selection Evolution</i> , 2013 , 45, 15	4.9	7
74	Massive screening of copy number population-scale variation in <i>Bos taurus</i> genome. <i>BMC Genomics</i> , 2013 , 14, 124	4.5	33

73	Association between single nucleotide polymorphisms (SNPs) and milk production traits in Italian Brown cattle. <i>Livestock Science</i> , 2013 , 157, 93-99	1.7	8
72	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, 465-74	4.3	7
71	Mitochondrial DNA of seven Italian sheep breeds shows faint signatures of domestication and suggests recent breed formation. <i>Mitochondrial DNA</i> , 2013 , 24, 577-83		20
70	Recent advance in DNA-based traceability and authentication of livestock meat PDO and PGI products. <i>Recent Patents on Food, Nutrition & Agriculture</i> , 2013 , 5, 9-18	1.9	20
69	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	3.7	12
68	Genome wide analysis of fertility and production traits in Italian Holstein cattle. <i>PLoS ONE</i> , 2013 , 8, e80249	3.9	52
67	Effect of microsatellite outliers on the genetic structure of eight Italian goat breeds. <i>Small Ruminant Research</i> , 2012 , 103, 99-107	1.7	13
66	Molecular tools and analytical approaches for the characterization of farm animal genetic diversity. <i>Animal Genetics</i> , 2012 , 43, 483-502	2.5	82
65	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, 3390-400	4	12
64	Genetic diversity in widespread species is not congruent with species richness in alpine plant communities. <i>Ecology Letters</i> , 2012 , 15, 1439-48	10	108
63	Origin and spread of <i>Bos taurus</i> : new clues from mitochondrial genomes belonging to haplogroup T1. <i>PLoS ONE</i> , 2012 , 7, e38601	3.7	58
62	Genetic diversity of sheep breeds from Albania, Greece, and Italy assessed by mitochondrial DNA and nuclear polymorphisms (SNPs). <i>Scientific World Journal, The</i> , 2011 , 11, 1641-59	2.2	17
61	Genome wide scan for somatic cell counts in holstein bulls. <i>BMC Proceedings</i> , 2011 , 5 Suppl 4, S17	2.3	5
60	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	3.7	67
59	Spatial Trends of Genetic Variation of Domestic Ruminants in Europe. <i>Diversity</i> , 2010 , 2, 932-945	2.5	19
58	Identification of selection signatures in cattle breeds selected for dairy production. <i>Genetics</i> , 2010 , 185, 1451-61	4	93
57	On the origin of cattle: How aurochs became cattle and colonized the world. <i>Evolutionary Anthropology</i> , 2010 , 19, 148-157	4.7	139
56	The other side of comparative genomics: genes with no orthologs between the cow and other mammalian species. <i>BMC Genomics</i> , 2009 , 10, 604	4.5	6

55	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	2.6	46
54	Geographical patterning of sixteen goat breeds from Italy, Albania and Greece assessed by Single Nucleotide Polymorphisms. <i>BMC Ecology</i> , 2009 , 9, 20	2.7	20
53	Assessing SNP markers for assigning individuals to cattle populations. <i>Animal Genetics</i> , 2009 , 40, 18-26	2.5	36
52	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, 486-91	2.5	23
51	Revealing the history of sheep domestication using retrovirus integrations. <i>Science</i> , 2009 , 324, 532-6	33.3	292
50	Genome-wide survey of SNP variation uncovers the genetic structure of cattle breeds. <i>Science</i> , 2009 , 324, 528-32	33.3	612
49	The multifaceted origin of taurine cattle reflected by the mitochondrial genome. <i>PLoS ONE</i> , 2009 , 4, e5753	3.7	123
48	Are cattle, sheep, and goats endangered species?. <i>Molecular Ecology</i> , 2008 , 17, 275-84	5.7	168
47	Assessment of AFLP marker behaviour in enriching STS radiation hybrid maps. <i>Animal Genetics</i> , 2008 , 39, 383-94	2.5	1
46	Mitochondrial genomes of extinct aurochs survive in domestic cattle. <i>Current Biology</i> , 2008 , 18, R157-8	6.3	181
45	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	6.8	27
44	Traceability of four European Protected Geographic Indication (PGI) beef products using Single Nucleotide Polymorphisms (SNP) and Bayesian statistics. <i>Meat Science</i> , 2008 , 80, 1212-7	6.4	39
43	Internal controls for quantitative polymerase chain reaction of swine mammary glands during pregnancy and lactation. <i>Journal of Dairy Science</i> , 2008 , 91, 3057-66	4	33
42	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, 430-8	1.6	4
41	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, 17659-64	11.5	199
40	Traceability of the PGI product 'Vitellone Bianco dell'Appennino Centrale' by SNP markers. <i>Italian Journal of Animal Science</i> , 2007 , 6, 174-174	2.2	2
39	Differentiation of European cattle by AFLP fingerprinting. <i>Animal Genetics</i> , 2007 , 38, 60-6	2.5	41
38	Breed assignment of Italian cattle using biallelic AFLP markers. <i>Animal Genetics</i> , 2007 , 38, 147-53	2.5	24

