Gary A Churchill

List of Publications by Year
in descending order

287 papers	31,223 citations	7568 77 h-index	5679 162 g-index
323 all docs	323 docs citations	323 times ranked	29533 citing authors

#	Article	IF	Citations
1	R/qtl: QTL mapping in experimental crosses. Bioinformatics, 2003, 19, 889-890.	4.1	3,197
2	Analysis of Variance for Gene Expression Microarray Data. Journal of Computational Biology, 2000, 7, 819-837.	1.6	1,158
3	The Collaborative Cross, a community resource for the genetic analysis of complex traits. Nature Genetics, 2004, 36, 1133-1137.	21.4	1,034
4	Identification of conserved gene expression features between murine mammary carcinoma models and human breast tumors. Genome Biology, 2007, 8, R76.	9.6	1,009
5	Characterization of human embryonic stem cell lines by the International Stem Cell Initiative. Nature Biotechnology, 2007, 25, 803-816.	17.5	983
6	Fundamentals of experimental design for cDNA microarrays. Nature Genetics, 2002, 32, 490-495.	21.4	979
7	A Hidden Markov Model approach to variation among sites in rate of evolution. Molecular Biology and Evolution, 1996, 13, 93-104.	8.9	768
8	Statistical tests for differential expression in cDNA microarray experiments. Genome Biology, 2003, 4, 210.	9.6	741
9	Variation in gene expression within and among natural populations. Nature Genetics, 2002, 32, 261-266.	21.4	637
10	A Statistical Framework for Quantitative Trait Mapping. Genetics, 2001, 159, 371-387.	2.9	565
11	Statistical design and the analysis of gene expression microarray data. Genetical Research, 2001, 77, 123-128.	0.9	513
12	Improved statistical tests for differential gene expression by shrinking variance components estimates. Biostatistics, 2005, 6, 59-75.	1.5	450
13	Subspecific origin and haplotype diversity in the laboratory mouse. Nature Genetics, 2011, 43, 648-655.	21.4	439
14	High-Resolution Genetic Mapping Using the Mouse Diversity Outbred Population. Genetics, 2012, 190, 437-447.	2.9	437
15	Bootstrapping cluster analysis: Assessing the reliability of conclusions from microarray experiments. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 8961-8965.	7.1	414
16	The diversity outbred mouse population. Mammalian Genome, 2012, 23, 713-718.	2.2	406
17	The nature and identification of quantitative trait loci: a community's view. Nature Reviews Genetics, 2003, 4, 911-916.	16.3	390
18	Aging in inbred strains of mice: study design and interim report on median lifespans and circulating IGF1 levels. Aging Cell, 2009, 8, 277-287.	6.7	359

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19	Defining the consequences of genetic variation on a proteome-wide scale. Nature, 2016, 534, 500-505.	27.8	335
20	R/qtl2: Software for Mapping Quantitative Trait Loci with High-Dimensional Data and Multiparent Populations. Genetics, 2019, 211, 495-502.	2.9	333
21	Genetic analysis of complex traits in the emerging Collaborative Cross. Genome Research, 2011, 21, 1213-1222.	5.5	327
22	Macromolecule biosynthesis: a key function of sleep. Physiological Genomics, 2007, 31, 441-457.	2.3	322
23	Stochastic models for heterogeneous DNA sequences. Bulletin of Mathematical Biology, 1989, 51, 79-94.	1.9	302
24	On the subspecific origin of the laboratory mouse. Nature Genetics, 2007, 39, 1100-1107.	21.4	281
25	The mouse as a model for human biology: a resource guide for complex trait analysis. Nature Reviews Genetics, 2007, 8, 58-69.	16.3	270
26	The Collaborative Cross at Oak Ridge National Laboratory: developing a powerful resource for systems genetics. Mammalian Genome, 2008, 19, 382-389.	2.2	245
27	Quantitative Trait Loci for Femoral and Lumbar Vertebral Bone Mineral Density in C57BL/6J and C3H/HeJ Inbred Strains of Mice. Journal of Bone and Mineral Research, 2001, 16, 1195-1206.	2.8	236
28	A customized and versatile high-density genotyping array for the mouse. Nature Methods, 2009, 6, 663-666.	19.0	236
29	Genetic properties of the MAGIC maize population: a new platform for high definition QTL mapping in Zea mays. Genome Biology, 2015, 16, 167.	8.8	225
30	Genome-Wide Epistatic Interaction Analysis Reveals Complex Genetic Determinants of Circadian Behavior in Mice. Genome Research, 2001, 11, 959-980.	5.5	211
31	A New Standard Genetic Map for the Laboratory Mouse. Genetics, 2009, 182, 1335-1344.	2.9	202
32	The Mouse Universal Genotyping Array: From Substrains to Subspecies. G3: Genes, Genomes, Genetics, 2016, 6, 263-279.	1.8	199
33	C57BL/6N Mutation in *Cytoplasmic FMRP interacting protein 2* Regulates Cocaine Response. Science, 2013, 342, 1508-1512.	12.6	198
34	Statistical design and the analysis of gene expression microarray data. Genetical Research, 2007, 89, 509-514.	0.9	195
35	Quantitative Trait Locus Mapping Methods for Diversity Outbred Mice. G3: Genes, Genomes, Genetics, 2014, 4, 1623-1633.	1.8	195
36	Concordance of Murine Quantitative Trait Loci for Salt-Induced Hypertension with Rat and Human Loci. Genomics, 2001, 71, 70-77.	2.9	194

