

Miguel Perez-Enciso

List of Publications by Year in descending order

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123
papers

6,592
citations

70961

41
h-index

71532

76
g-index

132
all docs

132
docs citations

132
times ranked

7244
citing authors

#	ARTICLE	IF	CITATIONS
1	Phenomes: the current frontier in animal breeding. <i>Genetics Selection Evolution</i> , 2021, 53, 22.	1.2	16
2	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
3	Automatic Fruit Morphology Phenome and Genetic Analysis: An Application in the Octoploid Strawberry. <i>Plant Phenomics</i> , 2021, 2021, 9812910.	2.5	14
4	Opportunities and limits of combining microbiome and genome data for complex trait prediction. <i>Genetics Selection Evolution</i> , 2021, 53, 65.	1.2	17
5	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
6	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
7	Exploring Deep Learning for Complex Trait Genomic Prediction in Polyploid Outcrossing Species. <i>Frontiers in Plant Science</i> , 2020, 11, 25.	1.7	85
8	SeqBreed: a python tool to evaluate genomic prediction in complex scenarios. <i>Genetics Selection Evolution</i> , 2020, 52, 7.	1.2	9
9	A Guide for Using Deep Learning for Complex Trait Genomic Prediction. <i>Genes</i> , 2019, 10, 553.	1.0	116
10	HIV drug resistance prediction with weighted categorical kernel functions. <i>BMC Bioinformatics</i> , 2019, 20, 410.	1.2	17
11	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
12	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
13	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
14	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
15	Can Deep Learning Improve Genomic Prediction of Complex Human Traits?. <i>Genetics</i> , 2018, 210, 809-819.	1.2	160
16	RAPID COMMUNICATION: A haplotype information theory method reveals genes of evolutionary interest in European vs. Asian pigs1. <i>Journal of Animal Science</i> , 2018, 96, 3064-3069.	0.2	3
17	A Pathway-Centered Analysis of Pig Domestication and Breeding in Eurasia. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 2171-2184.	0.8	16
18	Evaluating Sequence-Based Genomic Prediction with an Efficient New Simulator. <i>Genetics</i> , 2017, 205, 939-953.	1.2	39

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19	The "heritability" of domestication and its functional partitioning in the pig. <i>Heredity</i> , 2017, 118, 160-168.	1.2	7
20	Genome-wide SNP data unveils the globalization of domesticated pigs. <i>Genetics Selection Evolution</i> , 2017, 49, 71.	1.2	114
21	Influence of epistasis on response to genomic selection using complete sequence data. <i>Genetics Selection Evolution</i> , 2017, 49, 66.	1.2	23
22	Pipeliner: software to evaluate the performance of bioinformatics pipelines for next-generation resequencing. <i>Molecular Ecology Resources</i> , 2015, 15, 99-106.	2.2	10
23	Sequence- vs. chip-assisted genomic selection: accurate biological information is advised. <i>Genetics Selection Evolution</i> , 2015, 47, 43.	1.2	130
24	Genome data from a sixteenth century pig illuminate modern breed relationships. <i>Heredity</i> , 2015, 114, 175-184.	1.2	39
25	On genetic differentiation between domestic pigs and Tibetan wild boars. <i>Nature Genetics</i> , 2015, 47, 190-192.	9.4	4
26	The chimerical genome of <i>scpi</i> del <i>scpc</i> oco feral pigs (<i>scpc</i> ota) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 46 <i>Ecology</i> , 2015, 24, 2364-2378.	2.0	15
27	A Deep Catalog of Autosomal Single Nucleotide Variation in the Pig. <i>PLoS ONE</i> , 2015, 10, e0118867.	1.1	22
28	10th WCGALP in beautiful Vancouver. <i>Journal of Animal Breeding and Genetics</i> , 2014, 131, 409-412.	0.8	0
29	Genomic relationships computed from either next-generation sequence or array SNP data. <i>Journal of Animal Breeding and Genetics</i> , 2014, 131, 85-96.	0.8	24
30	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
31	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
32	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
33	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
34	Worldwide genetic relationships of pigs as inferred from X chromosome SNPs. <i>Animal Genetics</i> , 2013, 44, 130-138.	0.6	9
35	Dissecting structural and nucleotide genome-wide variation in inbred Iberian pigs. <i>BMC Genomics</i> , 2013, 14, 148.	1.2	45
36	Population genomics from pool sequencing. <i>Molecular Ecology</i> , 2013, 22, 5561-5576.	2.0	133

