

Miguel Perez-Enciso

List of Publications by Year in descending order

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Version: 2024-02-01

123
papers

6,592
citations

71061

41
h-index

71651

76
g-index

132
all docs

132
docs citations

132
times ranked

7244
citing authors

#	ARTICLE	IF	CITATIONS
1	Analyses of pig genomes provide insight into porcine demography and evolution. <i>Nature</i> , 2012, 491, 393-398.	13.7	1,190
2	Prediction of clinical outcome with microarray data: a partial least squares discriminant analysis (PLS-DA) approach. <i>Human Genetics</i> , 2003, 112, 581-92.	1.8	325
3	Pig Domestication and Human-Mediated Dispersal in Western Eurasia Revealed through Ancient DNA and Geometric Morphometrics. <i>Molecular Biology and Evolution</i> , 2013, 30, 824-832.	3.5	196
4	Regulatory impact factors: unraveling the transcriptional regulation of complex traits from expression data. <i>Bioinformatics</i> , 2010, 26, 896-904.	1.8	193
5	Can Deep Learning Improve Genomic Prediction of Complex Human Traits?. <i>Genetics</i> , 2018, 210, 809-819.	1.2	160
6	A comparison of carcass, meat quality and histochemical characteristics of Iberian (Guadyerbas line) and Landrace pigs. <i>Livestock Science</i> , 1998, 56, 215-223.	1.2	158
7	Genome-Wide Footprints of Pig Domestication and Selection Revealed through Massive Parallel Sequencing of Pooled DNA. <i>PLoS ONE</i> , 2011, 6, e14782.	1.1	135
8	Population genomics from pool sequencing. <i>Molecular Ecology</i> , 2013, 22, 5561-5576.	2.0	133
9	Sequence- vs. chip-assisted genomic selection: accurate biological information is advised. <i>Genetics Selection Evolution</i> , 2015, 47, 43.	1.2	130
10	Exploring the gonad transcriptome of two extreme male pigs with RNA-seq. <i>BMC Genomics</i> , 2011, 12, 552.	1.2	127
11	Qxpak: a versatile mixed model application for genetical genomics and QTL analyses. <i>Bioinformatics</i> , 2004, 20, 2792-2798.	1.8	126
12	Sheep genome functional annotation reveals proximal regulatory elements contributed to the evolution of modern breeds. <i>Nature Communications</i> , 2018, 9, 859.	5.8	126
13	A QTL on pig chromosome 4 affects fatty acid metabolism: evidence from an Iberian by Landrace intercross.. <i>Journal of Animal Science</i> , 2000, 78, 2525.	0.2	122
14	Liver transcriptome profile in pigs with extreme phenotypes of intramuscular fatty acid composition. <i>BMC Genomics</i> , 2012, 13, 547.	1.2	118
15	A Guide for Using Deep Learning for Complex Trait Genomic Prediction. <i>Genes</i> , 2019, 10, 553.	1.0	116
16	Genome-wide SNP data unveils the globalization of domesticated pigs. <i>Genetics Selection Evolution</i> , 2017, 49, 71.	1.2	114
17	Integrating Y-Chromosome, Mitochondrial, and Autosomal Data to Analyze the Origin of Pig Breeds. <i>Molecular Biology and Evolution</i> , 2009, 26, 2061-2072.	3.5	103
18	Copy number variation in the porcine genome inferred from a 60 k SNP BeadChip. <i>BMC Genomics</i> , 2010, 11, 593.	1.2	102