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37	Genomes of the Mouse Collaborative Cross. Genetics, 2017, 206, 537-556.	2.9	189
38	The Collaborative Cross: A Recombinant Inbred Mouse Population for the Systems Genetic Era. ILAR Journal, 2011, 52, 24-31.	1.8	183
39	Modeling Host Genetic Regulation of Influenza Pathogenesis in the Collaborative Cross. PLoS Pathogens, 2013, 9, e1003196.	4.7	183
40	A multi-tissue full lifespan epigenetic clock for mice. Aging, 2018, 10, 2832-2854.	3.1	166
41	MAANOVA: A Software Package for the Analysis of Spotted cDNA Microarray Experiments. Statistics in the Health Sciences, 2003, , 313-341.	0.2	165
42	Gene expression patterns in the hippocampus and amygdala of endogenous depression and chronic stress models. Molecular Psychiatry, 2012, 17, 49-61.	7.9	165
43	Multiple trait measurements in 43 inbred mouse strains capture the phenotypic diversity characteristic of human populations. Journal of Applied Physiology, 2007, 102, 2369-2378.	2.5	160
44	Genetic analysis in the Collaborative Cross breeding population. Genome Research, 2011, 21, 1223-1238.	5.5	158
45	PPARÎ³2 nuclear receptor controls multiple regulatory pathways of osteoblast differentiation from marrow mesenchymal stem cells. Journal of Cellular Biochemistry, 2009, 106, 232-246.	2.6	156
46	Maternal Environment and Genotype Interact to Establish Diabesity in Mice. Genome Research, 2000, 10, 1568-1578.	5.5	155
47	Quantitative trait loci for bone density in C57BL/6J and CAST/EiJ inbred mice. Mammalian Genome, 1999, 10, 1043-1049.	2.2	153
48	Structural Model Analysis of Multiple Quantitative Traits. PLoS Genetics, 2006, 2, e114.	3.5	152
49	The impact of reduced frequency of cage changes on the health of mice housed in ventilated cages. Laboratory Animals, 2001, 35, 58-73.	1.0	141
50	Genetic Analysis of a New Mouse Model for Non-Insulin-Dependent Diabetes. Genomics, 2001, 74, 273-286.	2.9	138
51	Using ANOVA to Analyze Microarray Data. BioTechniques, 2004, 37, 173-177.	1.8	138
52	Genome Wide Identification of SARS-CoV Susceptibility Loci Using the Collaborative Cross. PLoS Genetics, 2015, 11, e1005504.	3.5	137
53	Sex- and lineage-specific inheritance of depression-like behavior in the rat. Mammalian Genome, 2004, 15, 648-662.	2.2	129
54	Ten Years of the Collaborative Cross. Genetics, 2012, 190, 291-294.	2.9	128

