Johann SÃ¶lkner

List of Publications by Year
in descending order

195 papers	6,252 citations	76294 40 h-index	95218 68 g-index
200 all docs	200 docs citations	200 times ranked	4804 citing authors

#	Article	IF	Citations
1	Experiences from the Implementation of Community-Based Goat Breeding Programs in Malawi and Uganda: A Potential Approach for Conservation and Improvement of Indigenous Small Ruminants in Smallholder Farms. Sustainability, 2021, 13, 1494.	1.6	6
2	Population structure, inbreeding and admixture in local cattle populations managed by communityâ€based breeding programs in Burkina Faso. Journal of Animal Breeding and Genetics, 2021, 138, 379-388.	0.8	9
3	Genetic Improvement of Local Cattle Breeds in West Africa: A Review of Breeding Programs. Sustainability, 2021, 13, 2125.	1.6	9
4	Investigation of ancestral alleles in the Bovinae subfamily. BMC Genomics, 2021, 22, 108.	1.2	4
5	Livestock Keepersâ€™ Attitudes: Keystone of Effective Community-Based Breeding Programs. Sustainability, 2021, 13, 2499.	1.6	7
6	Community-Based Livestock Breeding: Coordinated Action or Relational Process?. Frontiers in Veterinary Science, 2021, 8, 613505.	0.9	12
7	Values and Beliefs That Shape Cattle Breeding in Southwestern Burkina Faso. Human Ecology, 2021, 49, 429-441.	0.7	1
8	A Mix of Old British and Modern European Breeds: Genomic Prediction of Breed Composition of Smallholder Pigs in Uganda. Frontiers in Genetics, 2021, 12, 676047.	1.1	7
9	Genomeâ€wide SNP analysis clearly distinguished the Belarusian Red cattle from other European cattle breeds. Animal Genetics, 2021, 52, 720-724.	0.6	8
10	Comparative Study of the Genetic Diversity of Local Steppe Cattle Breeds from Russia, Kazakhstan and Kyrgyzstan by Microsatellite Analysis of Museum and Modern Samples. Diversity, 2021, 13, 351.	0.7	6
11	Post-genotyping optimization of dataset formation could affect genetic diversity parameters: an example of analyses with alpine goat breeds. BMC Genomics, 2021, 22, 546.	1.2	8
12	Genome-wide association study of trypanosome prevalence and morphometric traits in purebred and crossbred BaoulÃ© cattle of Burkina Faso. PLoS ONE, 2021, 16, e0255089.	1.1	6
13	Local Ancestry to Identify Selection in Response to Trypanosome Infection in BaoulÃ© x Zebu Crossbred Cattle in Burkina Faso. Frontiers in Genetics, 2021, 12, 670390.	1.1	3
14	PSXIV-26 Selection footprints in Russian red cattle identified by linkage disequilibrium blocks based on SNP data. Journal of Animal Science, 2021, 99, 255-256.	0.2	2
15	Assessing Bos taurus introgression in the UOA Bos indicus assembly. Genetics Selection Evolution, 2021, 53, 96.	1.2	3
16	Breeding objectives and practices in three local cattle breed production systems in Burkina Faso with implication for the design of breeding programs. Livestock Science, 2020, 232, 103910.	0.6	15
17	Genetic diversity, population structure and runs of homozygosity in Ethiopian short fat-tailed and Awassi sheep breeds using genome-wide 50k SNP markers. Livestock Science, 2020, 232, 103899.	0.6	9
18	Association of missense variants in GDF9 with litter size in Entlebucher Mountain dogs. Animal Genetics, 2020, 51, 78-86.	0.6	3

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19	Indigenous knowledge of veterinary medicinal plant use in cattle treatment in southwestern Burkina Faso (West Africa). South African Journal of Botany, 2020, 128, 189-199.	1.2	11
20	Morphometric characterization of purebred and crossbred BaoulÃ© cattle in Burkina Faso. Acta Agriculturae Scandinavica - Section A: Animal Science, 2020, 69, 193-202.	0.2	3
