John Wm Bastiaansen

List of Publications by Year
in descending order

56 papers	**1,960** citations	236833 **25** h-index	265120 **42** g-index
57 all docs	**57** docs citations	**57** times ranked	**2640** citing authors

#	Article	IF	Citations
1	Murine Gut Microbiota Is Defined by Host Genetics and Modulates Variation of Metabolic Traits. PLoS ONE, 2012, 7, e39191.	1.1	198
2	New alleles in calpastatin gene are associated with meat quality traits in pigs1. Journal of Animal Science, 2004, 82, 2829-2839.	0.2	128
3	A QTL resource and comparison tool for pigs: PigQTLDB. Mammalian Genome, 2005, 16, 792-800.	1.0	125
4	Evolutionary dynamics of copy number variation in pig genomes in the context of adaptation and domestication. BMC Genomics, 2013, 14, 449.	1.2	118
5	Comparison of linkage disequilibrium and haplotype diversity on macro- and microchromosomes in chicken. BMC Genetics, 2009, 10, 86.	2.7	72
6	Investigation of Obesity Candidate Genes On Porcine Fat Deposition Quantitative Trait Loci Regions. Obesity, 2004, 12, 1981-1994.	4.0	68
7	Whole genome SNP discovery and analysis of genetic diversity in Turkey (Meleagris gallopavo). BMC Genomics, 2012, 13, 391.	1.2	63
8	Accuracy of genomic prediction using imputed whole€genome sequence data in white layers. Journal of Animal Breeding and Genetics, 2016, 133, 167-179.	0.8	61
9	A Genome-Wide Association Study Reveals Dominance Effects on Number of Teats in Pigs. PLoS ONE, 2014, 9, e105867.	1.1	59
10	Genomic associations with somatic cell score in first-lactation Holstein cows. Journal of Dairy Science, 2012, 95, 899-908.	1.4	47
11	Long-term response to genomic selection: effects of estimation method and reference population structure for different genetic architectures. Genetics Selection Evolution, 2012, 44, 3.	1.2	47
12	Sire evaluation for total number born in pigs using a genomic reaction norms approach1. Journal of Animal Science, 2014, 92, 3825-3834.	0.2	46
13	Genome-wide associations for fertility traits in Holstein€"Friesian dairy cows using data from experimental research herds in four European countries. Animal, 2012, 6, 1206-1215.	1.3	42
14	Genetic parameters for semen quality and quantity traits in five pig lines1. Journal of Animal Science, 2017, 95, 4251-4259.	0.2	42
15	Sensitivity of methods for estimating breeding values using genetic markers to the number of QTL and distribution of QTL variance. Genetics Selection Evolution, 2010, 42, 9.	1.2	41
16	Accuracy of Predicted Genomic Breeding Values in Purebred and Crossbred Pigs. G3: Genes, Genomes, Genetics, 2015, 5, 1575-1583.	0.8	41
17	Standard error of the genetic correlation: how much data do we need to estimate a purebred-crossbred genetic correlation?. Genetics Selection Evolution, 2014, 46, 79.	1.2	40
18	A major SNP resource for dissection of phenotypic and genetic variation in Pacific white shrimp (<i>Litopenaeus vannamei</i>). Animal Genetics, 2010, 41, 39-47.	0.6	37

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19	Identification of Mendelian inconsistencies between SNP and pedigree information of sibs. Genetics Selection Evolution, 2011, 43, 34.	1.2	37
20	A SNP based linkage map of the turkey genome reveals multiple intrachromosomal rearrangements between the Turkey and Chicken genomes. BMC Genomics, 2010, 11, 647.	1.2	35
21	Bayesian GWAS and network analysis revealed new candidate genes for number of teats in pigs. Journal of Applied Genetics, 2015, 56, 123-132.	1.0	35
22	Systematic differences in the response of genetic variation to pedigree and genome-based selection methods. Heredity, 2014, 113, 503-513.	1.2	34
23	Linkage disequilibrium patterns and persistence of phase in purebred and crossbred pig (Sus scrofa) populations. BMC Genetics, 2014, 15, 126.	2.7	33
24	Environmental and economic impacts of using co-products in the diets of finishing pigs in Brazil. Journal of Cleaner Production, 2017, 162, 247-259.	4.6	33
25	Genetic variances, heritabilities and maternal effects on body weight, breast meat yield, meat quality traits and the shape of the growth curve in turkey birds. BMC Genetics, 2011, 12, 14.	2.7	31
26	Genome-wide association study using deregressed breeding values for cryptorchidism and scrotal/inguinal hernia in two pig lines. Genetics Selection Evolution, 2015, 47, 18.	1.2	26
27	Genetic correlations between feed efficiency traits, and growth performance and carcass traits in purebred and crossbred pigs. Journal of Animal Science, 2018, 96, 817-829.	0.2	26
28	Artificial selection on introduced Asian haplotypes shaped the genetic architecture in European commercial pigs. Proceedings of the Royal Society B: Biological Sciences, 2015, 282, 20152019.	1.2	25
29	Accuracy of genomic prediction of purebreds for cross bred performance in pigs. Journal of Animal Breeding and Genetics, 2016, 133, 443-451.	0.8	24
30	Impact of fitting dominance and additive effects on accuracy of genomic prediction of breeding values in layers. Journal of Animal Breeding and Genetics, 2016, 133, 334-346.	0.8	24
31	Using markers with large effect in genetic and genomic predictions1. Journal of Animal Science, 2017, 95, 59-71.	0.2	24
32	Relationship Between Immune Cell Phenotypes and Pig Growth in a Commercial Farm. Animal Biotechnology, 2006, 17, 81-98.	0.7	23
33	Mapping and association studies of diabetes related genes in the pig. Animal Genetics, 2005, 36, 36-42.	0.6	21
34	Genome‐wide association study of insect bite hypersensitivity in <scp>D</scp>utch <scp>S</scp>hetland pony mares. Animal Genetics, 2013, 44, 44-52.	0.6	21
35	The impact of genome editing on the introduction of monogenic traits in livestock. Genetics Selection Evolution, 2018, 50, 18.	1.2	21
36	Genetic parameters for natural antibody isotype titers in milk of Dutch Holstein‐Friesians. Animal Genetics, 2013, 44, 485-492.	0.6	18