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55	FXR and ABCG5/ABCG8 as determinants of cholesterol gallstone formation from quantitative trait locus mapping in mice. Gastroenterology, 2003, 125, 868-881.	1.3	122
56	Bayesian Model Selection for Genome-Wide Epistatic Quantitative Trait Loci Analysis. Genetics, 2005, 170, 1333-1344.	2.9	120
57	The Role of Subjectivity in Reconstructing Ancestral Character States: A Bayesian Approach to Unknown Rates, States, and Transformation Asymmetries. Systematic Biology, 1999, 48, 651-664.	5.6	115
58	The Collaborative Cross, developing a resource for mammalian systems genetics: A status report of the Wellcome Trust cohort. Mammalian Genome, 2008, 19, 379-381.	2.2	111
59	Diversity Outbred Mice Identify Population-Based Exposure Thresholds and Genetic Factors that Influence Benzene-Induced Genotoxicity. Environmental Health Perspectives, 2015, 123, 237-245.	6.0	111
60	High‐precision genetic mapping of behavioral traits in the diversity outbred mouse population. Genes, Brain and Behavior, 2013, 12, 424-437.	2.2	110
61	Crossover Interference in the Mouse. Genetics, 2002, 160, 1123-1131.	2.9	109
62	A major quantitative trait locus on chromosome 3 controls colitis severity in IL-10-deficient mice. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 13820-13825.	7.1	103
63	Hierarchical analysis of RNA-seq reads improves the accuracy of allele-specific expression. Bioinformatics, 2018, 34, 2177-2184.	4.1	101
64	Hidden Markov chains and the analysis of genome structure. Computers & Chemistry, 1992, 16, 107-115.	1.2	100
65	Mapping Quantitative Trait Loci for Vertebral Trabecular Bone Volume Fraction and Microarchitecture in Mice. Journal of Bone and Mineral Research, 2003, 19, 587-599.	2.8	98
66	Multiple mechanisms limit the duration of wakefulness in Drosophila brain. Physiological Genomics, 2006, 27, 337-350.	2.3	97
67	Combining Data From Multiple Inbred Line Crosses Improves the Power and Resolution of Quantitative Trait Loci Mapping. Genetics, 2005, 169, 1699-1709.	2.9	96
68	Statistical aspects of genetic mapping in autopolyploids. Gene, 1999, 235, 31-41.	2.2	95
69	Genetic Analysis of Susceptibility to Dextran Sulfate Sodium-Induced Colitis in Mice. Genomics, 1999, 55, 147-156.	2.9	94
70	A collaborative database of inbred mouse strain characteristics. Bioinformatics, 2004, 20, 2857-2859.	4.1	94
71	Aging Research Using Mouse Models. Current Protocols in Mouse Biology, 2015, 5, 95-133.	1.2	92
72	Transformations for cDNA Microarray Data. Statistical Applications in Genetics and Molecular Biology, 2003, 2, Article4.	0.6	90

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73	Evidence of a Large-Scale Functional Organization of Mammalian Chromosomes. PLoS Genetics, 2005, 1, e33.	3.5	88
74	Gonadal sex reversal in mutant *Dax1* XY mice: a failure to upregulate *Sox9* in pre-Sertoli cells. Development (Cambridge), 2005, 132, 3045-3054.	2.5	86
75	High-Resolution Sex-Specific Linkage Maps of the Mouse Reveal Polarized Distribution of Crossovers in Male Germline. Genetics, 2014, 197, 91-106.	2.9	85
76	Pooled-sampling makes high-resolution mapping practical with DNA markers.. Proceedings of the National Academy of Sciences of the United States of America, 1993, 90, 16-20.	7.1	83
77	Discovery of blood transcriptomic markers for depression in animal models and pilot validation in subjects with early-onset major depression. Translational Psychiatry, 2012, 2, e101-e101.	4.8	83
78	A comparison of cDNA, oligonucleotide, and Affymetrix GeneChip gene expression microarray platforms. Journal of Biomolecular Techniques, 2004, 15, 276-84.	1.5	83
79	Clinicopathologic features and prognosis for wilms' tumor patients with metastases at diagnosis. Cancer, 1986, 58, 2501-2511.	4.1	82
80	Overexpression of innate immune response genes in a model of recessive polycystic kidney disease. Kidney International, 2008, 73, 63-76.	5.2	82
81	RNA-Seq Alignment to Individualized Genomes Improves Transcript Abundance Estimates in Multiparent Populations. Genetics, 2014, 198, 59-73.	2.9	82
82	Using Advanced Intercross Lines for High-Resolution Mapping of HDL Cholesterol Quantitative Trait Loci. Genome Research, 2003, 13, 1654-1664.	5.5	81
83	Heterogeneity in Rates of Recombination Across the Mouse Genome. Genetics, 1996, 142, 537-548.	2.9	81
84	Genetic Modulation of Tau Phosphorylation in the Mouse. Journal of Neuroscience, 2003, 23, 187-192.	3.6	80
85	Genetic Analysis of Hematological Parameters in Incipient Lines of the Collaborative Cross. G3: Genes, Genomes, Genetics, 2012, 2, 157-165.	1.8	80
86	Sensitivity to hepatotoxicity due to epigallocatechin gallate is affected by genetic background in diversity outbred mice. Food and Chemical Toxicology, 2015, 76, 19-26.	3.6	80
87	An imputed genotype resource for the laboratory mouse. Mammalian Genome, 2008, 19, 199-208.	2.2	79
88	Influence of sex and diet on quantitative trait loci for HDL cholesterol levels in an SM/J by NZB/BlNJ intercross population. Journal of Lipid Research, 2004, 45, 881-888.	4.2	78
89	Ten Years of the Collaborative Cross. G3: Genes, Genomes, Genetics, 2012, 2, 153-156.	1.8	78
90	Strain-Specific Effects of Rosiglitazone on Bone Mass, Body Composition, and Serum Insulin-Like Growth Factor-I. Endocrinology, 2009, 150, 1330-1340.	2.8	77

