

# Fernando Pardo-Manuel de Villena

## List of Publications by Year in descending order

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96  
papers

8,030  
citations

87723

38  
h-index

58464

82  
g-index

117  
all docs

117  
docs citations

117  
times ranked

8159  
citing authors

#	ARTICLE	IF	CITATIONS
1	Host-pathogen genetic interactions underlie tuberculosis susceptibility in genetically diverse mice. <i>ELife</i> , 2022, 11, .	2.8	44
2	eQTL mapping using allele-specific count data is computationally feasible, powerful, and provides individual-specific estimates of genetic effects. <i>PLoS Genetics</i> , 2022, 18, e1010076.	1.5	13
3	Ictal neural oscillatory alterations precede sudden unexpected death in epilepsy. <i>Brain Communications</i> , 2022, 4, fcac073.	1.5	7
4	The evolutionary significance of meiotic drive. <i>Heredity</i> , 2022, 129, 44-47.	1.2	8
5	An interaction of inorganic arsenic exposure with body weight and composition on type 2 diabetes indicators in Diversity Outbred mice. <i>Mammalian Genome</i> , 2022, 33, 575-589.	1.0	4
6	Baseline T cell immune phenotypes predict virologic and disease control upon SARS-CoV infection in Collaborative Cross mice. <i>PLoS Pathogens</i> , 2021, 17, e1009287.	2.1	22
7	Diverse genetic backgrounds play a prominent role in the metabolic phenotype of CC021/Unc and CC027/GeniUNC mice exposed to inorganic arsenic. <i>Toxicology</i> , 2021, 452, 152696.	2.0	2
8	Bayesian modeling of skewed X inactivation in genetically diverse mice identifies a novel <i>Xce</i> allele associated with copy number changes. <i>Genetics</i> , 2021, 218, .	1.2	5
9	Correlation of Regulatory T Cell Numbers with Disease Tolerance upon Virus Infection. <i>ImmunoHorizons</i> , 2021, 5, 157-169.	0.8	1
10	A k -mer query tool for assessing population diversity in pangenomes. , 2021, , .		0
11	Regulation of protein abundance in genetically diverse mouse populations. <i>Cell Genomics</i> , 2021, 1, 100003.	3.0	27
12	<i>Onchocerca volvulus</i> bivalent subunit vaccine induces protective immunity in genetically diverse collaborative cross recombinant inbred intercross mice. <i>Npj Vaccines</i> , 2021, 6, 17.	2.9	11
13	Immune predictors of mortality following RNA virus infection. <i>Journal of Infectious Diseases</i> , 2020, 221, 882-889.	1.9	10
14	Characterization of genetically complex Collaborative Cross mouse strains that model divergent locomotor activating and reinforcing properties of cocaine. <i>Psychopharmacology</i> , 2020, 237, 979-996.	1.5	25
15	Genetic Basis of Aerobically Supported Voluntary Exercise: Results from a Selection Experiment with House Mice. <i>Genetics</i> , 2020, 216, 781-804.	1.2	15
16	Complex Genetic Architecture Underlies Regulation of Influenza-A-Virus-Specific Antibody Responses in the Collaborative Cross. <i>Cell Reports</i> , 2020, 31, 107587.	2.9	31
17	A New Polygenic Model for Nonfamilial Colorectal Cancer Inheritance Based on the Genetic Architecture of the Azoxymethane-Induced Mouse Model. <i>Genetics</i> , 2020, 214, 691-702.	1.2	5
18	Collaborative Cross mice reveal extreme epilepsy phenotypes and genetic loci for seizure susceptibility. <i>Epilepsia</i> , 2020, 61, 2010-2021.	2.6	23