21	Unsupervised detection of ancestry tracks with the GHap <scp>r</scp> package. Methods in Ecology and Evolution, 2020, 11, 1448-1454.	2.2	6
22	Evaluation of increased feed supply and different fattening strategies for an Ethiopian sheep population by system dynamics modelling. Animal Production Science, 2020, 60, 2050.	0.6	3
23	From farmers to livestock keepers: a typology of cattle production systems in south-western Burkina Faso. Tropical Animal Health and Production, 2020, 52, 2179-2189.	0.5	14
24	Editorial: Why Livestock Genomics for Developing Countries Offers Opportunities for Success. Frontiers in Genetics, 2020, 11, 626.	1.1	2
25	Inbreeding depression for kit survival at birth in a rabbit population under long-term selection. Genetics Selection Evolution, 2020, 52, 39.	1.2	4
26	Short communication: Investigation of the temporal relationships between milk mid-infrared predicted biomarkers and lameness events in later lactation. Journal of Dairy Science, 2020, 103, 4475-4482.	1.4	10
27	Tangible and intangible benefits of local goats rearing in smallholder farms in Malawi. Small Ruminant Research, 2020, 187, 106095.	0.6	27
28	Selection signatures in two oldest Russian native cattle breeds revealed using high-density single nucleotide polymorphism analysis. PLoS ONE, 2020, 15, e0242200.	1.1	22
29	Prediction of pregnancy state from milk mid-infrared (MIR) spectroscopy in dairy cows. Acta Fytotechnica Et Zootechnica, 2020, 23, 224-232.	0.1	4
30	Genotype by Environment interactions for egg number and egg weight of five dual-purpose chicken breeds in different zones of Oromia region in Ethiopia. Acta Fytotechnica Et Zootechnica, 2020, 23, 205-213.	0.1	4
31	PSXII-21 Genome-wide search for genomic regions under putative selection in two Russian native cattle breeds using high-density SNP Bead Chip. Journal of Animal Science, 2020, 98, 242-243.	0.2	1
32	A complex structural variant at the <scp>KIT</scp> locus in cattle with the Pinzgauer spotting pattern. Animal Genetics, 2019, 50, 423-429.	0.6	12
33	Timing and Extent of Inbreeding in African Goats. Frontiers in Genetics, 2019, 10, 537.	1.1	15
34	Indigenous knowledge, practices and preferences in control of gastrointestinal nematodes in Bonga and Horro sheep of Ethiopia. Small Ruminant Research, 2019, 175, 110-116.	0.6	3
35	Genetic associations of lactose and its ratios to other milk solids with health traits in Austrian Fleckvieh cows. Journal of Dairy Science, 2019, 102, 4238-4248.	1.4	38
36	AUTALASSO: an automatic adaptive LASSO for genome-wide prediction. BMC Bioinformatics, 2019, 20, 167.	1.2	20

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37	Is the introgression of Lobi/Baoul cattle by zebuine genes in Burkina Faso Lobi cattle threatened?. African Journal of Biotechnology, 2019, 18, 77-85.	0.3	4
38	On the genomic regions associated with milk lactose in Fleckvieh cattle. Journal of Dairy Science, 2019, 102, 10088-10099.	1.4	17
39	Population Structure and Genetic Diversity of Sheep Breeds in the Kyrgyzstan. Frontiers in Genetics, 2019, 10, 1311.	1.1	34
40	Elevated haplotypes frequencies reveal similarities for selection signatures in Western and Russian Simmental populations. Journal of Central European Agriculture, 2019, 20, 1-11.	0.3	7
41	Genetic and environmental risk factors for vitiligo and melanoma in Pura Raza EspaÃ±ol horses. Equine Veterinary Journal, 2019, 51, 606-611.	0.9	13
42	Mastitis Detection from Milk Mid-Infrared (MIR) Spectroscopy in Dairy Cows. Acta Universitatis Agriculturae Et Silviculturae Mendelianae Brunensis, 2019, 67, 1221-1226.	0.2	10