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19	Many QTLs with minor additive effects are associated with a large difference in growth between two selection lines in chickens. <i>Genetical Research</i> , 2005, 86, 115-125.	0.3	99
20	A QTL for intramuscular fat and backfat thickness is located on porcine Chromosome 6. <i>Mammalian Genome</i> , 2000, 11, 344-346.	1.0	95
21	On Marker-Assisted Prediction of Genetic Value: Beyond the Ridge. <i>Genetics</i> , 2003, 163, 347-365.	1.2	94
22	Qxpak.5: Old mixed model solutions for new genomics problems. <i>BMC Bioinformatics</i> , 2011, 12, 202.	1.2	87
23	Conservation genomic analysis of domestic and wild pig populations from the Iberian Peninsula. <i>BMC Genetics</i> , 2013, 14, 106.	2.7	87
24	Exploring Deep Learning for Complex Trait Genomic Prediction in Polyploid Outcrossing Species. <i>Frontiers in Plant Science</i> , 2020, 11, 25.	1.7	85
25	Test for positional candidate genes for body composition on pig chromosome 6. <i>Genetics Selection Evolution</i> , 2002, 34, 465-79.	1.2	75
26	Detection of QTL affecting fatty acid composition in the pig. <i>Mammalian Genome</i> , 2003, 14, 650-656.	1.0	74
27	QTL mapping for growth and carcass traits in an Iberian by Landrace pig intercross: additive, dominant and epistatic effects. <i>Genetical Research</i> , 2002, 80, 145-154.	0.3	68
28	A functional regulatory variant of MYH3 influences muscle fiber-type composition and intramuscular fat content in pigs. <i>PLoS Genetics</i> , 2019, 15, e1008279.	1.5	66
29	SNP calling by sequencing pooled samples. <i>BMC Bioinformatics</i> , 2012, 13, 239.	1.2	63
30	Genome-wide association study for intramuscular fatty acid composition in an Iberian \times Landrace cross1. <i>Journal of Animal Science</i> , 2012, 90, 2883-2893.	0.2	63
31	A comparison of normal and nonnormal mixed models for number of lambs born in Norwegian sheep. <i>Journal of Animal Science</i> , 1994, 72, 1166-1173.	0.2	58
32	Porcine colonization of the Americas: a 60k SNP story. <i>Heredity</i> , 2013, 110, 321-330.	1.2	58
33	Sparse Matrix Inversion for Restricted Maximum Likelihood Estimation of Variance Components by Expectation-Maximization. <i>Journal of Dairy Science</i> , 1993, 76, 1479-1483.	1.4	54
34	Assessment of genetic variation explained by markers for wool traits in sheep via a segment mapping approach. <i>Mammalian Genome</i> , 2001, 12, 569-572.	1.0	53
35	Quantitative Trait Loci Mapping in F2 Crosses Between Outbred Lines. <i>Genetics</i> , 2000, 155, 391-405.	1.2	53
36	Fine Mapping of Complex Trait Genes Combining Pedigree and Linkage Disequilibrium Information: A Bayesian Unified Framework. <i>Genetics</i> , 2003, 163, 1497-1510.	1.2	53

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37	Identification of rumen microbial biomarkers linked to methane emission in Holstein dairy cows. <i>Journal of Animal Breeding and Genetics</i> , 2020, 137, 49-59.	0.8	51
38	Transcriptome architecture across tissues in the pig. <i>BMC Genomics</i> , 2008, 9, 173.	1.2	45
39	Dissecting structural and nucleotide genome-wide variation in inbred Iberian pigs. <i>BMC Genomics</i> , 2013, 14, 148.	1.2	45
40	Resequencing studies of nonmodel organisms using closely related reference genomes: optimal experimental designs and bioinformatics approaches for population genomics. <i>Molecular Ecology</i> , 2014, 23, 1764-1779.	2.0	45
41	Massive parallel sequencing in animal genetics: wherefroms and wheretos. <i>Animal Genetics</i> , 2010, 41, 561-569.	0.6	44
42	Whole-genome sequence analysis reveals differences in population management and selection of European low-input pig breeds. <i>BMC Genomics</i> , 2014, 15, 601.	1.2	44
43	From SNP co-association to RNA co-expression: Novel insights into gene networks for intramuscular fatty acid composition in porcine. <i>BMC Genomics</i> , 2014, 15, 232.	1.2	44
44	Selection in the Making: A Worldwide Survey of Haplotypic Diversity Around a Causative Mutation in Porcine <i>IGF2</i> . <i>Genetics</i> , 2008, 178, 1639-1652.	1.2	42
45	Bayes factors for detection of Quantitative Trait Loci. <i>Genetics Selection Evolution</i> , 2001, 33, 133-52.	1.2	40
46	Estrogen receptor polymorphism in Landrace pigs and its association with litter size performance. <i>Livestock Science</i> , 2003, 82, 53-59.	1.2	39
47	A quantitative trait locus genome scan for porcine muscle fiber traits reveals overdominance and epistasis1. <i>Journal of Animal Science</i> , 2008, 86, 3290-3299.	0.2	39
48	Genome data from a sixteenth century pig illuminate modern breed relationships. <i>Heredity</i> , 2015, 114, 175-184.	1.2	39
49	Evaluating Sequence-Based Genomic Prediction with an Efficient New Simulator. <i>Genetics</i> , 2017, 205, 939-953.	1.2	39
50	Characterization of the porcine acyl-CoA synthetase long-chain 4 gene and its association with growth and meat quality traits. <i>Animal Genetics</i> , 2006, 37, 219-224.	0.6	35
51	Unexpected High Polymorphism at the FABP4 Gene Unveils a Complex History for Pig Populations. <i>Genetics</i> , 2006, 174, 2119-2127.	1.2	35
52	Optimal Neutrality Tests Based on the Frequency Spectrum. <i>Genetics</i> , 2010, 186, 353-365.	1.2	34
53	On growth, fatness, and form: A further look at porcine Chromosome 4 in an Iberian × Landrace cross. <i>Mammalian Genome</i> , 2005, 16, 374-382.	1.0	33
54	Characterization of the porcine FABP5 gene and its association with the FAT1 QTL in an Iberian by Landrace cross. <i>Animal Genetics</i> , 2006, 37, 589-591.	0.6	33