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19	<i>Gabra2</i> is a genetic modifier of <i>Scn8a</i> encephalopathy in the mouse*. <i>Epilepsia</i> , 2020, 61, 2847-2856.	2.6	15
20	Dissecting the Genetic Architecture of Cystatin C in Diversity Outbred Mice. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2529-2541.	0.8	9
21	Genetic Background Shapes Phenotypic Response to Diet for Adiposity in the Collaborative Cross. <i>Frontiers in Genetics</i> , 2020, 11, 615012.	1.1	10
22	Instability of the Pseudoautosomal Boundary in House Mice. <i>Genetics</i> , 2019, 212, 469-487.	1.2	15
23	Effects of Preconception and in Utero Inorganic Arsenic Exposure on the Metabolic Phenotype of Genetically Diverse Collaborative Cross Mice. <i>Chemical Research in Toxicology</i> , 2019, 32, 1487-1490.	1.7	7
24	Differential metabolism of inorganic arsenic in mice from genetically diverse Collaborative Cross strains. <i>Archives of Toxicology</i> , 2019, 93, 2811-2822.	1.9	15
25	Identification of a Locus in Mice that Regulates the Collateral Damage and Lethality of Virus Infection. <i>Cell Reports</i> , 2019, 27, 1387-1396.e5.	2.9	5
26	A Diallel of the Mouse Collaborative Cross Founders Reveals Strong Strain-Specific Maternal Effects on Litter Size. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1613-1622.	0.8	11
27	Whole Genome Sequencing and Progress Toward Full Inbreeding of the Mouse Collaborative Cross Population. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1303-1311.	0.8	39
28	Functionally Overlapping Variants Control Tuberculosis Susceptibility in Collaborative Cross Mice. <i>MBio</i> , 2019, 10, .	1.8	36
29	Genetic diversity between mouse strains allows identification of the CC027/GeniUnc strain as an orally reactive model of peanut allergy. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 143, 1027-1037.e7.	1.5	40
30	Quantitative trait mapping in Diversity Outbred mice identifies two genomic regions associated with heart size. <i>Mammalian Genome</i> , 2018, 29, 80-89.	1.0	27
31	Bayesian Diallel Analysis Reveals <i>Mx1</i> -Dependent and <i>Mx1</i> -Independent Effects on Response to Influenza A Virus in Mice. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 427-445.	0.8	27
32	Reciprocal F1 Hybrids of Two Inbred Mouse Strains Reveal Parent-of-Origin and Perinatal Diet Effects on Behavior and Expression. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3447-3468.	0.8	12
33	CC002/Unc females are mouse models of exercise-induced paradoxical fat response. <i>Physiological Reports</i> , 2018, 6, e13716.	0.7	9
34	Toward Personalized Gene Therapy: Characterizing the Host Genetic Control of Lentiviral-Vector-Mediated Hepatic Gene Delivery. <i>Molecular Therapy - Methods and Clinical Development</i> , 2017, 5, 83-92.	1.8	14
35	Structural Variation Shapes the Landscape of Recombination in Mouse. <i>Genetics</i> , 2017, 206, 603-619.	1.2	51
36	Male Infertility Is Responsible for Nearly Half of the Extinction Observed in the Mouse Collaborative Cross. <i>Genetics</i> , 2017, 206, 557-572.	1.2	66

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37	Genomes of the Mouse Collaborative Cross. <i>Genetics</i> , 2017, 206, 537-556.	1.2	189
38	High-Resolution Maps of Mouse Reference Populations. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3427-3434.	0.8	27
39	Wild Mouse Gut Microbiota Promotes Host Fitness and Improves Disease Resistance. <i>Cell</i> , 2017, 171, 1015-1028.e13.	13.5	603
40	Sequence and Structural Diversity of Mouse Y Chromosomes. <i>Molecular Biology and Evolution</i> , 2017, 34, 3186-3204.	3.5	54
41	Genetic architecture of atherosclerosis dissected by QTL analyses in three F2 intercrosses of apolipoprotein E-null mice on C57BL/6J, DBA/2J and 129S6/SvEvTac backgrounds. <i>PLoS ONE</i> , 2017, 12, e0182882.	1.1	4
42	Inbred Strain Variant Database (ISVdb): A Repository for Probabilistically Informed Sequence Differences Among the Collaborative Cross Strains and Their Founders. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1623-1630.	0.8	26
43	Oas1b-dependent Immune Transcriptional Profiles of West Nile Virus Infection in the Collaborative Cross. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1665-1682.	0.8	38
44	Allelic Variation in the Toll-Like Receptor Adaptor Protein <i>Ticam2</i> Contributes to SARS-Coronavirus Pathogenesis in Mice. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1653-1663.	0.8	75
45	The Mouse Universal Genotyping Array: From Substrains to Subspecies. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 263-279.	0.8	199
46	Whole Genome Sequence of Two Wild-Derived <i>Mus musculus domesticus</i> Inbred Strains, LEWES/Eij and ZALENDE/Eij, with Different Diploid Numbers. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 4211-4216.	0.8	12
47	Diversity Outbred Mice at 21: Maintaining Allelic Variation in the Face of Selection. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3893-3902.	0.8	66
48	Long-term exercise in mice has sex-dependent benefits on body composition and metabolism during aging. <i>Physiological Reports</i> , 2016, 4, e13011.	0.7	49
49	Transcriptional profiles of WNV neurovirulence in a genetically diverse Collaborative Cross population. <i>Genomics Data</i> , 2016, 10, 137-140.	1.3	9
50	Genetics of murine craniofacial morphology: diallel analysis of the eight founders of the Collaborative Cross. <i>Journal of Anatomy</i> , 2016, 228, 96-112.	0.9	29
51	The Evolutionary Fates of a Large Segmental Duplication in Mouse. <i>Genetics</i> , 2016, 204, 267-285.	1.2	21
52	<i>R2d2</i> Drives Selfish Sweeps in the House Mouse. <i>Molecular Biology and Evolution</i> , 2016, 33, 1381-1395.	3.5	55
53	The Founder Strains of the Collaborative Cross Express a Complex Combination of Advantageous and Deleterious Traits for Male Reproduction. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 2671-2683.	0.8	28
54	Genome Wide Identification of SARS-CoV Susceptibility Loci Using the Collaborative Cross. <i>PLoS Genetics</i> , 2015, 11, e1005504.	1.5	137