43	Genome-wide mapping of the dominance effects based on breed ancestry for semen traits in admixed Swiss Fleckvieh bulls. Journal of Dairy Science, 2019, 102, 11217-11224.	1.4	7
44	Future of beekeeping in Northwestern Ethiopia: Scenarios, local adaptation measures and its implications for farmersâ€™ livelihoods. Biodiversitas, 2019, 20, .	0.2	0
45	Deviation Patterns of Observed and Expected Haplotype Blocks Associated with Potential Recessive Disorders in Tyrol Grey Cattle. Acta Universitatis Agriculturae Et Silviculturae Mendelianae Brunensis, 2019, 67, 1183-1188.	0.2	0
46	Detection of Autosomal Hemizygous Regions in the Fleckvieh Population Based on SNP-chip Data and Parent Offspring Pairs. Acta Universitatis Agriculturae Et Silviculturae Mendelianae Brunensis, 2019, 67, 1447-1452.	0.2	0
47	Effects of breed proportion and components of heterosis for semen traits in a composite cattle breed. Journal of Animal Breeding and Genetics, 2018, 135, 45-53.	0.8	4
48	Conservation of a domestic metapopulation structured into related and partly admixed strains. Molecular Ecology, 2018, 27, 1633-1650.	2.0	23
49	Meta-analysis of genome-wide association studies for cattle stature identifies common genes that regulate body size in mammals. Nature Genetics, 2018, 50, 362-367.	9.4	286
50	Short communication: Genomic prediction using imputed whole-genome sequence variants in Brown Swiss Cattle. Journal of Dairy Science, 2018, 101, 1292-1296.	1.4	35
51	Genomeâ€wide association study and heritability estimate for ectopic ureters in Entlebucher mountain dogs. Animal Genetics, 2018, 49, 645-650.	0.6	5
52	Misidentification of runs of homozygosity islands in cattle caused by interference with copy number variation or large intermarker distances. Genetics Selection Evolution, 2018, 50, 43.	1.2	32
53	Genomic response to natural selection within alpine cattle breeds. Czech Journal of Animal Science, 2018, 63, 136-143.	0.5	6
54	Whole-genome SNP analysis elucidates the genetic structure of Russian cattle and its relationship with Eurasian taurine breeds. Genetics Selection Evolution, 2018, 50, 37.	1.2	34

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55	Genomeâ€wide <scp>SNP</scp> analysis unveils genetic structure and phylogeographic history of snow sheep (Ovis nivicola) populations inhabiting the Verkhoyansk Mountains and Momsky Ridge (northeastern Siberia). Ecology and Evolution, 2018, 8, 8000-8010.	0.8	9
56	Genetic association between somatic cell score and milk lactose in early- to mid-lactation of first calving Fleckvieh cows. Journal of Central European Agriculture, 2018, 19, 791-797.	0.3	4
57	Genomic characterization of Pinzgau cattle: genetic conservation and breeding perspectives. Conservation Genetics, 2017, 18, 893-910.	0.8	39
58	Genome-wide mapping and estimation of inbreeding depression of semen quality traits in a cattle population. Journal of Dairy Science, 2017, 100, 4721-4730.	1.4	89
59	The use of mid-infrared spectrometry to estimate the ration composition of lactating dairy cows. Journal of Dairy Science, 2017, 100, 5411-5421.	1.4	14
60	Accuracy of genomic predictions in Gyr (Bos indicus) dairy cattle. Journal of Dairy Science, 2017, 100, 5479-5490.	1.4	32
61	Assessment of sportive longevity in Pura Raza EspaÃ±ol dressage horses. Livestock Science, 2017, 203, 69-75.	0.6	6
62	A PLAG1 mutation contributed to stature recovery in modern cattle. Scientific Reports, 2017, 7, 17140.	1.6	42