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91	A Multi-Megabase Copy Number Gain Causes Maternal Transmission Ratio Distortion on Mouse Chromosome 2. PLoS Genetics, 2015, 11, e1004850.	3.5	76
92	Genetic determinants of gut microbiota composition and bile acid profiles in mice. PLoS Genetics, 2019, 15, e1008073.	3.5	75
93	Mapping quantitative trait loci for serum insulin-like growth factor-1 levels in mice. Bone, 2000, 27, 521-528.	2.9	74
94	Generation of a New Congenic Mouse Strain to Test the Relationships Among Serum Insulin-like Growth Factor I, Bone Mineral Density, and Skeletal Morphology In Vivo. Journal of Bone and Mineral Research, 2002, 17, 570-579.	2.8	73
95	Adaptive Evolution and Effective Population Size in Wild House Mice. Molecular Biology and Evolution, 2012, 29, 2949-2955.	8.9	73
96	Quantitative Trait Loci Analysis for Plasma HDL-Cholesterol Concentrations and Atherosclerosis Susceptibility Between Inbred Mouse Strains C57BL/6J and 129S1/SvImJ. Arteriosclerosis, Thrombosis, and Vascular Biology, 2004, 24, 161-166.	2.4	72
97	What are microarrays teaching us about sleep?. Trends in Molecular Medicine, 2009, 15, 79-87.	6.7	70
98	Spontaneous voiding by mice reveals strain-specific lower urinary tract function to be a quantitative genetic trait. American Journal of Physiology - Renal Physiology, 2014, 306, F1296-F1307.	2.7	68
99	Pleiotropy, Homeostasis, and Functional Networks Based on Assays of Cardiovascular Traits in Genetically Randomized Populations. Genome Research, 2003, 13, 2082-2091.	5.5	67
100	Quantitative trait locus analysis for obesity reveals multiple networks of interacting loci. Mammalian Genome, 2006, 17, 22-36.	2.2	67
101	The accuracy of DNA sequences: Estimating sequence quality. Genomics, 1992, 14, 89-98.	2.9	66
102	The X Chromosome in Quantitative Trait Locus Mapping. Genetics, 2006, 174, 2151-2158.	2.9	66
103	The future of model organisms in human disease research. Nature Reviews Genetics, 2011, 12, 575-582.	16.3	66
104	Collaborative Cross and Diversity Outbred data resources in the Mouse Phenome Database. Mammalian Genome, 2015, 26, 511-520.	2.2	66
105	Diversity Outbred Mice at 21: Maintaining Allelic Variation in the Face of Selection. G3: Genes, Genomes, Genetics, 2016, 6, 3893-3902.	1.8	66
106	Estimating p-values in small microarray experiments. Bioinformatics, 2007, 23, 38-43.	4.1	65
107	Identification of quantitative trait loci associated with acylsugar accumulation using intraspecific populations of the wild tomato, Lycopersicon pennellii. Theoretical and Applied Genetics, 1998, 96, 458-467.	3.6	63
108	QTL analysis of self-selected macronutrient diet intake: fat, carbohydrate, and total kilocalories. Physiological Genomics, 2002, 11, 205-217.	2.3	62

