Joaquim Casellas

List of Publications by Year
in descending order

114 papers	1,674 citations	304602 22 h-index	414303 32 g-index
116 all docs	116 docs citations	116 times ranked	1847 citing authors

#	Article	IF	Citations
1	Inbred mouse strains and genetic stability: a review. Animal, 2011, 5, 1-7.	1.3	89
2	Differences in Muscle Transcriptome among Pigs Phenotypically Extreme for Fatty Acid Composition. PLoS ONE, 2014, 9, e99720.	1.1	66
3	Analysis of founder-specific inbreeding depression on birth weight in Ripollesa lambs1. Journal of Animal Science, 2009, 87, 72-79.	0.2	61
4	Population structure of eleven Spanish ovine breeds and detection of selective sweeps with BayeScan and hapFLK. Scientific Reports, 2016, 6, 27296.	1.6	52
5	Genetic analysis of rennet coagulation time, curd-firming rate, and curd firmness assessed over an extended testing period using mechanical and near-infrared instruments. Journal of Dairy Science, 2013, 96, 50-62.	1.4	45
6	Genetic and environmental relationships of detailed milk fatty acids profile determined by gas chromatography in Brown Swiss cows. Journal of Dairy Science, 2016, 99, 1315-1330.	1.4	43
7	Bayesian analysis of parent-specific transmission ratio distortion in seven Spanish beef cattle breeds. Animal Genetics, 2017, 48, 93-96.	0.6	42
8	Genetic and environmental factors influencing mortality up to weaning of Bruna dels Pirineus beef calves in mountain areas. A survival analysis1. Journal of Animal Science, 2005, 83, 543-551.	0.2	41
9	High amino acid variation in the intracellular domain of the pig prolactin receptor (PRLR) and its relation to ovulation rate and piglet survival traits1. Journal of Animal Science, 2006, 84, 1991-1998.	0.2	36
10	Effect of leg conformation on survivability of Duroc, Landrace, and Large White sows1. Journal of Animal Science, 2008, 86, 2392-2400.	0.2	35
11	Genetic analysis of beef fatty acid composition predicted by near-infrared spectroscopy1. Journal of Animal Science, 2012, 90, 429-438.	0.2	34
12	Survival analysis from birth to slaughter of Ripollesa lambs under semi-intensive management1. Journal of Animal Science, 2007, 85, 512-517.	0.2	33
13	Candidate gene association analysis for milk yield, composition, urea nitrogen and somatic cell scores in Brown Swiss cows. Animal, 2014, 8, 1062-1070.	1.3	32
14	Bayes factor analyses of heritability for serum and muscle lipid traits in Duroc pigs1. Journal of Animal Science, 2010, 88, 2246-2254.	0.2	31
15	Genome Scans for Transmission Ratio Distortion Regions in Mice. Genetics, 2012, 191, 247-259.	1.2	31
16	Additive genetic relationship of longevity with fertility and production traits in Nellore cattle based on bivariate models. Genetics and Molecular Research, 2010, 9, 176-187.	0.3	30
17	A Genetic Predictive Model for Canine Hip Dysplasia: Integration of Genome Wide Association Study (GWAS) and Candidate Gene Approaches. PLoS ONE, 2015, 10, e0122558.	1.1	28
18	Recombination rates across porcine autosomes inferred from high€density linkage maps. Animal Genetics, 2012, 43, 620-623.	0.6	27