37	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> , 2007 , 39, 41-49	1.9	7
36	Nanotechnologies applied to the analysis of the animal genome. <i>Veterinary Research Communications</i> , 2007 , 31 Suppl 1, 153-9	2.9	7
35	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, 1175-9	4.4	61
34	Detecting footprints of selection in <i>Ovis aries</i> by a spatial analysis approach. <i>Italian Journal of Animal Science</i> , 2007 , 6, 171-173	2.2	1
33	A second generation radiation hybrid map to aid the assembly of the bovine genome sequence. <i>BMC Genomics</i> , 2006 , 7, 283	4.5	23
32	Characterization of 37 breed-specific single-nucleotide polymorphisms in sheep. <i>Journal of Heredity</i> , 2006 , 97, 531-4	2.4	22
31	Tuscany autochthonous cattle breeds: an original genetic resource investigated by AFLP markers. <i>Journal of Animal Breeding and Genetics</i> , 2006 , 123, 10-6	2.9	14
30	Allele frequencies and diversity parameters of 27 single nucleotide polymorphisms within and across goat breeds. <i>Molecular Ecology Notes</i> , 2006 , 6, 992-997		15
29	Characterization of single nucleotide polymorphisms in sheep and their variation as evidence of selection. <i>Animal Genetics</i> , 2006 , 37, 290-2	2.5	17
28	Geographical partitioning of goat diversity in Europe and the Middle East. <i>Animal Genetics</i> , 2006 , 37, 327-34	2.5	145
27	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, 117-20	3.2	19
26	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> , 2005 , 122, 62-8	2.9	46
25	Safety risks for animals fed genetic modified (GM) plants. <i>Veterinary Research Communications</i> , 2005 , 29 Suppl 2, 13-8	2.9	15
24	Pattern of ancient goat migration revealed by AFLP molecular markers. <i>Italian Journal of Animal Science</i> , 2005 , 4, 55-57	2.2	2
23	Application of AFLP technology to radiation hybrid mapping. <i>Chromosome Research</i> , 2004 , 12, 285-97	4.4	8
22	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, 103-9	2.5	65
21	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, 392-5	3.2	67
20	Establishment and characterization of two new pig cell lines for use in virological diagnostic laboratories. <i>Journal of Virological Methods</i> , 2003 , 107, 205-12	2.6	55

19	Signatures of selection? Patterns of microsatellite diversity on a chromosome containing a selected locus. <i>Heredity</i> , 2003 , 90, 350-8	3.6	22
18	Genetic distances within and across cattle breeds as indicated by biallelic AFLP markers. <i>Animal Genetics</i> , 2002 , 33, 280-6	2.5	30
17	Construction and Use of Genetic Maps in Cereals 2002 , 347-369		2
16	Identification of QTLs for grain yield and grain-related traits of maize (Zeamays L.) using an AFLP map, different testers, and cofactor analysis. <i>Theoretical and Applied Genetics</i> , 2001 , 102, 230-243	6	42
15	Assessing genetic diversity in Italian goat populations using AFLP markers. <i>Animal Genetics</i> , 2001 , 32, 281-8	2.5	45
14	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 ^{2.9}		13
13	AFLP markers in a molecular linkage map of maize: codominant scoring and linkage group distribution. <i>Theoretical and Applied Genetics</i> , 1999 , 99, 425-31	6	118
12	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	6	140
11	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	6	363
10	AFLP markers for DNA fingerprinting in cattle. <i>Animal Genetics</i> , 1997 , 28, 418-26	2.5	116
9	Analysis of stable events of transformation in wheat via PEG-mediated DNA uptake into protoplasts. <i>Plant Science</i> , 1993 , 93, 85-94	5.3	10
8	Genetic diversity of maize inbred lines within and among heterotic groups revealed by RFLPs. <i>Theoretical and Applied Genetics</i> , 1992 , 84, 17-25	6	52
7	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	5.1	8
6	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	2.1	16
5	The b-32 protein from maize endosperm: characterization of genomic sequences encoding two alternative central domains. <i>Plant Molecular Biology</i> , 1990 , 14, 1031-40	4.6	29
4	Multiple adaptive solutions to face climatic constraints: novel insights in the debate over the role of convergence in local adaptation		1
3	BITE: an R package for biodiversity analyses		25
2	Phylogeny and distribution of Y-chromosomal haplotypes in domestic, ancient and wild goats		2

- 1 Combining landscape genomics and ecological modelling to investigate local adaptation of indigenous Ugandan cattle to East Coast fever

1