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37	Porcine colonization of the Americas: a 60k SNP story. <i>Heredity</i> , 2013, 110, 321-330.	1.2	58
38	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
39	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
40	Conservation genomic analysis of domestic and wild pig populations from the Iberian Peninsula. <i>BMC Genetics</i> , 2013, 14, 106.	2.7	87
41	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
42	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
43	Analyses of pig genomes provide insight into porcine demography and evolution. <i>Nature</i> , 2012, 491, 393-398.	13.7	1,190
44	SNP calling by sequencing pooled samples. <i>BMC Bioinformatics</i> , 2012, 13, 239.	1.2	63
45	Liver transcriptome profile in pigs with extreme phenotypes of intramuscular fatty acid composition. <i>BMC Genomics</i> , 2012, 13, 547.	1.2	118
46	Genome-wide association study for intramuscular fatty acid composition in an Iberian Landrace cross. <i>Journal of Animal Science</i> , 2012, 90, 2883-2893.	0.2	63
47	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 ETQqD.0.784314 rgBT		
48	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
49	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
50	Mitochondrial DNA diversity in wild boar from the Primorsky Krai Region (East Russia). <i>Animal Genetics</i> , 2011, 42, 96-99.	0.6	9
51	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
52	Evolutionary study of a potential selection target region in the pig. <i>Heredity</i> , 2011, 106, 330-338.	1.2	15
53	Partial short-read sequencing of a highly inbred Iberian pig and genomics inference thereof. <i>Heredity</i> , 2011, 107, 256-264.	1.2	16
54	Association between plasma metabolites and gene expression profiles in five porcine endocrine tissues. <i>Genetics Selection Evolution</i> , 2011, 43, 28.	1.2	9

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55	Qxpak.5: Old mixed model solutions for new genomics problems. BMC Bioinformatics, 2011, 12, 202.	1.2	87
56	Exploring the gonad transcriptome of two extreme male pigs with RNA-seq. BMC Genomics, 2011, 12, 552.	1.2	127
57	Copy number variation in the porcine genome inferred from a 60 k SNP BeadChip. BMC Genomics, 2010, 11, 593.	1.2	102
58	Massive parallel sequencing in animal genetics: wherefroms and wheretos. Animal Genetics, 2010, 41, 561-569.	0.6	44
59	Large-scale SNP genotyping in crosses between outbred lines: how useful is it?. Heredity, 2010, 105, 173-182.	1.2	21
60	Leipzig: the dawn of the genomes era. Journal of Animal Breeding and Genetics, 2010, 127, 338-338.	0.8	4
61	Optimal Neutrality Tests Based on the Frequency Spectrum. Genetics, 2010, 186, 353-365.	1.2	34
62	Regulatory impact factors: unraveling the transcriptional regulation of complex traits from expression data. Bioinformatics, 2010, 26, 896-904.	1.8	193
63	Explaining the Genetic Basis of Complex Quantitative Traits through Prediction Models. Journal of Computational Biology, 2010, 17, 1711-1723.	0.8	2
64	Exploratory Study on the Transcriptional Profile of Pigs Subclinically Infected with Porcine Circovirus Type 2. Animal Biotechnology, 2009, 20, 96-109.	0.7	12
65	Plant Polyphenol Intake Alters Gene Expression in Canine Leukocytes. Journal of Nutrigenetics and Nutrigenomics, 2009, 2, 43-52.	1.8	7
66	Integrating Y-Chromosome, Mitochondrial, and Autosomal Data to Analyze the Origin of Pig Breeds. Molecular Biology and Evolution, 2009, 26, 2061-2072.	3.5	103
67	Genomic scan for quantitative trait loci of chemical and physical body composition and deposition on pig chromosome X including the pseudoautosomal region of males. Genetics Selection Evolution, 2009, 41, 27.	1.2	9
68	Impact of breed and sex on porcine endocrine transcriptome: a bayesian biometrical analysis. BMC Genomics, 2009, 10, 89.	1.2	21
69	A Genome Wide Detection of Quantitative Trait Loci on Pig Maternal Infanticide Behavior in a Large Scale White Duroc—Erhualian Resource Population. Behavior Genetics, 2009, 39, 213-219.	1.4	19
70	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. Animal Genetics, 2009, 40, 813-820.	0.6	28
71	Evaluation of <i>FABP2</i> as candidate gene for a fatty acid composition QTL in porcine chromosome 8. Journal of Animal Breeding and Genetics, 2009, 126, 52-58.	0.8	10
72	Population and quantitative genetics for a cause. Journal of Animal Breeding and Genetics, 2008, 125, 217-218.	0.8	0