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19	Genetic variation and effects of candidate-gene polymorphisms on coagulation properties, curd firmness modeling and acidity in milk from Brown Swiss cows. Animal, 2015, 9, 1104-1112.	1.3	27
20	Comparing the mRNA expression profile and the genetic determinism of intramuscular fat traits in the porcine gluteus medius and longissimus dorsi muscles. BMC Genomics, 2019, 20, 170.	1.2	27
21	Viability of Iberian Ã— Meishan F2 newborn pigs. II. Survival analysis up to weaning1. Journal of Animal Science, 2004, 82, 1925-1930.	0.2	26
22	Association analyses between the prion protein locus and reproductive and lamb weight traits in Ripollesa sheep1. Journal of Animal Science, 2007, 85, 592-597.	0.2	24
23	A genome-wide association analysis for porcine serum lipid traits reveals the existence of age-specific genetic determinants. BMC Genomics, 2014, 15, 758.	1.2	24
24	Bayesian threshold analysis of direct and maternal genetic parameters for piglet mortality at farrowing in Large White, Landrace, and Pietrain populations1. Journal of Animal Science, 2009, 87, 80-87.	0.2	23
25	Evidence of maternal QTL affecting growth and obesity in adult mice. Mammalian Genome, 2009, 20, 269-280.	1.0	23
26	Morphological analysis and subpopulation characterization of Ripollesa sheep breed. Animal Genetic Resources = Ressources Genetiques Animales = Recursos Geneticos Animales, 2011, 49, 9-17.	0.2	22
27	Within-Generation Mutation Variance for Litter Size in Inbred Mice. Genetics, 2008, 179, 2147-2155.	1.2	21
28	Genetics of serum and muscle lipids in pigs. Animal Genetics, 2013, 44, 609-619.	0.6	21
29	A Flexible Bayesian Model for Testing for Transmission Ratio Distortion. Genetics, 2014, 198, 1357-1367.	1.2	21
30	Response of lactating dairy ewes to various levels of dietary calcium soaps of fatty acids. Animal Feed Science and Technology, 2006, 131, 312-332.	1.1	19
31	Retention of different sizes of electronic identification boluses in the forestomachs of sheep1,2. Journal of Animal Science, 2006, 84, 2865-2872.	0.2	19
32	Transcriptional analysis of intramuscular fatty acid composition in the longissimus thoracis muscle of <scp>I</scp>berianÃÃ—Â<scp>L</scp>andrace backâ€crossed pigs. Animal Genetics, 2013, 44, 648-660.	0.6	19
33	Implementation of Bayesian methods to identify SNP and haplotype regions with transmission ratio distortion across the whole genome: TRDscan v.1.0. Journal of Dairy Science, 2019, 102, 3175-3188.	1.4	19
34	Viability of Iberian Ã— Meishan F2 newborn pigs. I. Analysis of physiological and vitality variables1. Journal of Animal Science, 2004, 82, 1919-1924.	0.2	18
35	Genetic inbreeding depression load for morphological traits and defects in the Pura Raza EspaÃ±ola horse. Genetics Selection Evolution, 2020, 52, 62.	1.2	18
36	Fine mapping and association analysis of a quantitative trait locus for milk production traits on Bos taurus autosome 4. Journal of Dairy Science, 2009, 92, 758-764.	1.4	17