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55	IsoDOT Detects Differential RNA-Isoform Expression/Usage With Respect to a Categorical or Continuous Covariate With High Sensitivity and Specificity. <i>Journal of the American Statistical Association</i> , 2015, 110, 975-986.	1.8	10
56	The "Omics"™ of Voluntary Exercise: Systems Approaches to a Complex Phenotype. <i>Trends in Endocrinology and Metabolism</i> , 2015, 26, 673-675.	3.1	9
57	Coexistent ARID1A"PIK3CA mutations promote ovarian clear-cell tumorigenesis through pro-tumorigenic inflammatory cytokine signalling. <i>Nature Communications</i> , 2015, 6, 6118.	5.8	247
58	A Multi-Megabase Copy Number Gain Causes Maternal Transmission Ratio Distortion on Mouse Chromosome 2. <i>PLoS Genetics</i> , 2015, 11, e1004850.	1.5	76
59	Analyses of allele-specific gene expression in highly divergent mouse crosses identifies pervasive allelic imbalance. <i>Nature Genetics</i> , 2015, 47, 353-360.	9.4	204
60	Identification of microRNAs associated with allergic airway disease using a genetically diverse mouse population. <i>BMC Genomics</i> , 2015, 16, 633.	1.2	22
61	Genetic Regulation of <i>Zfp30</i> , <i>CXCL1</i> , and Neutrophilic Inflammation in Murine Lung. <i>Genetics</i> , 2014, 198, 735-745.	1.2	44
62	Annotation of long non-coding RNAs expressed in Collaborative Cross founder mice in response to respiratory virus infection reveals a new class of interferon-stimulated transcripts. <i>RNA Biology</i> , 2014, 11, 875-890.	1.5	122
63	Genetics of Adverse Reactions to Haloperidol in a Mouse Diallel: A Drug"Placebo Experiment and Bayesian Causal Analysis. <i>Genetics</i> , 2014, 196, 321-347.	1.2	30
64	High-Resolution Sex-Specific Linkage Maps of the Mouse Reveal Polarized Distribution of Crossovers in Male Germline. <i>Genetics</i> , 2014, 197, 91-106.	1.2	85
65	The Collaborative Cross as a Resource for Modeling Human Disease: <i>CC011/Unc</i> , a New Mouse Model for Spontaneous Colitis. <i>Mammalian Genome</i> , 2014, 25, 95-108.	1.0	78
66	Host genetic diversity enables Ebola hemorrhagic fever pathogenesis and resistance. <i>Science</i> , 2014, 346, 987-991.	6.0	262
67	Genomic Profiling of Collaborative Cross Founder Mice Infected with Respiratory Viruses Reveals Novel Transcripts and Infection-Related Strain-Specific Gene and Isoform Expression. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1429-1444.	0.8	25
68	C57BL/6N Mutation in <i>Cytoplasmic FMRP interacting protein 2</i> Regulates Cocaine Response. <i>Science</i> , 2013, 342, 1508-1512.	6.0	198
69	Deconstructing <i>Mus gemischus</i> : advances in understanding ancestry, structure, and variation in the genome of the laboratory mouse. <i>Mammalian Genome</i> , 2013, 24, 1-20.	1.0	56
70	Genetic Architecture of Skewed X Inactivation in the Laboratory Mouse. <i>PLoS Genetics</i> , 2013, 9, e1003853.	1.5	41
71	Modeling Host Genetic Regulation of Influenza Pathogenesis in the Collaborative Cross. <i>PLoS Pathogens</i> , 2013, 9, e1003196.	2.1	183
72	Expression Quantitative Trait Loci for Extreme Host Response to Influenza A in Pre-Collaborative Cross Mice. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 213-221.	0.8	78

