Fernando Pardo-Manuel de Villena

List of Publications by Year
in descending order

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	The Collaborative Cross, a community resource for the genetic analysis of complex traits. Nature Genetics, 2004, 36, 1133-1137.	9.4	1,034
2	Wild Mouse Gut Microbiota Promotes Host Fitness and Improves Disease Resistance. Cell, 2017, 171, 1015-1028.e13.	13.5	603
3	Subspecific origin and haplotype diversity in the laboratory mouse. Nature Genetics, 2011, 43, 648-655.	9.4	439
4	Genetic analysis of complex traits in the emerging Collaborative Cross. Genome Research, 2011, 21, 1213-1222.	2.4	327
5	On the subspecific origin of the laboratory mouse. Nature Genetics, 2007, 39, 1100-1107.	9.4	281
6	Host genetic diversity enables Ebola hemorrhagic fever pathogenesis and resistance. Science, 2014, 346, 987-991.	6.0	262
7	Coexistent ARID1A–PIK3CA mutations promote ovarian clear-cell tumorigenesis through pro-tumorigenic inflammatory cytokine signalling. Nature Communications, 2015, 6, 6118.	5.8	247
8	The polymorphism architecture of mouse genetic resources elucidated using genome-wide resequencing data: implications for QTL discovery and systems genetics. Mammalian Genome, 2007, 18, 473-481.	1.0	237
9	A customized and versatile high-density genotyping array for the mouse. Nature Methods, 2009, 6, 663-666.	9.0	236
10	Female Meiosis Drives Karyotypic Evolution in Mammals. Genetics, 2001, 159, 1179-1189.	1.2	224
11	Nonrandom segregation during meiosis: the unfairness of females. Mammalian Genome, 2001, 12, 331-339.	1.0	209
12	Analyses of allele-specific gene expression in highly divergent mouse crosses identifies pervasive allelic imbalance. Nature Genetics, 2015, 47, 353-360.	9.4	204
13	The Mouse Universal Genotyping Array: From Substrains to Subspecies. G3: Genes, Genomes, Genetics, 2016, 6, 263-279.	0.8	199
14	C57BL/6N Mutation in *Cytoplasmic FMRP interacting protein 2* Regulates Cocaine Response. Science, 2013, 342, 1508-1512.	6.0	198
15	Genomes of the Mouse Collaborative Cross. Genetics, 2017, 206, 537-556.	1.2	189
16	The Collaborative Cross: A Recombinant Inbred Mouse Population for the Systems Genetic Era. ILAR Journal, 2011, 52, 24-31.	1.8	183
17	Modeling Host Genetic Regulation of Influenza Pathogenesis in the Collaborative Cross. PLoS Pathogens, 2013, 9, e1003196.	2.1	183
18	Collaborative Cross mice and their power to map host susceptibility to *Aspergillus fumigatus* infection. Genome Research, 2011, 21, 1239-1248.	2.4	138