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109	Proteomic and transcriptomic profiling reveal different aspects of aging in the kidney. ELife, 2021, 10, .	6.0	62
110	Discovery of novel variants in genotyping arrays improves genotype retention and reduces ascertainment bias. BMC Genomics, 2012, 13, 34.	2.8	61
111	Gene loci associated with insulin secretion in islets from nondiabetic mice. Journal of Clinical Investigation, 2019, 129, 4419-4432.	8.2	60
112	Naive Application of Permutation Testing Leads to Inflated Type I Error Rates. Genetics, 2008, 178, 609-610.	2.9	59
113	Critical reasoning on causal inference in genome-wide linkage and association studies. Trends in Genetics, 2010, 26, 493-498.	6.7	59
114	Selective Phenotyping for Increased Efficiency in Genetic Mapping Studies. Genetics, 2004, 168, 2285-2293.	2.9	58
115	R/qtlDesign: inbred line cross experimental design. Mammalian Genome, 2007, 18, 87-93.	2.2	58
116	Architecture of energy balance traits in emerging lines of the Collaborative Cross. American Journal of Physiology - Endocrinology and Metabolism, 2011, 300, E1124-E1134.	3.5	58
117	Report of the National Heart, Lung, and Blood Institute Working Group on Sex Differences Research in Cardiovascular Disease. Hypertension, 2016, 67, 802-807.	2.7	58
118	A Markov Chain Model of Coalescence with Recombination. Theoretical Population Biology, 1997, 52, 43-59.	1.1	57
119	Genetic identification of thiosulfate sulfurtransferase as an adipocyte-expressed antidiabetic target in mice selected for leanness. Nature Medicine, 2016, 22, 771-779.	30.7	57
120	Genetics of Colitis Susceptibility in IL-10-Deficient Mice: Backcross versus F2 Results Contrasted by Principal Component Analysis. Genomics, 2002, 80, 274-282.	2.9	56
121	*PPARG* by Dietary Fat Interaction Influences Bone Mass in Mice and Humans. Journal of Bone and Mineral Research, 2008, 23, 1398-1408.	2.8	56
122	QTL associated with blood pressure, heart rate, and heart weight in CBA/CaJ and BALB/cJ mice. Physiological Genomics, 2002, 10, 5-12.	2.3	55
123	Kinesin Family Member 12 Is a Candidate Polycystic Kidney Disease Modifier in the cpk Mouse. Journal of the American Society of Nephrology: JASN, 2005, 16, 905-916.	6.1	55
124	*R2d2* Drives Selfish Sweeps in the House Mouse. Molecular Biology and Evolution, 2016, 33, 1381-1395.	8.9	55
125	Precise genetic mapping and integrative bioinformatics in Diversity Outbred mice reveals Hydin as a novel pain gene. Mammalian Genome, 2014, 25, 211-222.	2.2	54
126	Genetic Drivers of Pancreatic Islet Function. Genetics, 2018, 209, 335-356.	2.9	54