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37	Genetic diversity measures of the bovine Alberes breed using microsatellites: variability among herds and types of coat colour*. Journal of Animal Breeding and Genetics, 2004, 121, 101-110.	0.8	16
38	Skew distribution of founder-specific inbreeding depression effects on the longevity of Landrace sows. Genetical Research, 2008, 90, 499-508.	0.3	15
39	Genetic parameters and direct, maternal and heterosis effects on litter size in a diallel cross among three commercial varieties of Iberian pig. Animal, 2019, 13, 2765-2772.	1.3	15
40	Analysis of litter size and days to lambing in the Ripollesa ewe. I. Comparison of models with linear and threshold approaches1. Journal of Animal Science, 2007, 85, 618-624.	0.2	14
41	Bayesian inference in a piecewise Weibull proportional hazards model with unknown change points. Journal of Animal Breeding and Genetics, 2007, 124, 176-184.	0.8	14
42	Application of the microarray technology to the transcriptional analysis of muscle phenotypes in pigs. Animal Genetics, 2014, 45, 311-321.	0.6	14
43	Effect of medium- and long-chain triglyceride supplementation on small newborn-pig survival. Preventive Veterinary Medicine, 2005, 67, 213-221.	0.7	13
44	Parametric bootstrap for testing model fitting in the proportional hazards framework: An application to the survival analysis of Bruna dels Pirineus beef calves1. Journal of Animal Science, 2006, 84, 2609-2616.	0.2	13
45	Evaluation of the retention of electronic identification boluses in the forestomachs of cattle1,2. Journal of Animal Science, 2006, 84, 2260-2268.	0.2	13
46	Survey of SSC12 Regions Affecting Fatty Acid Composition of Intramuscular Fat Using High-Density SNP Data. Frontiers in Genetics, 2011, 2, 101.	1.1	12
47	Fetal programming by co-twin rivalry in sheep1. Journal of Animal Science, 2014, 92, 64-71.	0.2	12
48	Impact of incomplete pedigree data and independent culling level pre-selection on the genetic evaluation of livestock: A simulation study on lamb growth. Livestock Science, 2017, 198, 76-81.	0.6	12
49	Discovering lethal alleles across the turkey genome using a transmission ratio distortion approach. Animal Genetics, 2020, 51, 876-889.	0.6	12
50	Discriminating between allele‐and genotype‐specific transmission ratio distortion. Animal Genetics, 2020, 51, 847-854.	0.6	12
51	Polymorphisms of the porcine dopaminebeta-hydroxylase gene and their relation to reproduction and piglet survivability in an Iberian x Meishan F2 intercross. Animal Genetics, 2006, 37, 279-282.	0.6	11
52	Bayesian analysis of quantitative traits using skewed distributions. Genetical Research, 2008, 90, 179-190.	0.3	11
53	Genetic background and phenotypic characterization over two farrowings of leg conformation defects in Landrace and Large White sows1. Journal of Animal Science, 2009, 87, 1606-1612.	0.2	11
54	Epistasis for Founder-Specific Inbreeding Depression in Rabbits. Journal of Heredity, 2011, 102, 157-164.	1.0	11

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55	Inbreeding depression load for litter size in Entrepelado and Retinto Iberian pig varieties1. Journal of Animal Science, 2019, 97, 1979-1986.	0.2	11
56	Genetic determinism for within-litter birth weight variation and its relationship with litter weight and litter size in the Ripollesa ewe breed. Animal, 2007, 1, 637-644.	1.3	10
57	Lack of Socs2 expression reduces lifespan in high-growth mice. Age, 2008, 30, 245-249.	3.0	10
58	geamm v.1.4: a versatile program for mixed model analysis of gene expression data. Animal Genetics, 2008, 39, 89-90.	0.6	10
59	A multivariate analysis with direct additive and inbreeding depression load effects. Genetics Selection Evolution, 2019, 51, 78.	1.2	10
60	Analysis of litter size and days to lambing in the Ripollesa ewe. II. Estimation of variance components and response to phenotypic selection on litter size1. Journal of Animal Science, 2007, 85, 625-631.	0.2	9
61	Consistency and influence on performance of behavioural differences in Large White and Landrace purebred pigs. Applied Animal Behaviour Science, 2009, 117, 13-19.	0.8	9
62	Backfat thickness and longissimus dorsi real-time ultrasound measurements in light lambs1. Journal of Animal Science, 2012, 90, 5047-5055.	0.2	9
63	Accuracy and expected genetic gain under genetic or genomic evaluation in sheep flocks with different amounts of pedigree, genomic and phenotypic data. Livestock Science, 2015, 182, 58-63.	0.6	9
64	On individual-specific prediction of hidden inbreeding depression load. Journal of Animal Breeding and Genetics, 2018, 135, 37-44.	0.8	9
65	Bayes factor analysis for the genetic background of physiological and vitality variables of F2 Iberian × Meishan newborn piglets1. Journal of Animal Science, 2005, 83, 334-339.	0.2	8
66	An association study between polymorphisms of the porcine bone morphogenetic protein receptor type1beta(BMPR1B) and reproductive performance of Iberian x Meishan F2 sows. Animal Genetics, 2006, 37, 297-298.	0.6	8
67	Bayes factor for testing between different structures of random genetic groups: A case study using weaning weight in Bruna dels Pirineus beef cattle. Genetics Selection Evolution, 2007, 39, 39.	1.2	8
68	Competing risk analyses of longevity in Duroc sows with a special emphasis on leg conformation. Animal, 2009, 3, 446-453.	1.3	8
69	Expression patterns and genetic variation of the ovine skeletal muscle transcriptome of sheep from five Spanish meat breeds. Scientific Reports, 2018, 8, 10486.	1.6	8
70	Low genome-wide homozygosity in 11 Spanish ovine breeds. Animal Genetics, 2019, 50, 501-511.	0.6	8
71	Bayes factor for testing the genetic background of quantitative threshold traits. Journal of Animal Breeding and Genetics, 2006, 123, 301-306.	0.8	7
72	Accounting for additive genetic mutations on litter size in Ripollesa sheep1. Journal of Animal Science, 2010, 88, 1248-1255.	0.2	7