#	ARTICLE	IF	CITATIONS
19	Genome Wide Identification of SARS-CoV Susceptibility Loci Using the Collaborative Cross. PLoS Genetics, 2015, 11, e1005504.	1.5	137
20	Status and access to the Collaborative Cross population. Mammalian Genome, 2012, 23, 706-712.	1.0	134
21	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. RNA Biology, 2014, 11, 875-890.	1.5	122
22	Genetic and Haplotype Diversity Among Wild-Derived Mouse Inbred Strains. Genome Research, 2004, 14, 1880-1887.	2.4	90
23	High-Resolution Sex-Specific Linkage Maps of the Mouse Reveal Polarized Distribution of Crossovers in Male Germline. Genetics, 2014, 197, 91-106.	1.2	85
24	Genetic Analysis of Hematological Parameters in Incipient Lines of the Collaborative Cross. G3: Genes, Genomes, Genetics, 2012, 2, 157-165.	0.8	80
25	Expression Quantitative Trait Loci for Extreme Host Response to Influenza A in Pre-Collaborative Cross Mice. G3: Genes, Genomes, Genetics, 2012, 2, 213-221.	0.8	78
26	The Collaborative Cross as a Resource for Modeling Human Disease: CC011/Unc, a New Mouse Model for Spontaneous Colitis. Mammalian Genome, 2014, 25, 95-108.	1.0	78
27	A Multi-Megabase Copy Number Gain Causes Maternal Transmission Ratio Distortion on Mouse Chromosome 2. PLoS Genetics, 2015, 11, e1004850.	1.5	76
28	Allelic Variation in the Toll-Like Receptor Adaptor Protein *Ticam2* Contributes to SARS-Coronavirus Pathogenesis in Mice. G3: Genes, Genomes, Genetics, 2017, 7, 1653-1663.	0.8	75
29	Diversity Outbred Mice at 21: Maintaining Allelic Variation in the Face of Selection. G3: Genes, Genomes, Genetics, 2016, 6, 3893-3902.	0.8	66
30	Male Infertility Is Responsible for Nearly Half of the Extinction Observed in the Mouse Collaborative Cross. Genetics, 2017, 206, 557-572.	1.2	66
31	Discovery of novel variants in genotyping arrays improves genotype retention and reduces ascertainment bias. BMC Genomics, 2012, 13, 34.	1.2	61
32	Architecture of energy balance traits in emerging lines of the Collaborative Cross. American Journal of Physiology - Endocrinology and Metabolism, 2011, 300, E1124-E1134.	1.8	58
33	Deconstructing Mus gemischus: advances in understanding ancestry, structure, and variation in the genome of the laboratory mouse. Mammalian Genome, 2013, 24, 1-20.	1.0	56
34	*R2d2* Drives Selfish Sweeps in the House Mouse. Molecular Biology and Evolution, 2016, 33, 1381-1395.	3.5	55
35	Comparative analysis and visualization of multiple collinear genomes. BMC Bioinformatics, 2012, 13, S13.	1.2	54
36	Sequence and Structural Diversity of Mouse Y Chromosomes. Molecular Biology and Evolution, 2017, 34, 3186-3204.	3.5	54

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37	Structural Variation Shapes the Landscape of Recombination in Mouse. Genetics, 2017, 206, 603-619.	1.2	51
38	Long‐term exercise in mice has sex‐dependent benefits on body composition and metabolism during aging. Physiological Reports, 2016, 4, e13011.	0.7	49
39	Genetic Regulation of *Zfp30*, CXCL1, and Neutrophilic Inflammation in Murine Lung. Genetics, 2014, 198, 735-745.	1.2	44
40	Host-pathogen genetic interactions underlie tuberculosis susceptibility in genetically diverse mice. ELife, 2022, 11, .	2.8	44
41	Efficient genome ancestry inference in complex pedigrees with inbreeding. Bioinformatics, 2010, 26, i199-i207.	1.8	42
42	Imputation of Single-Nucleotide Polymorphisms in Inbred Mice Using Local Phylogeny. Genetics, 2012, 190, 449-458.	1.2	42
43	Genetic Architecture of Skewed X Inactivation in the Laboratory Mouse. PLoS Genetics, 2013, 9, e1003853.	1.5	41
44	Genetic diversity between mouse strains allows identification of the CC027/GeniUnc strain as an orally reactive model of peanut allergy. Journal of Allergy and Clinical Immunology, 2019, 143, 1027-1037.e7.	1.5	40
45	Whole Genome Sequencing and Progress Toward Full Inbreeding of the Mouse Collaborative Cross Population. G3: Genes, Genomes, Genetics, 2019, 9, 1303-1311.	0.8	39
46	Oas1b-dependent Immune Transcriptional Profiles of West Nile Virus Infection in the Collaborative Cross. G3: Genes, Genomes, Genetics, 2017, 7, 1665-1682.	0.8	38
47	Functionally Overlapping Variants Control Tuberculosis Susceptibility in Collaborative Cross Mice. MBio, 2019, 10, .	1.8	36
48	The Paternal Gene of the DDK Syndrome Maps to the Schlafen Gene Cluster on Mouse Chromosome 11. Genetics, 2006, 172, 411-423.	1.2	32
49	Complex Genetic Architecture Underlies Regulation of Influenza-A-Virus-Specific Antibody Responses in the Collaborative Cross. Cell Reports, 2020, 31, 107587.	2.9	31
50	Genetics of Adverse Reactions to Haloperidol in a Mouse Diallel: A Drug–Placebo Experiment and Bayesian Causal Analysis. Genetics, 2014, 196, 321-347.	1.2	30
51	Genetics of murine craniofacial morphology: diallel analysis of the eight founders of the Collaborative Cross. Journal of Anatomy, 2016, 228, 96-112.	0.9	29
52	The Founder Strains of the Collaborative Cross Express a Complex Combination of Advantageous and Deleterious Traits for Male Reproduction. G3: Genes, Genomes, Genetics, 2015, 5, 2671-2683.	0.8	28
53	High-Resolution Maps of Mouse Reference Populations. G3: Genes, Genomes, Genetics, 2017, 7, 3427-3434.	0.8	27
54	Quantitative trait mapping in Diversity Outbred mice identifies two genomic regions associated with heart size. Mammalian Genome, 2018, 29, 80-89.	1.0	27