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73	Transcriptome Atlases of Mouse Brain Reveals Differential Expression Across Brain Regions and Genetic Backgrounds. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 203-211.	0.8	18
74	Inferring ancestry in admixed populations using microarray probe intensities. , 2012, , .		16
75	Genetic Analysis of Hematological Parameters in Incipient Lines of the Collaborative Cross. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 157-165.	0.8	80
76	Imputation of Single-Nucleotide Polymorphisms in Inbred Mice Using Local Phylogeny. <i>Genetics</i> , 2012, 190, 449-458.	1.2	42
77	Status and access to the Collaborative Cross population. <i>Mammalian Genome</i> , 2012, 23, 706-712.	1.0	134
78	Discovery of novel variants in genotyping arrays improves genotype retention and reduces ascertainment bias. <i>BMC Genomics</i> , 2012, 13, 34.	1.2	61
79	Comparative analysis and visualization of multiple collinear genomes. <i>BMC Bioinformatics</i> , 2012, 13, S13.	1.2	54
80	Subspecific origin and haplotype diversity in the laboratory mouse. <i>Nature Genetics</i> , 2011, 43, 648-655.	9.4	439
81	Dynamic visualization and comparative analysis of multiple collinear genomic data. , 2011, 2011, 335-339.		2
82	Genetic analysis of complex traits in the emerging Collaborative Cross. <i>Genome Research</i> , 2011, 21, 1213-1222.	2.4	327
83	The Collaborative Cross: A Recombinant Inbred Mouse Population for the Systems Genetic Era. <i>ILAR Journal</i> , 2011, 52, 24-31.	1.8	183
84	Architecture of energy balance traits in emerging lines of the Collaborative Cross. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2011, 300, E1124-E1134.	1.8	58
85	Collaborative Cross mice and their power to map host susceptibility to <i>Aspergillus fumigatus</i> infection. <i>Genome Research</i> , 2011, 21, 1239-1248.	2.4	138
86	Efficient genome ancestry inference in complex pedigrees with inbreeding. <i>Bioinformatics</i> , 2010, 26, i199-i207.	1.8	42
87	A customized and versatile high-density genotyping array for the mouse. <i>Nature Methods</i> , 2009, 6, 663-666.	9.0	236
88	TreeQA: quantitative genome wide association mapping using local perfect phylogeny trees. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2009, , 415-26.	0.7	10
89	TREEQA: QUANTITATIVE GENOME WIDE ASSOCIATION MAPPING USING LOCAL PERFECT PHYLOGENY TREES. , 2008, , .		9
90	On the subspecific origin of the laboratory mouse. <i>Nature Genetics</i> , 2007, 39, 1100-1107.	9.4	281

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91	The polymorphism architecture of mouse genetic resources elucidated using genome-wide resequencing data: implications for QTL discovery and systems genetics. <i>Mammalian Genome</i> , 2007, 18, 473-481.	1.0	237
92	The Paternal Gene of the DDK Syndrome Maps to the Schlafen Gene Cluster on Mouse Chromosome 11. <i>Genetics</i> , 2006, 172, 411-423.	1.2	32
93	Genetic and Haplotype Diversity Among Wild-Derived Mouse Inbred Strains. <i>Genome Research</i> , 2004, 14, 1880-1887.	2.4	90
94	The Collaborative Cross, a community resource for the genetic analysis of complex traits. <i>Nature Genetics</i> , 2004, 36, 1133-1137.	9.4	1,034
95	Nonrandom segregation during meiosis: the unfairness of females. <i>Mammalian Genome</i> , 2001, 12, 331-339.	1.0	209
96	Female Meiosis Drives Karyotypic Evolution in Mammals. <i>Genetics</i> , 2001, 159, 1179-1189.	1.2	224