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37	Meta‐analysis of results from quantitative trait loci mapping studies on pig chromosome 4. Animal Genetics, 2011, 42, 280-292.	0.6	17
38	Accuracy of imputation using the most common sires as reference population in layer chickens. BMC Genetics, 2015, 16, 101.	2.7	15
39	Genomic prediction of growth in pigs based on a model including additive and dominance effects. Journal of Animal Breeding and Genetics, 2016, 133, 180-186.	0.8	15
40	Genotype by feed interaction for feed efficiency and growth performance traits in pigs1. Journal of Animal Science, 2018, 96, 4125-4135.	0.2	15
41	Effects of incorporating environmental cost and risk aversion on economic values of pig breeding goal traits. Journal of Animal Breeding and Genetics, 2018, 135, 194-207.	0.8	13
42	Using markers with large effect in genetic and genomic predictions. Journal of Animal Science, 2017, 95, 59.	0.2	13
43	Whole genome QTL mapping for growth, meat quality and breast meat yield traits in turkey. BMC Genetics, 2011, 12, 61.	2.7	12
44	A stochastic bio-economic pig farm model to assess the impact of innovations on farm performance. Animal, 2018, 12, 819-830.	1.3	12
45	Accuracy of genomic prediction using deregressed breeding values estimated from purebred and crossbred offspring phenotypes in pigs1. Journal of Animal Science, 2015, 93, 3313-3321.	0.2	10
46	Genes located on a SSC17 meat quality QTL region are associated with growth in outbred pig populations. Animal Genetics, 2009, 40, 774-778.	0.6	9
47	Fine mapping and single nucleotide polymorphism effects estimation on pig chromosomes 1, 4, 7, 8, 17 and X. Genetics and Molecular Biology, 2013, 36, 511-519.	0.6	9
48	Accuracy of genome-enabled prediction exploring purebred and crossbred pig populations1. Journal of Animal Science, 2015, 93, 4684-4691.	0.2	9
49	Genome‐wide association study reveals regions associated with gestation length in two pig populations. Animal Genetics, 2016, 47, 223-226.	0.6	9
50	Regional regulation of transcription in the chicken genome. BMC Genomics, 2010, 11, 28.	1.2	7
51	Genome-wide candidate regions for selective sweeps revealed through massive parallel sequencing of DNA across ten turkey populations. BMC Genetics, 2014, 15, 117.	2.7	7
52	On the relationship between an Asian haplotype on chromosome 6 that reduces androstenone levels in boars and the differential expression of SULT2A1 in the testis. BMC Genetics, 2014, 15, 4.	2.7	7
53	Accounting for genetic architecture in single‐and multipopulation genomic prediction using weights from genomewide association studies in pigs. Journal of Animal Breeding and Genetics, 2016, 133, 187-196.	0.8	7
54	Quantitative genotyping to estimate genetic contributions to pooled samples and genetic merit of the contributing entities. Acta Agriculturae Scandinavica - Section A: Animal Science, 2010, 60, 3-12.	0.2	3

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55	Prior genetic architecture impacting genomic regions under selection: An example using genomic selection in two poultry breeds. Livestock Science, 2015, 171, 1-11.	0.6	3
56	Asian low‑androstenone haplotype on pig chromosome 6 does not unfavorably affect production and reproduction traits. Animal Genetics, 2014, 45, 874-877.	0.6	1