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55	Bayesian Diallel Analysis Reveals *Mx1*-Dependent and *Mx1*-Independent Effects on Response to Influenza A Virus in Mice. G3: Genes, Genomes, Genetics, 2018, 8, 427-445.	0.8	27
56	Regulation of protein abundance in genetically diverse mouse populations. Cell Genomics, 2021, 1, 100003.	3.0	27
57	Inbred Strain Variant Database (ISVdb): A Repository for Probabilistically Informed Sequence Differences Among the Collaborative Cross Strains and Their Founders. G3: Genes, Genomes, Genetics, 2017, 7, 1623-1630.	0.8	26
58	Genomic Profiling of Collaborative Cross Founder Mice Infected with Respiratory Viruses Reveals Novel Transcripts and Infection-Related Strain-Specific Gene and Isoform Expression. G3: Genes, Genomes, Genetics, 2014, 4, 1429-1444.	0.8	25
59	Characterization of genetically complex Collaborative Cross mouse strains that model divergent locomotor activating and reinforcing properties of cocaine. Psychopharmacology, 2020, 237, 979-996.	1.5	25
60	Collaborative Cross mice reveal extreme epilepsy phenotypes and genetic loci for seizure susceptibility. Epilepsia, 2020, 61, 2010-2021.	2.6	23
61	Identification of microRNAs associated with allergic airway disease using a genetically diverse mouse population. BMC Genomics, 2015, 16, 633.	1.2	22
62	Baseline T cell immune phenotypes predict virologic and disease control upon SARS-CoV infection in Collaborative Cross mice. PLoS Pathogens, 2021, 17, e1009287.	2.1	22
63	The Evolutionary Fates of a Large Segmental Duplication in Mouse. Genetics, 2016, 204, 267-285.	1.2	21
64	Transcriptome Atlases of Mouse Brain Reveals Differential Expression Across Brain Regions and Genetic Backgrounds. G3: Genes, Genomes, Genetics, 2012, 2, 203-211.	0.8	18
65	Inferring ancestry in admixed populations using microarray probe intensities. , 2012, , .		16
66	Instability of the Pseudoautosomal Boundary in House Mice. Genetics, 2019, 212, 469-487.	1.2	15
67	Differential metabolism of inorganic arsenic in mice from genetically diverse Collaborative Cross strains. Archives of Toxicology, 2019, 93, 2811-2822.	1.9	15
68	Genetic Basis of Aerobically Supported Voluntary Exercise: Results from a Selection Experiment with House Mice. Genetics, 2020, 216, 781-804.	1.2	15
69	*Gabra2* is a genetic modifier of *Scn8a* encephalopathy in the mouse*. Epilepsia, 2020, 61, 2847-2856.	2.6	15
70	Toward Personalized Gene Therapy: Characterizing the Host Genetic Control of Lentiviral-Vector-Mediated Hepatic Gene Delivery. Molecular Therapy - Methods and Clinical Development, 2017, 5, 83-92.	1.8	14
71	eQTL mapping using allele-specific count data is computationally feasible, powerful, and provides individual-specific estimates of genetic effects. PLoS Genetics, 2022, 18, e1010076.	1.5	13
72	Whole Genome Sequence of Two Wild-Derived *Mus musculus domesticus* Inbred Strains, LEWES/EiJ and ZALENDE/EiJ, with Different Diploid Numbers. G3: Genes, Genomes, Genetics, 2016, 6, 4211-4216.	0.8	12