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127	Test- and behavior-specific genetic factors affect WKY hypoactivity in tests of emotionality. Behavioural Brain Research, 2006, 169, 220-230.	2.2	53
128	Mouse BMD quantitative trait loci show improved concordance with human genome-wide association loci when recalculated on a new, common mouse genetic map. Journal of Bone and Mineral Research, 2010, 25, 1808-1820.	2.8	53
129	Exploration of Low-Dose Estrogen Effects: Identification of No Observed Transcriptional Effect Level (NOTEL). Toxicologic Pathology, 2004, 32, 482-492.	1.8	53
130	Effects of atherogenic diet on hepatic gene expression across mouse strains. Physiological Genomics, 2009, 39, 172-182.	2.3	52
131	Structural Variation Shapes the Landscape of Recombination in Mouse. Genetics, 2017, 206, 603-619.	2.9	51
132	Quantitative trait loci that determine plasma lipids and obesity in C57BL/6J and 129S1/SvImJ inbred mice. Journal of Lipid Research, 2004, 45, 1624-1632.	4.2	50
133	Genetic analysis of the stress-responsive adrenocortical axis. Physiological Genomics, 2006, 27, 362-369.	2.3	50
134	Epistatic Networks Jointly Influence Phenotypes Related to Metabolic Disease and Gene Expression in Diversity Outbred Mice. Genetics, 2017, 206, 621-639.	2.9	50
135	Sex, flies and microarrays. Nature Genetics, 2001, 29, 355-356.	21.4	49
136	Genetic analysis of blood pressure in C3H/HeJ and SWR/J mice. Physiological Genomics, 2004, 17, 215-220.	2.3	49
137	The Genome of C57BL/6J â€œEveâ€‚ the Mother of the Laboratory Mouse Genome Reference Strain. G3: Genes, Genomes, Genetics, 2019, 9, 1795-1805.	1.8	49
138	A General Bayesian Approach to Analyzing Diallel Crosses of Inbred Strains. Genetics, 2012, 190, 413-435.	2.9	47
139	Major Locus on Mouse Chromosome 17 and Minor Locus on Chromosome 9 are Linked with Alopecia Areata in C3H/HeJ Mice. Journal of Investigative Dermatology, 2003, 120, 771-775.	0.7	46
140	Quantitative trait loci that determine lipoprotein cholesterol levels in DBA/2J and CAST/Ei inbred mice,. Journal of Lipid Research, 2003, 44, 953-967.	4.2	46
141	Quantitative Trait Loci Modulate Renal Cystic Disease Severity in the Mouse bpk Model. Journal of the American Society of Nephrology: JASN, 2000, 11, 1253-1260.	6.1	46
142	Bayesian model selection reveals biological origins of zero inflation in single-cell transcriptomics. Genome Biology, 2020, 21, 183.	8.8	45
143	Methods for inferring phylogenies from nucleic acid sequence data by using maximum likelihood and linear invariants.. Molecular Biology and Evolution, 1991, 8, 128-43.	8.9	45
144	Genetic Regulation of *Zfp30*, CXCL1, and Neutrophilic Inflammation in Murine Lung. Genetics, 2014, 198, 735-745.	2.9	44

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145	Mapping Complex Traits in a Diversity Outbred F1 Mouse Population Identifies Germline Modifiers of Metastasis in Human Prostate Cancer. Cell Systems, 2017, 4, 31-45.e6.	6.2	44
146	A large-scale genome–lipid association map guides lipid identification. Nature Metabolism, 2020, 2, 1149-1162.	11.9	43
147	Applying Gene Expression, Proteomics and Single-Nucleotide Polymorphism Analysis for Complex Trait Gene Identification. Genetics, 2008, 178, 1795-1805.	2.9	42
148	Genome-Wide Association Mapping of Quantitative Traits in Outbred Mice. G3: Genes, Genomes, Genetics, 2012, 2, 167-174.	1.8	42
149	Imputation of Single-Nucleotide Polymorphisms in Inbred Mice Using Local Phylogeny. Genetics, 2012, 190, 449-458.	2.9	42
150	The Reconstruction of Ancestral Character States. Evolution; International Journal of Organic Evolution, 1996, 50, 504.	2.3	41
151	Genetic Modifiers of Polycystic Kidney Disease in Intersubspecific KAT2J Mutants. Genomics, 1999, 58, 129-137.	2.9	41
152	Locating Ath8, a locus for murine atherosclerosis susceptibility and testing several of its candidate genes in mice and humans. Atherosclerosis, 2004, 177, 443-450.	0.8	41
153	Interacting genetic loci cause airway hyperresponsiveness. Physiological Genomics, 2005, 21, 105-111.	2.3	41
154	High-fat diet leads to tissue-specific changes reflecting risk factors for diseases in DBA/2J mice. Physiological Genomics, 2010, 42, 55-66.	2.3	41
155	Doxorubicin-Induced Cardiotoxicity in Collaborative Cross (CC) Mice Recapitulates Individual Cardiotoxicity in Humans. G3: Genes, Genomes, Genetics, 2019, 9, 2637-2646.	1.8	41
156	Network models for sequence evolution. Journal of Molecular Evolution, 1993, 37, 77-85.	1.8	39
157	Interacting QTLs for cholesterol gallstones and gallbladder mucin in AKR and SWR strains of mice. Physiological Genomics, 2002, 8, 67-77.	2.3	39
158	Quantitative Trait Loci That Determine BMD in C57BL/6J and 129S1/SvImJ Inbred Mice. Journal of Bone and Mineral Research, 2005, 21, 105-112.	2.8	39
159	Genetic analysis of resistance to Type-1 Diabetes in ALR/Lt mice, a NOD-related strain with defenses against autoimmune-mediated diabetogenic stress. Immunogenetics, 2003, 55, 491-496.	2.4	38
160	Association of a lithogenic Abcg5/Abcg8 allele on Chromosome 17 (Lith9) with cholesterol gallstone formation in PERA/EiJ mice. Mammalian Genome, 2005, 16, 495-504.	2.2	38
161	Naive Pluripotent Stem Cells Exhibit Phenotypic Variability that Is Driven by Genetic Variation. Cell Stem Cell, 2020, 27, 470-481.e6.	11.1	38
162	Integrative Genetic Analysis of Allergic Inflammation in the Murine Lung. American Journal of Respiratory Cell and Molecular Biology, 2014, 51, 436-445.	2.9	37