63	Heritability and factors associated with number of harness race starts in the Spanish Trotter horse population. Equine Veterinary Journal, 2017, 49, 288-293.	0.9	10
64	Identifying highly informative genetic markers for quantification of ancestry proportions in crossbred sheep populations: implications for choosing optimum levels of admixture. BMC Genetics, 2017, 18, 80.	2.7	10
65	System dynamics modeling in designing breeding schemes: The case of Menz sheep in Ethiopian highlands1. Journal of Animal Science, 2017, 95, 2367-2378.	0.2	0
66	Genome-wide association studies of fertility and calving traits in Brown Swiss cattle using imputed whole-genome sequences. BMC Genomics, 2017, 18, 910.	1.2	36
67	Genome-wide association study for birth, weaning and yearling weight in Colombian Brahman cattle. Genetics and Molecular Biology, 2017, 40, 453-459.	0.6	23
68	Genomic dissection of inbreeding depression: a gate to new opportunities. Revista Brasileira De Zootecnia, 2017, 46, 773-782.	0.3	26
69	System dynamics modeling in designing breeding schemes: The case of Menz sheep in Ethiopian highlands. Journal of Animal Science, 2017, 95, 2367.	0.2	0
70	Assessing footprints of natural selection through PCA analysis in cattle. Acta Fytotechnica Et Zootechnica, 2017, 20, 23-27.	0.1	1
71	P4014 Global and local admixture analyses of baladi cattle. Journal of Animal Science, 2016, 94, 85-86.	0.2	0
72	Review of sheep crossbreeding based on exotic sires and among indigenous breeds in the tropics: An Ethiopian perspective. African Journal of Agricultural Research Vol Pp, 2016, 11, 901-911.	0.2	23

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73	Revealing misassembled segments in the bovine reference genome by high resolution linkage disequilibrium scan. BMC Genomics, 2016, 17, 705.	1.2	41
74	0837 Community-based breeding programs: A sustainable solution for livestock keepers?. Journal of Animal Science, 2016, 94, 402-403.	0.2	1
75	The use of coancestry based on shared segments for maintaining genetic diversity. Journal of Animal Breeding and Genetics, 2016, 133, 357-365.	0.8	6
76	Direct and maternal genetic effects on growth, reproduction, and ultrasound traits in zebu Brahman cattle in Colombia1. Journal of Animal Science, 2016, 94, 2761-2769.	0.2	11
77	Locusâ€specific ancestry to detect recent response to selection in admixed Swiss Fleckvieh cattle. Animal Genetics, 2016, 47, 637-646.	0.6	17
78	Whole genome SNP scanning of snow sheep (Ovis nivicola). Doklady Biochemistry and Biophysics, 2016, 469, 288-293.	0.3	4
79	Pleiotropic Genes Affecting Carcass Traits in Bos indicus (Nellore) Cattle Are Modulators of Growth. PLoS ONE, 2016, 11, e0158165.	1.1	23
80	STUDY OF GENETIC DIVERSITY AND POPULATION STRUCTURE OF FIVE RUSSIAN CATTLE BREEDS USING WHOLE-GENOME SNP ANALYSIS. Sel'skokhozyaistvennaya Biologiya, 2016, 51, 788-800.	0.1	9
81	Smallholder experiences with dairy cattle crossbreeding in the tropics: from introduction to impact. Animal, 2015, 9, 150-157.	1.3	24
82	PREDICTION OF GLOBAL AND LOCAL SIMMENTAL AND RED HOLSTEIN FRIESIAN ADMIXTURE LEVELS IN SWISS FLECKVIEH CATTLE. Poljoprivreda, 2015, 21, 63-67.	0.2	2
83	GENOMIC BACKGROUND OF ENTROPION IN FLECKVIEH CATTLE. Poljoprivreda, 2015, 21, 48-51.	0.2	4
84	Trypanosomosis: potential driver of selection in African cattle. Frontiers in Genetics, 2015, 6, 137.	1.1	32
85	Genomic analysis for managing small and endangered populations: a case study in Tyrol Grey cattle. Frontiers in Genetics, 2015, 6, 173.	1.1	46
86	Genomic regions influencing coat color saturation and facial markings in Fleckvieh cattle. Animal Genetics, 2015, 46, 65-68.	0.6	29