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55	In Silico Study of Transcriptome Genetic Variation in Outbred Populations. <i>Genetics</i> , 2004, 166, 547-554.	1.2	30
56	Characterization of the porcine nutrient and taste receptor gene repertoire in domestic and wild populations across the globe. <i>BMC Genomics</i> , 2014, 15, 1057.	1.2	30
57	Estimates of genetic parameters for litter size in six strains of Iberian pigs. <i>Livestock Science</i> , 1992, 32, 283-293.	1.2	28
58	A non-synonymous mutation in a conserved site of the <i>MTTP</i> gene is strongly associated with protein activity and fatty acid profile in pigs. <i>Animal Genetics</i> , 2009, 40, 813-820.	0.6	28
59	Computation of identity by descent probabilities conditional on DNA markers via a Monte Carlo Markov Chain method. <i>Genetics Selection Evolution</i> , 2000, 32, 467-82.	1.2	27
60	Linkage disequilibrium fine mapping of quantitative trait loci: A simulation study. <i>Genetics Selection Evolution</i> , 2003, 35, 513-32.	1.2	27
61	Adipocyte fatty-acid binding protein is closely associated to the porcine <i>FAT1</i> locus on chromosome 41. <i>Journal of Animal Science</i> , 2006, 84, 2907-2913.	0.2	26
62	Combining Gene Expression and Molecular Marker Information for Mapping Complex Trait Genes: A Simulation Study. <i>Genetics</i> , 2003, 164, 1597-1606.	1.2	26
63	Genetic evaluation with uncertain parentage: a comparison of methods. <i>Theoretical and Applied Genetics</i> , 1992, 84, 173-179.	1.8	25
64	A comparison between linear and poisson mixed models for litter size in iberian pigs. <i>Livestock Science</i> , 1993, 35, 303-316.	1.2	25
65	Genomic relationships computed from either next-generation sequence or array <i>sc</i> SNP data. <i>Journal of Animal Breeding and Genetics</i> , 2014, 131, 85-96.	0.8	24
66	Influence of epistasis on response to genomic selection using complete sequence data. <i>Genetics Selection Evolution</i> , 2017, 49, 66.	1.2	23
67	Exploring Alternative Models for Sex-Linked Quantitative Trait Loci in Outbred Populations: Application to an Iberian Landrace Pig Intercross. <i>Genetics</i> , 2002, 161, 1625-1632.	1.2	23
68	A Deep Catalog of Autosomal Single Nucleotide Variation in the Pig. <i>PLoS ONE</i> , 2015, 10, e0118867.	1.1	22
69	Genetical genomics: use all data. <i>BMC Genomics</i> , 2007, 8, 69.	1.2	21
70	Impact of breed and sex on porcine endocrine transcriptome: a bayesian biometrical analysis. <i>BMC Genomics</i> , 2009, 10, 89.	1.2	21
71	Large-scale SNP genotyping in crosses between outbred lines: how useful is it?. <i>Heredity</i> , 2010, 105, 173-182.	1.2	21
72	Accuracy of genomic predictions using different imputation error rates in aquaculture breeding programs: A simulation study. <i>Aquaculture</i> , 2019, 503, 225-230.	1.7	21