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163	High-Density Genotypes of Inbred Mouse Strains: Improved Power and Precision of Association Mapping. G3: Genes, Genomes, Genetics, 2015, 5, 2021-2026.	1.8	37
164	A Bayesian Framework for Inference of the Genotype–Phenotype Map for Segregating Populations. Genetics, 2011, 187, 1163-1170.	2.9	36
165	The distribution of restriction enzyme sites inEscherichia coli. Nucleic Acids Research, 1990, 18, 589-597.	14.5	35
166	Femur Mechanical Properties in the F2 Progeny of an NZB/B1NJ Ã— RF/J Cross Are Regulated Predominantly by Genetic Loci That Regulate Bone Geometry. Journal of Bone and Mineral Research, 2006, 21, 1256-1266.	2.8	35
167	Inheritance Patterns of Transcript Levels in F1 Hybrid Mice. Genetics, 2006, 174, 627-637.	2.9	35
168	Genetic analysis of albuminuria in a cross between C57BL/6J and DBA/2J mice. American Journal of Physiology - Renal Physiology, 2007, 293, F1649-F1656.	2.7	35
169	Four additional mouse crosses improve the lipid QTL landscape and identify Lipg as a QTL gene. Journal of Lipid Research, 2009, 50, 2083-2094.	4.2	35
170	Sample size for a phylogenetic inference.. Molecular Biology and Evolution, 1992, 9, 753-69.	8.9	33
171	Genetic Analysis of Blood Pressure in 8 Mouse Intercross Populations. Hypertension, 2009, 54, 802-809.	2.7	33
172	Randomization in Laboratory Procedure Is Key to Obtaining Reproducible Microarray Results. PLoS ONE, 2008, 3, e3724.	2.5	33
173	Identification of QTLs controlling acylsugar fatty acid composition in an intraspecific population of Lycopersicon pennellii (Corr.) D'Arcy. Theoretical and Applied Genetics, 1999, 99, 373-381.	3.6	32
174	X-linked and lineage-dependent inheritance of coping responses to stress. Mammalian Genome, 2003, 14, 748-757.	2.2	32
175	Identification of genetic determinants of IGF–1 levels and longevity among mouse inbred strains. Aging Cell, 2010, 9, 823-836.	6.7	32
176	Accessing Data Resources in the Mouse Phenome Database for Genetic Analysis of Murine Life Span and Health Span. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2016, 71, 170-177.	3.6	32
177	Complex Genetic Architecture Revealed by Analysis of High-Density Lipoprotein Cholesterol in Chromosome Substitution Strains and F2 Crosses. Genetics, 2006, 174, 999-1007.	2.9	31
178	Mapping the Effects of Genetic Variation on Chromatin State and Gene Expression Reveals Loci That Control Ground State Pluripotency. Cell Stem Cell, 2020, 27, 459-469.e8.	11.1	31
179	Quantitative Trait Locus Analysis Using J/qtl. Methods in Molecular Biology, 2009, 573, 175-188.	0.9	31
180	Quantitative Trait Locus Study Design From an Information Perspective. Genetics, 2005, 170, 447-464.	2.9	29

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181	Gene expression analysis of mouse chromosome substitution strains. Mammalian Genome, 2006, 17, 598-614.	2.2	29
182	Importance of randomization in microarray experimental designs with Illumina platforms. Nucleic Acids Research, 2009, 37, 5610-5618.	14.5	29
183	How mice are indispensable for understanding obesity and diabetes genetics. Current Opinion in Endocrinology, Diabetes and Obesity, 2017, 24, 83-91.	2.3	29
184	Fasting blood glucose as a predictor of mortality: Lost in translation. Cell Metabolism, 2021, 33, 2189-2200.e3.	16.2	29
185	Coordinated Expression Domains in Mammalian Genomes. PLoS ONE, 2010, 5, e12158.	2.5	29
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