87	Assessment of autozygosity in Nellore cows (Bos indicus) through high-density SNP genotypes. Frontiers in Genetics, 2015, 6, 5.	1.1	69
88	Genomic data as the Ã¢â‚¬Å“hitchhiker's guideÃ¢â‚¬Â• to cattle adaptation: tracking the milestones of past selection in the bovine genome. Frontiers in Genetics, 2015, 6, 36.	1.1	23
89	Strategies for single nucleotide polymorphism (SNP) genotyping to enhance genotype imputation in Gyr (Bos indicus) dairy cattle: Comparison of commercially available SNP chips. Journal of Dairy Science, 2015, 98, 4969-4989.	1.4	29
90	Relative resistance of Menz and Washera sheep breeds to artificial infection with Haemonchus contortus in the highlands of Ethiopia. Tropical Animal Health and Production, 2015, 47, 961-968.	0.5	16

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91	Low levels of taurine introgression in the current Brazilian Nelore and Gir indicine cattle populations. Genetics Selection Evolution, 2015, 47, 31.	1.2	29
92	Survival analysis of genetic and non-genetic factors influencing ewe longevity and lamb survival of Ethiopian sheep breeds. Livestock Science, 2015, 176, 22-32.	0.6	22
93	Communityâ€based livestock breeding programmes: essentials and examples. Journal of Animal Breeding and Genetics, 2015, 132, 155-168.	0.8	109
94	Quantitative genetics, spread of genes and genetic improvement: papers in honour of John James. Journal of Animal Breeding and Genetics, 2015, 132, 85-88.	0.8	1
95	<scp>grain</scp>: a computer program to calculate ancestral and partial inbreeding coefficients using a gene dropping approach. Journal of Animal Breeding and Genetics, 2015, 132, 100-108.	0.8	33
96	Recovery of Native Genetic Background in Admixed Populations Using Haplotypes, Phenotypes, and Pedigree Information â€“ Using Cika Cattle as a Case Breed. PLoS ONE, 2015, 10, e0123253.	1.1	19
97	Accuracy of genotype imputation in Nelore cattle. Genetics Selection Evolution, 2014, 46, 69.	1.2	86
98	Animal breeding strategies in Africa: current issues and the way forward. Journal of Animal Breeding and Genetics, 2014, 131, 327-328.	0.8	9
99	Accuracy of genomic predictions in Bos indicus (Nellore) cattle. Genetics Selection Evolution, 2014, 46, 17.	1.2	77
100	Linear vs. piecewise Weibull model for genetic evaluation of sires for longevity in Simmental cattle. Mljekarstvo, 2014, , 141-149.	0.2	10
101	Imputation of non-genotyped individuals using genotyped progeny in Nellore, a Bos indicus cattle breed. Livestock Science, 2014, 166, 176-189.	0.6	10
102	Effect of genetic improvement of body weight on herd dynamics and profitability of Ethiopian meat sheep: A dynamic simulation model. Small Ruminant Research, 2014, 117, 15-24.	0.6	8
103	Assessing signatures of selection through variation in linkage disequilibrium between taurine and indicine cattle. Genetics Selection Evolution, 2014, 46, 19.	1.2	79
104	Linkage disequilibrium levels in Bos indicus and Bos taurus cattle using medium and high density SNP chip data and different minor allele frequency distributions. Livestock Science, 2014, 166, 121-132.	0.6	69
105	Inbreeding and runs of homozygosity: A possible solution to an old problem. Livestock Science, 2014, 166, 26-34.	0.6	283
106	Genome-Wide Mapping of Loci Explaining Variance in Scrotal Circumference in Nellore Cattle. PLoS ONE, 2014, 9, e88561.	1.1	33
107	Joint genealogical analysis as a tool for diversity evaluation in Pinzgau cattle populations. Archives Animal Breeding, 2014, 57, 1-12.	0.5	2