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73	On the mapping of quantitative trait loci at marker and non-marker locations. <i>Genetical Research</i> , 2002, 79, 97-106.	0.3	19
74	A Genome Wide Detection of Quantitative Trait Loci on Pig Maternal Infanticide Behavior in a Large Scale White Duroc—Ærhuatian Resource Population. <i>Behavior Genetics</i> , 2009, 39, 213-219.	1.4	19
75	pSBVB: A Versatile Simulation Tool To Evaluate Genomic Selection in Polyploid Species. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 327-334.	0.8	19
76	HIV drug resistance prediction with weighted categorical kernel functions. <i>BMC Bioinformatics</i> , 2019, 20, 410.	1.2	17
77	Opportunities and limits of combining microbiome and genome data for complex trait prediction. <i>Genetics Selection Evolution</i> , 2021, 53, 65.	1.2	17
78	Partial short-read sequencing of a highly inbred Iberian pig and genomics inference thereof. <i>Heredity</i> , 2011, 107, 256-264.	1.2	16
79	A Pathway-Centered Analysis of Pig Domestication and Breeding in Eurasia. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2171-2184.	0.8	16
80	Phenomes: the current frontier in animal breeding. <i>Genetics Selection Evolution</i> , 2021, 53, 22.	1.2	16
81	Quantitative Trait Locus Analysis in Crosses Between Outbred Lines With Dominance and Inbreeding. <i>Genetics</i> , 2001, 159, 413-422.	1.2	16
82	Evolutionary study of a potential selection target region in the pig. <i>Heredity</i> , 2011, 106, 330-338.	1.2	15
83	The chimerical genome of <i>scp>l</scp>sla del <scp>C</scp>oco feral pigs (<scp>C</scp>osta) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Ecology, 2015, 24, 2364-2378.</i>	2.0	15
84	Nucleotide variability and linkage disequilibrium patterns at the porcine <i>FABP5</i> gene. <i>Animal Genetics</i> , 2008, 39, 468-473.	0.6	14
85	Estimating Conformational Traits in Dairy Cattle With DeepAPS: A Two-Step Deep Learning Automated Phenotyping and Segmentation Approach. <i>Frontiers in Genetics</i> , 2020, 11, 513.	1.1	14
86	Automatic Fruit Morphology Phenome and Genetic Analysis: An Application in the Octoploid Strawberry. <i>Plant Phenomics</i> , 2021, 2021, 9812910.	2.5	14
87	Exploratory Study on the Transcriptional Profile of Pigs Subclinically Infected with Porcine Circovirus Type 2. <i>Animal Biotechnology</i> , 2009, 20, 96-109.	0.7	12
88	Polymorphisms of the porcine dopamine-beta-hydroxylase gene and their relation to reproduction and piglet survivability in an Iberian x Meishan F2 intercross. <i>Animal Genetics</i> , 2006, 37, 279-282.	0.6	11
89	Assignment of the 2,4-dienoyl-CoA reductase (DECR) gene to porcine chromosome 4. <i>Animal Genetics</i> , 2002, 33, 164-165.	0.6	10
90	Evaluation of <i>FABP2</i> as candidate gene for a fatty acid composition QTL in porcine chromosome 8. <i>Journal of Animal Breeding and Genetics</i> , 2009, 126, 52-58.	0.8	10