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73	Reciprocal F1 Hybrids of Two Inbred Mouse Strains Reveal Parent-of-Origin and Perinatal Diet Effects on Behavior and Expression. G3: Genes, Genomes, Genetics, 2018, 8, 3447-3468.	0.8	12
74	A Diallel of the Mouse Collaborative Cross Founders Reveals Strong Strain-Specific Maternal Effects on Litter Size. G3: Genes, Genomes, Genetics, 2019, 9, 1613-1622.	0.8	11
75	Onchocerca volvulus bivalent subunit vaccine induces protective immunity in genetically diverse collaborative cross recombinant inbred intercross mice. Npj Vaccines, 2021, 6, 17.	2.9	11
76	IsoDOT Detects Differential RNA-Isoform Expression/Usage With Respect to a Categorical or Continuous Covariate With High Sensitivity and Specificity. Journal of the American Statistical Association, 2015, 110, 975-986.	1.8	10
77	Immune predictors of mortality following RNA virus infection. Journal of Infectious Diseases, 2020, 221, 882-889.	1.9	10
78	Genetic Background Shapes Phenotypic Response to Diet for Adiposity in the Collaborative Cross. Frontiers in Genetics, 2020, 11, 615012.	1.1	10
79	TreeQA: quantitative genome wide association mapping using local perfect phylogeny trees. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2009, , 415-26.	0.7	10
80	TREEQA: QUANTITATIVE GENOME WIDE ASSOCIATION MAPPING USING LOCAL PERFECT PHYLOGENY TREES. , 2008, , .		9
81	The 'Omics' of Voluntary Exercise: Systems Approaches to a Complex Phenotype. Trends in Endocrinology and Metabolism, 2015, 26, 673-675.	3.1	9
82	Transcriptional profiles of WNV neurovirulence in a genetically diverse Collaborative Cross population. Genomics Data, 2016, 10, 137-140.	1.3	9
83	CC002/Unc females are mouse models of exercise-induced paradoxical fat response. Physiological Reports, 2018, 6, e13716.	0.7	9
84	Dissecting the Genetic Architecture of Cystatin C in Diversity Outbred Mice. G3: Genes, Genomes, Genetics, 2020, 10, 2529-2541.	0.8	9
85	The evolutionary significance of meiotic drive. Heredity, 2022, 129, 44-47.	1.2	8
86	Effects of Preconception and in Utero Inorganic Arsenic Exposure on the Metabolic Phenotype of Genetically Diverse Collaborative Cross Mice. Chemical Research in Toxicology, 2019, 32, 1487-1490.	1.7	7
87	Ictal neural oscillatory alterations precede sudden unexpected death in epilepsy. Brain Communications, 2022, 4, fcac073.	1.5	7
88	Identification of a Locus in Mice that Regulates the Collateral Damage and Lethality of Virus Infection. Cell Reports, 2019, 27, 1387-1396.e5.	2.9	5
89	A New Polygenic Model for Nonfamilial Colorectal Cancer Inheritance Based on the Genetic Architecture of the Azoxymethane-Induced Mouse Model. Genetics, 2020, 214, 691-702.	1.2	5
90	Bayesian modeling of skewed X inactivation in genetically diverse mice identifies a novel *Xce* allele associated with copy number changes. Genetics, 2021, 218, .	1.2	5

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91	Genetic architecture of atherosclerosis dissected by QTL analyses in three F2 intercrosses of apolipoprotein E-null mice on C57BL6/J, DBA/2J and 129S6/SvEvTac backgrounds. PLoS ONE, 2017, 12, e0182882.	1.1	4
92	An interaction of inorganic arsenic exposure with body weight and composition on type 2 diabetes indicators in Diversity Outbred mice. Mammalian Genome, 2022, 33, 575-589.	1.0	4
93	Dynamic visualization and comparative analysis of multiple collinear genomic data. , 2011, 2011, 335-339.		2
94	Diverse genetic backgrounds play a prominent role in the metabolic phenotype of CC021/Unc and CC027/GeniUNC mice exposed to inorganic arsenic. Toxicology, 2021, 452, 152696.	2.0	2
95	Correlation of Regulatory T Cell Numbers with Disease Tolerance upon Virus Infection. ImmunoHorizons, 2021, 5, 157-169.	0.8	1
96	A k -mer query tool for assessing population diversity in pangenomes. , 2021, , .		0