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73	Short communication: Effect of mutation age on genomic predictions. Journal of Dairy Science, 2011, 94, 4224-4229.	1.4	7
74	Consequences of paternally inherited effects on the genetic evaluation of maternal effects. Genetics Selection Evolution, 2015, 47, 63.	1.2	7
75	Modeling Skewness in Human Transcriptomes. PLoS ONE, 2012, 7, e38919.	1.1	7
76	Analysis of temperament development during the fattening period in the semi-feral bovine calves of theAlberesMassif. Animal Research, 2006, 55, 389-395.	0.6	6
77	Empirical Bayes factor analyses of quantitative trait loci for gestation length in Iberian Ã— Meishan F2 sows. Animal, 2008, 2, 177-183.	1.3	6
78	Whole genome sequencing identifies allelic ratio distortion in sperm involving genes related to spermatogenesis in a swine model. DNA Research, 2020, 27, .	1.5	6
79	Correction factors for weight productive traits up to weaning in the Bruna dels Pirineus beef cattle breed. Animal Research, 2002, 51, 43-50.	0.6	6
80	Genomic differentiation among varieties of Iberian pig. Spanish Journal of Agricultural Research, 2020, 18, e0401.	0.3	6
81	Survival Quantitative Trait Locus Fine Mapping by Measuring and Testing for Hardyâ€"Weinberg and Linkage Disequilibrium. Genetics, 2007, 176, 721-724.	1.2	5
82	Quantitative trait loci for fatness at growing and reproductive stages in Iberianâ€ƒÃ—â€ƒMeishan F$_2$ sows. Animal Genetics, 2011, 42, 548-551.	0.6	5
83	Canalization analysis of birth weight in Bruna dels Pirineus beef cattle1. Journal of Animal Science, 2013, 91, 3070-3078.	0.2	5
84	Genetic evaluation of age at first calving for GuzerÃ¡ beef cattle using linear, threshold, and survival Bayesian models. Journal of Animal Science, 2018, 96, 2517-2524.	0.2	5
85	An Association Analysis Between a Silent C558T Polymorphism at the Pig Vascular Cell Adhesion Molecule 1 Locus and Sow Reproduction and Piglet Survivability Traits. Reproduction in Domestic Animals, 2008, 43, 542-546.	0.6	4
86	Analysis of lambing distribution in the Ripollesa sheep breed. II. Environmental and genetic sources of variation. Animal, 2019, 13, 2140-2145.	1.3	4
87	Between-groups within-gene heterogeneity of residual variances in microarray gene expression data. BMC Genomics, 2008, 9, 319.	1.2	3
88	Segregation Analysis of a Sex Ratio Distortion Locus in Congenic Mice. Journal of Heredity, 2010, 101, 351-359.	1.0	3
89	Dairy Cattle Breeding Simulation Program: A simulation program to teach animal breeding principles and practices. Journal of Dairy Science, 2010, 93, 2816-2826.	1.4	3
90	Comparison of linear, skewed-linear, and proportional hazard models for the analysis of lambing interval in Ripollesa ewes1. Journal of Animal Science, 2012, 90, 1788-1797.	0.2	3