108	Optimization of selection for growth in Menz Sheep while minimizing inbreeding depression in fitness traits. Genetics Selection Evolution, 2013, 45, 20.	1.2	12

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109	Genome-wide association study for birth weight in Nellore cattle points to previously described orthologous genes affecting human and bovine height. BMC Genetics, 2013, 14, 52.	2.7	111
110	The Survival Kit: Software to analyze survival data including possibly correlated random effects. Computer Methods and Programs in Biomedicine, 2013, 110, 503-510.	2.6	56
111	Estimates of autozygosity derived from runs of homozygosity: empirical evidence from selected cattle populations. Journal of Animal Breeding and Genetics, 2013, 130, 286-293.	0.8	196
112	Trypanosomosis: a priority disease in tsetse-challenged areas of Burkina Faso. Tropical Animal Health and Production, 2013, 45, 497-503.	0.5	20
113	A Novel qPCR Assay for the Detection of African Animal Trypanosomosis in Trypanotolerant and Trypanosusceptible Cattle Breeds. PLoS Neglected Tropical Diseases, 2013, 7, e2345.	1.3	19
114	Complex Inheritance of Melanoma and Pigmentation of Coat and Skin in Grey Horses. PLoS Genetics, 2013, 9, e1003248.	1.5	55
115	Estimating autozygosity from high-throughput information: effects of SNP density and genotyping errors. Genetics Selection Evolution, 2013, 45, 42.	1.2	227
116	Detecting Loci under Recent Positive Selection in Dairy and Beef Cattle by Combining Different Genome-Wide Scan Methods. PLoS ONE, 2013, 8, e64280.	1.1	84
117	Evaluation of the lasso and the elastic net in genome-wide association studies. Frontiers in Genetics, 2013, 4, 270.	1.1	169
118	Analysis of longevity in the Slovak Pinzgau population - extension to the animal model. Czech Journal of Animal Science, 2013, 58, 289-295.	0.5	11
119	Genetic evaluation for longevity of Croatian Simmental bulls using a piecewise Weibull model. Archives Animal Breeding, 2013, 56, 89-101.	0.5	7
120	Serial translocation by means of circular intermediates underlies colour sidedness in cattle. Nature, 2012, 482, 81-84.	13.7	137
121	Copy number expansion of the STX17 duplication in melanoma tissue from Grey horses. BMC Genomics, 2012, 13, 365.	1.2	34
122	Pasture use and management strategies in the Ankole pastoral system in Uganda. Grass and Forage Science, 2012, 67, 199-209.	1.2	7
123	Estimates of economic values for important traits of two indigenous Ethiopian sheep breeds. Small Ruminant Research, 2012, 105, 154-160.	0.6	13
124	Molecular tools and analytical approaches for the characterization of farm animal genetic diversity. Animal Genetics, 2012, 43, 483-502.	0.6	104
125	Prediction of breed composition in an admixed cattle population. Animal Genetics, 2012, 43, 696-703.	0.6	54
126	Communityâ€based alternative breeding plans for indigenous sheep breeds in four agroâ€ecological zones of Ethiopia. Journal of Animal Breeding and Genetics, 2012, 129, 244-253.	0.8	47

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127	Short communication: Genomic selection using a multi-breed, across-country reference population. Journal of Dairy Science, 2011, 94, 2625-2630.	1.4	77
128	Identification of smallholder farmers and pastoralistsâ€™ preferences for sheep breeding traits: choice model approach. Animal, 2011, 5, 1984-1992.	1.3	42
129	Important aspects and limitations in considering community-based breeding programs for low-input smallholder livestock systems. Small Ruminant Research, 2011, 98, 170-175.	0.6	65