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91	Pipelinier: software to evaluate the performance of bioinformatics pipelines for next-generation resequencing. <i>Molecular Ecology Resources</i> , 2015, 15, 99-106.	2.2	10
92	Genomic scan for quantitative trait loci of chemical and physical body composition and deposition on pig chromosome X including the pseudoautosomal region of males. <i>Genetics Selection Evolution</i> , 2009, 41, 27.	1.2	9
93	Building phenotype networks to improve QTL detection: a comparative analysis of fatty acid and fat traits in pigs. <i>Journal of Animal Breeding and Genetics</i> , 2011, 128, 329-343.	0.8	9
94	Mitochondrial DNA diversity in wild boar from the Primorsky Krai Region (East Russia). <i>Animal Genetics</i> , 2011, 42, 96-99.	0.6	9
95	Nucleotide variability of the porcine <i>SERPINA6</i> gene and the origin of a putative causal mutation associated with meat quality. <i>Animal Genetics</i> , 2011, 42, 235-241.	0.6	9
96	Association between plasma metabolites and gene expression profiles in five porcine endocrine tissues. <i>Genetics Selection Evolution</i> , 2011, 43, 28.	1.2	9
97	Worldwide genetic relationships of pigs as inferred from X chromosome SNPs. <i>Animal Genetics</i> , 2013, 44, 130-138.	0.6	9
98	SeqBreed: a python tool to evaluate genomic prediction in complex scenarios. <i>Genetics Selection Evolution</i> , 2020, 52, 7.	1.2	9
99	A worldwide map of swine short tandem repeats and their associations with evolutionary and environmental adaptations. <i>Genetics Selection Evolution</i> , 2021, 53, 39.	1.2	9
100	A comparison between methods for linkage disequilibrium fine mapping of quantitative trait loci. <i>Genetical Research</i> , 2004, 83, 41-47.	0.3	8
101	A note on the use of mate selection in closed MOET breeding schemes. <i>Animal Science</i> , 1991, 53, 403-406.	1.3	7
102	Genetic implications of a bivariate threshold model for litter size components. <i>Journal of Animal Science</i> , 1994, 72, 2775.	0.2	7
103	Plant Polyphenol Intake Alters Gene Expression in Canine Leukocytes. <i>Journal of Nutrigenetics and Nutrigenomics</i> , 2009, 2, 43-52.	1.8	7
104	Disease Liability Prediction from Large Scale Genotyping Data Using Classifiers with a Reject Option. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 88-97.	1.9	7
105	The "heritability" of domestication and its functional partitioning in the pig. <i>Heredity</i> , 2017, 118, 160-168.	1.2	7
106	Effect of the data family structure, tank replication and the statistical model, on the estimation of genetic parameters for body weight at 28 days of age in the Pacific white shrimp (<i>Penaeus (Litopenaeus)</i>) Tj ETQq000 rgBT6/Overlock		
107	Sequential bulked typing: a rapid approach for detecting QTLs. <i>Theoretical and Applied Genetics</i> , 1998, 96, 551-557.	1.8	5
108	Interspecific Chromosome-Wide Transcription Profiles Reveal the Existence of Mammalian-Specific and Species-Specific Chromosome Domains. <i>Journal of Molecular Evolution</i> , 2004, 59, 317-328.	0.8	4

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109	Leipzig: the dawn of the genomes era. <i>Journal of Animal Breeding and Genetics</i> , 2010, 127, 338-338.	0.8	4
110	On genetic differentiation between domestic pigs and Tibetan wild boars. <i>Nature Genetics</i> , 2015, 47, 190-192.	9.4	4
111	Spanish practices. <i>Nature</i> , 1995, 378, 760-760.	13.7	3
112	A method for computing identity by descent probabilities and quantitative trait loci mapping with dominant (AFLP) markers. <i>Genetical Research</i> , 2002, 79, 247-258.	0.3	3
113	Multiple association analysis via simulated annealing (MASSA). <i>Bioinformatics</i> , 2006, 22, 573-580.	1.8	3
114	RAPID COMMUNICATION: A haplotype information theory method reveals genes of evolutionary interest in European vs. Asian pigs ¹ . <i>Journal of Animal Science</i> , 2018, 96, 3064-3069.	0.2	3
115	A note on prediction of response to artificial selection with indices of unequal information. <i>Livestock Science</i> , 1991, 29, 335-340.	1.2	2
116	Explaining the Genetic Basis of Complex Quantitative Traits through Prediction Models. <i>Journal of Computational Biology</i> , 2010, 17, 1711-1723.	0.8	2
117	Emerging tools in quantitative trait loci detection. <i>Acta Agriculturae Scandinavica - Section A: Animal Science</i> , 2007, 57, 202-207.	0.2	1
118	Assignment of RAD51C to porcine chromosome 12 and identification of intronic variability. <i>Animal Genetics</i> , 2005, 36, 461-462.	0.6	0
119	Atlas: A Java-Based Tool for Managing Genotypes. <i>Journal of Heredity</i> , 2005, 96, 623-625.	1.0	0
120	Population and quantitative genetics for a cause. <i>Journal of Animal Breeding and Genetics</i> , 2008, 125, 217-218.	0.8	0
121	International conference on quantitative genetics 4: big science for complex traits. <i>Journal of Animal Breeding and Genetics</i> , 2012, 129, 343-344.	0.8	0
122	Future implications of full-scale genomics for animal breeding: personalized indices?. <i>Journal of Animal Breeding and Genetics</i> , 2013, 130, 2-3.	0.8	0
123	10th WCGALP in beautiful Vancouver. <i>Journal of Animal Breeding and Genetics</i> , 2014, 131, 409-412.	0.8	0