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91	Short communication: Accounting for new mutations in genomic prediction models. Journal of Dairy Science, 2013, 96, 5398-5402.	1.4	3
92	Bayesian analysis of additive epistasis arising from new mutations in mice. Genetical Research, 2014, 96, e008.	0.3	3
93	Freemartinism in replacement ewe-lambs of the Ripollesa sheep breed. Journal of Veterinary Science, 2018, 19, 858.	0.5	3
94	Maternal Transmission Ratio Distortion in Two Iberian Pig Varieties. Genes, 2020, 11, 1050.	1.0	3
95	A cross-specific multiplicative binomial recursive model for the analysis of perinatal mortality in a diallel cross among three varieties of Iberian pig. Scientific Reports, 2020, 10, 21190.	1.6	3
96	Low-coverage whole-genome sequencing in livestock species for individual traceability and parentage testing. Livestock Science, 2021, 251, 104629.	0.6	3
97	Using haplotype probabilities in categorical survival analysis: a case study with three candidate genes in an Iberianâ€ƒÃ—â€ƒMeishan F_2 population of newborn piglets. Journal of Animal Breeding and Genetics, 2008, 125, 5-12.	0.8	2
98	Bayes factor between Student t and Gaussian mixed models within an animal breeding context. Genetics Selection Evolution, 2008, 40, 395.	1.2	2
99	Sources of sire-specific genetic variance for birth and weaning weight in Bruna dels Pirineus beef calves. Animal, 2012, 6, 1931-1938.	1.3	2
100	Comparison between linear and proportional hazard models for the analysis of age at first lambing in the Ripollesa breed. Animal, 2016, 10, 365-371.	1.3	2
101	Carcass traits and meat fatty acid composition in Mediterranean light lambs. Canadian Journal of Animal Science, 0, , .	0.7	2
102	Analysis of lambing distribution in the Ripollesa sheep breed. I. Development and comparison of circular von Mises models. Animal, 2019, 13, 2133-2139.	1.3	2
103	Markers with low GenTrain scores can generate spurious signals in genomeâ€wide scans for transmission ratio distortion. Animal Genetics, 2021, 52, 779-781.	0.6	2
104	Characterisation and conservation programme of the Alberes cattle breed in Catalonia (Spain). Animal Genetic Resources Information, 2008, 43, 1-14.	0.3	1
105	Variability-specific differential gene expression across reproductive stages in sows. Animal, 2013, 7, 378-385.	1.3	1
106	Bayes factor for testing between different structures of random genetic groups: A case study using weaning weight in Bruna dels Pirineus beef cattle. Genetics Selection Evolution, 2007, 39, 39-53.	1.2	1
107	Analyses of lambing dates in sheep breeds using von Mises distribution. Journal of Animal Breeding and Genetics, 2022, 139, 271-280.	0.8	1
108	Short Communication: Estimating abundance, survival and age structure of the Alberes cattle using recapture techniques. Canadian Journal of Animal Science, 2011, 91, 343-347.	0.7	0

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109	Bootstrap test for proportional hazard assumption on time-independent systematic effects of longevity data. Journal of Animal Breeding and Genetics, 2011, 128, 100-104.	0.8	0
110	Bayesian recursive mixed linear model for gene expression analyses with continuous covariates1. Journal of Animal Science, 2012, 90, 67-75.	0.2	0
111	Fine mapping by composite genome-wide association analysis. Genetical Research, 2017, 99, e4.	0.3	0
112	Technical note: PaGELL v.1.5: A flexible parametric program for the Bayesian analysis of longevity data within the context of animal breeding. Journal of Dairy Science, 2017, 100, 8282-8286.	1.4	0
113	Validation of a Bayesian approach for maternity identification in abandoned lambs. Italian Journal of Animal Science, 2017, 16, 405-411.	0.8	0
114	Analysis of reproductive seasonality in Entrepelado and Retinto Iberian pig varieties under intensive management. Livestock Science, 2021, 245, 104441.	0.6	0