130	Stochastic simulation model of Ankole pastoral production system: Model development and evaluation. Ecological Modelling, 2011, 222, 3692-3700.	1.2	5
131	An Unusual Splice Defect in the Mitofusin 2 Gene (MFN2) Is Associated with Degenerative Axonopathy in Tyrolean Grey Cattle. PLoS ONE, 2011, 6, e18931.	1.1	39
132	Influence of environmental and genetic factors on allergen-specific immunoglobulin-E levels in sera from Lipizzan horses. Equine Veterinary Journal, 2010, 33, 714-720.	0.9	40
133	Equine melanoma in a population of 296 grey Lipizzaner horses. Equine Veterinary Journal, 2010, 35, 153-157.	0.9	73
134	Heritability of longevity in Large White and Landrace sows using continuous time and grouped data models. Genetics Selection Evolution, 2010, 42, 13.	1.2	31
135	Yâ€šspecific microsatellites reveal an African subfamily in taurine (Bos taurus) cattle. Animal Genetics, 2010, 41, 232-241.	0.6	51
136	Multiple paternal origins of domestic cattle revealed by Y-specific interspersed multilocus microsatellites. Heredity, 2010, 105, 511-519.	1.2	50
137	Degenerative Axonopathy in a Tyrolean Grey Calf. Journal of Veterinary Internal Medicine, 2010, 24, 1519-1523.	0.6	5
138	Extensive Long-Range and Nonsyntenic Linkage Disequilibrium in Livestock Populations: Deconstruction of a Conundrum. Genetics, 2009, 181, 691-699.	1.2	16
139	Pedigree analysis in the Austrian Noriker draught horse: genetic diversity and the impact of breeding for coat colour on population structure. Journal of Animal Breeding and Genetics, 2009, 126, 348-356.	0.8	49
140	Breeding objectives and the relative importance of traits in plant and animal breeding: a comparative review. Euphytica, 2008, 161, 273-282.	0.6	33
141	A cis-acting regulatory mutation causes premature hair graying and susceptibility to melanoma in the horse. Nature Genetics, 2008, 40, 1004-1009.	9.4	271
142	Design of a village breeding programme for a llama population in the High Andes of Bolivia. Journal of Animal Breeding and Genetics, 2008, 125, 311-319.	0.8	23
143	Performance and fitness traits versus phenotypic appearance in the African Ankole Longhorn cattle: A novel approach to identify selection criteria for indigenous breeds. Livestock Science, 2008, 113, 234-242.	0.6	40
144	Morphological analysis and effect of selection for conformation in the Noriker draught horse population. Livestock Science, 2008, 115, 118-128.	0.6	36

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145	The Syrian Jabali goat and its production system. Journal of Arid Environments, 2008, 72, 384-391.	1.2	4
146	Multiple-Marker Mapping for Selective DNA Pooling Within Large Families. Journal of Dairy Science, 2008, 91, 2864-2873.	1.4	3
147	Quantitative Trait Loci Affecting Milk Yield and Protein Percentage in a Three-Country Brown Swiss Population. Journal of Dairy Science, 2008, 91, 767-783.	1.4	73
148	Genetic and morphological characterisation of the Ankole Longhorn cattle in the African Great Lakes region. Genetics Selection Evolution, 2008, 40, 467-490.	1.2	14
149	Genetic evaluation for length of productive life in Slovak Pinzgau cattle. Archives Animal Breeding, 2008, 51, 438-448.	0.5	22
150	Individual-based assessment of population structure and admixture in Austrian, Croatian and German draught horses. Heredity, 2007, 98, 114-122.	1.2	34
151	Genetic Parameters for Semen Production Traits in Austrian Dual-Purpose Simmental Bulls. Reproduction in Domestic Animals, 2007, 42, 326-328.	0.6	43
152	Evaluation of ancestral inbreeding coefficients: Ballouâ€™s formula versus gene dropping. Conservation Genetics, 2007, 8, 489-495.	0.8	20