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73	Nucleotide variability and linkage disequilibrium patterns at the porcine <i>FABP5</i> gene. <i>Animal Genetics</i> , 2008, 39, 468-473.	0.6	14
74	Transcriptome architecture across tissues in the pig. <i>BMC Genomics</i> , 2008, 9, 173.	1.2	45
75	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
76	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
77	Emerging tools in quantitative trait loci detection. <i>Acta Agriculturae Scandinavica - Section A: Animal Science</i> , 2007, 57, 202-207.	0.2	1
78	Genetical genomics: use all data. <i>BMC Genomics</i> , 2007, 8, 69.	1.2	21
79	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
80	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
81	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
82	Characterization of the porcine <i>FABP5</i> gene and its association with the <i>FAT1</i> QTL in an Iberian by Landrace cross. <i>Animal Genetics</i> , 2006, 37, 589-591.	0.6	33
83	Multiple association analysis via simulated annealing (MASSA). <i>Bioinformatics</i> , 2006, 22, 573-580.	1.8	3
84	Unexpected High Polymorphism at the <i>FABP4</i> Gene Unveils a Complex History for Pig Populations. <i>Genetics</i> , 2006, 174, 2119-2127.	1.2	35
85	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
86	Assignment of <i>RAD51C</i> to porcine chromosome 12 and identification of intronic variability. <i>Animal Genetics</i> , 2005, 36, 461-462.	0.6	0
87	On growth, fatness, and form: A further look at porcine Chromosome 4 in an Iberian \times Landrace cross. <i>Mammalian Genome</i> , 2005, 16, 374-382.	1.0	33
88	Atlas: A Java-Based Tool for Managing Genotypes. <i>Journal of Heredity</i> , 2005, 96, 623-625.	1.0	0
89	Qxpak: a versatile mixed model application for genetical genomics and QTL analyses. <i>Bioinformatics</i> , 2004, 20, 2792-2798.	1.8	126
90	In Silico Study of Transcriptome Genetic Variation in Outbred Populations. <i>Genetics</i> , 2004, 166, 547-554.	1.2	30

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91	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
92	A comparison between methods for linkage disequilibrium fine mapping of quantitative trait loci. <i>Genetical Research</i> , 2004, 83, 41-47.	0.3	8
93	Detection of QTL affecting fatty acid composition in the pig. <i>Mammalian Genome</i> , 2003, 14, 650-656.	1.0	74
94	Estrogen receptor polymorphism in Landrace pigs and its association with litter size performance. <i>Livestock Science</i> , 2003, 82, 53-59.	1.2	39
95	Linkage disequilibrium fine mapping of quantitative trait loci: A simulation study. <i>Genetics Selection Evolution</i> , 2003, 35, 513-32.	1.2	27
96	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
97	On Marker-Assisted Prediction of Genetic Value: Beyond the Ridge. <i>Genetics</i> , 2003, 163, 347-365.	1.2	94
98	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
99	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
100	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
101	On the mapping of quantitative trait loci at marker and non-marker locations. <i>Genetical Research</i> , 2002, 79, 97-106.	0.3	19
102	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
103	Test for positional candidate genes for body composition on pig chromosome 6. <i>Genetics Selection Evolution</i> , 2002, 34, 465-79.	1.2	75
104	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
105	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
106	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
107	Bayes factors for detection of Quantitative Trait Loci. <i>Genetics Selection Evolution</i> , 2001, 33, 133-52.	1.2	40
108	Quantitative Trait Locus Analysis in Crosses Between Outbred Lines With Dominance and Inbreeding. <i>Genetics</i> , 2001, 159, 413-422.	1.2	16

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109	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
110	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
111	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
112	Quantitative Trait Loci Mapping in F2 Crosses Between Outbred Lines. <i>Genetics</i> , 2000, 155, 391-405.	1.2	53
113	Sequential bulked typing: a rapid approach for detecting QTLs. <i>Theoretical and Applied Genetics</i> , 1998, 96, 551-557.	1.8	5
114	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
115	Spanish practices. <i>Nature</i> , 1995, 378, 760-760.	13.7	3
116	Genetic implications of a bivariate threshold model for litter size components.. <i>Journal of Animal Science</i> , 1994, 72, 2775.	0.2	7
117	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
118	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
119	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
120	Estimates of genetic parameters for litter size in six strains of Iberian pigs. <i>Livestock Science</i> , 1992, 32, 283-293.	1.2	28
121	Genetic evaluation with uncertain parentage: a comparison of methods. <i>Theoretical and Applied Genetics</i> , 1992, 84, 173-179.	1.8	25
122	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
123	A note on the use of mate selection in closed MOET breeding schemes. <i>Animal Science</i> , 1991, 53, 403-406.	1.3	7