153	Effects of age and environmental factors on semen production and semen quality of Austrian Simmental bulls. Animal Reproduction Science, 2006, 95, 27-37.	0.5	112
154	Genetic characterisation and breed assignment in Austrian sheep breeds using microsatellite marker information. Journal of Animal Breeding and Genetics, 2006, 123, 265-271.	0.8	64
155	Comparison of production systems and selection criteria of Ankole cattle by breeders in Burundi, Rwanda, Tanzania and Uganda. Tropical Animal Health and Production, 2006, 38, 571-581.	0.5	45
156	Genetic and non-genetic factors influencing fibre quality of Bolivian llamas. Small Ruminant Research, 2006, 61, 131-139.	0.6	14
157	Quantitative genetic aspects of coat color in horses1. Journal of Animal Science, 2006, 84, 2623-2628.	0.2	18
158	Feed Intake Behaviour of different Pig Breeds during Performance Testing on Station. Archives Animal Breeding, 2006, 49, 77-88.	0.5	11
159	Growth curves and genetic parameters for growth traits in Bolivian llamas. Livestock Science, 2005, 95, 73-81.	1.2	34
160	The BovMAS Consortium: identification of QTL for milk yield and milk protein percent on chromosome 14 in the Brown Swiss breed. Italian Journal of Animal Science, 2005, 4, 13-15.	0.8	2
161	Microsatellite diversity, population subdivision and gene flow in the Lipizzan horse. Animal Genetics, 2004, 35, 285-292.	0.6	69
162	Body weight of Awassi and indigenous Ethiopian sheep and their crosses. Small Ruminant Research, 2004, 55, 51-56.	0.6	17

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163	Effect of Maternal Age on Milk Production Traits, Fertility, and Longevity in Cattle. Journal of Dairy Science, 2004, 87, 2293-2298.	1.4	22
164	Analysis of alternative models treating herd Ã— year effects as fixed or random. Czech Journal of Animal Science, 2004, 49, 349-356.	0.5	4
165	Pedigree and marker information requirements to monitor genetic variability. Genetics Selection Evolution, 2003, 35, 369-83.	1.2	34
166	Genetic parameter estimates for birth weight, weaning weight and average daily gain in pure and crossbred sheep in Ethiopia. Journal of Animal Breeding and Genetics, 2003, 120, 29-38.	0.8	26
167	Inbreeding, Microsatellite Heterozygosity, and Morphological Traits in Lipizzan Horses. , 2003, 94, 125-132.		66
168	History of Lipizzan horse maternal lines as revealed by mtDNA analysis. Genetics Selection Evolution, 2002, 34, 635-48.	1.2	38
169	Optimization of progeny testing schemes when functional traits play an important role in the total merit index. Livestock Science, 2002, 77, 217-225.	1.2	23
170	Analysis of diversity and population structure in the Lipizzan horse breed based on pedigree information. Livestock Science, 2002, 77, 137-146.	1.2	94
171	Performance of crossbred and indigenous sheep under village conditions in the cool highlands of central-northern Ethiopia: growth, birth and body weights. Small Ruminant Research, 2002, 43, 195-202.	0.6	24
172	Effects of models with finite loci, selection, dominance, epistasis and linkage on inbreeding coefficients based on pedigree and genotypic information. Journal of Animal Breeding and Genetics, 2002, 119, 101-115.	0.8	13
173	Analysis of pedigrees of Tux-Zillertal, Carinthian Blond and Original Pinzgau cattle population in Austria. Journal of Animal Breeding and Genetics, 2002, 119, 175-181.	0.8	16
174	Optimization of a specialized beef breeding program with a crossbreeding component. Archives Animal Breeding, 2002, 45, 433-441.	0.5	3
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