

# Gary A Churchill

## List of Publications by Year in descending order

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287  
papers

31,223  
citations

8755

77  
h-index

6512

162  
g-index

323  
all docs

323  
docs citations

323  
times ranked

32976  
citing authors

#	ARTICLE	IF	CITATIONS
1	R/qlt: QTL mapping in experimental crosses. <i>Bioinformatics</i> , 2003, 19, 889-890.	1.8	3,197
2	Analysis of Variance for Gene Expression Microarray Data. <i>Journal of Computational Biology</i> , 2000, 7, 819-837.	0.8	1,158
3	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
4	Identification of conserved gene expression features between murine mammary carcinoma models and human breast tumors. <i>Genome Biology</i> , 2007, 8, R76.	13.9	1,009
5	Characterization of human embryonic stem cell lines by the International Stem Cell Initiative. <i>Nature Biotechnology</i> , 2007, 25, 803-816.	9.4	983
6	Fundamentals of experimental design for cDNA microarrays. <i>Nature Genetics</i> , 2002, 32, 490-495.	9.4	979
7	A Hidden Markov Model approach to variation among sites in rate of evolution. <i>Molecular Biology and Evolution</i> , 1996, 13, 93-104.	3.5	768
8	Statistical tests for differential expression in cDNA microarray experiments. <i>Genome Biology</i> , 2003, 4, 210.	13.9	741
9	Variation in gene expression within and among natural populations. <i>Nature Genetics</i> , 2002, 32, 261-266.	9.4	637
10	A Statistical Framework for Quantitative Trait Mapping. <i>Genetics</i> , 2001, 159, 371-387.	1.2	565
11	Statistical design and the analysis of gene expression microarray data. <i>Genetical Research</i> , 2001, 77, 123-128.	0.3	513
12	Improved statistical tests for differential gene expression by shrinking variance components estimates. <i>Biostatistics</i> , 2005, 6, 59-75.	0.9	450
13	Subspecific origin and haplotype diversity in the laboratory mouse. <i>Nature Genetics</i> , 2011, 43, 648-655.	9.4	439
14	High-Resolution Genetic Mapping Using the Mouse Diversity Outbred Population. <i>Genetics</i> , 2012, 190, 437-447.	1.2	437
15	Bootstrapping cluster analysis: Assessing the reliability of conclusions from microarray experiments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 8961-8965.	3.3	414
16	The diversity outbred mouse population. <i>Mammalian Genome</i> , 2012, 23, 713-718.	1.0	406
17	The nature and identification of quantitative trait loci: a community's view. <i>Nature Reviews Genetics</i> , 2003, 4, 911-916.	7.7	390
18	Aging in inbred strains of mice: study design and interim report on median lifespans and circulating IGF1 levels. <i>Aging Cell</i> , 2009, 8, 277-287.	3.0	359

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19	Defining the consequences of genetic variation on a proteome-wide scale. <i>Nature</i> , 2016, 534, 500-505.	13.7	335
20	R/qtl2: Software for Mapping Quantitative Trait Loci with High-Dimensional Data and Multiparent Populations. <i>Genetics</i> , 2019, 211, 495-502.	1.2	333
21	Genetic analysis of complex traits in the emerging Collaborative Cross. <i>Genome Research</i> , 2011, 21, 1213-1222.	2.4	327
22	Macromolecule biosynthesis: a key function of sleep. <i>Physiological Genomics</i> , 2007, 31, 441-457.	1.0	322
23	Stochastic models for heterogeneous DNA sequences. <i>Bulletin of Mathematical Biology</i> , 1989, 51, 79-94.	0.9	302
24	On the subspecific origin of the laboratory mouse. <i>Nature Genetics</i> , 2007, 39, 1100-1107.	9.4	281
25	The mouse as a model for human biology: a resource guide for complex trait analysis. <i>Nature Reviews Genetics</i> , 2007, 8, 58-69.	7.7	270
26	The Collaborative Cross at Oak Ridge National Laboratory: developing a powerful resource for systems genetics. <i>Mammalian Genome</i> , 2008, 19, 382-389.	1.0	245
27	Quantitative Trait Loci for Femoral and Lumbar Vertebral Bone Mineral Density in C57BL/6J and C3H/HeJ Inbred Strains of Mice. <i>Journal of Bone and Mineral Research</i> , 2001, 16, 1195-1206.	3.1	236
28	A customized and versatile high-density genotyping array for the mouse. <i>Nature Methods</i> , 2009, 6, 663-666.	9.0	236
29	Genetic properties of the MAGIC maize population: a new platform for high definition QTL mapping in <i>Zea mays</i> . <i>Genome Biology</i> , 2015, 16, 167.	3.8	225
30	Genome-Wide Epistatic Interaction Analysis Reveals Complex Genetic Determinants of Circadian Behavior in Mice. <i>Genome Research</i> , 2001, 11, 959-980.	2.4	211
31	A New Standard Genetic Map for the Laboratory Mouse. <i>Genetics</i> , 2009, 182, 1335-1344.	1.2	202
32	The Mouse Universal Genotyping Array: From Substrains to Subspecies. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 263-279.	0.8	199
33	C57BL/6N Mutation in <i>Cytoplasmic FMRP interacting protein 2</i> Regulates Cocaine Response. <i>Science</i> , 2013, 342, 1508-1512.	6.0	198
34	Statistical design and the analysis of gene expression microarray data. <i>Genetical Research</i> , 2007, 89, 509-514.	0.3	195
35	Quantitative Trait Locus Mapping Methods for Diversity Outbred Mice. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1623-1633.	0.8	195
36	Concordance of Murine Quantitative Trait Loci for Salt-Induced Hypertension with Rat and Human Loci. <i>Genomics</i> , 2001, 71, 70-77.	1.3	194

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37	Genomes of the Mouse Collaborative Cross. <i>Genetics</i> , 2017, 206, 537-556.	1.2	189
38	The Collaborative Cross: A Recombinant Inbred Mouse Population for the Systems Genetic Era. <i>ILAR Journal</i> , 2011, 52, 24-31.	1.8	183
39	Modeling Host Genetic Regulation of Influenza Pathogenesis in the Collaborative Cross. <i>PLoS Pathogens</i> , 2013, 9, e1003196.	2.1	183
40	A multi-tissue full lifespan epigenetic clock for mice. <i>Aging</i> , 2018, 10, 2832-2854.	1.4	166
41	MAANOVA: A Software Package for the Analysis of Spotted cDNA Microarray Experiments. <i>Statistics in the Health Sciences</i> , 2003, , 313-341.	0.2	165
42	Gene expression patterns in the hippocampus and amygdala of endogenous depression and chronic stress models. <i>Molecular Psychiatry</i> , 2012, 17, 49-61.	4.1	165
43	Multiple trait measurements in 43 inbred mouse strains capture the phenotypic diversity characteristic of human populations. <i>Journal of Applied Physiology</i> , 2007, 102, 2369-2378.	1.2	160
44	Genetic analysis in the Collaborative Cross breeding population. <i>Genome Research</i> , 2011, 21, 1223-1238.	2.4	158
45	PPAR $\beta$ nuclear receptor controls multiple regulatory pathways of osteoblast differentiation from marrow mesenchymal stem cells. <i>Journal of Cellular Biochemistry</i> , 2009, 106, 232-246.	1.2	156
46	Maternal Environment and Genotype Interact to Establish Diabesity in Mice. <i>Genome Research</i> , 2000, 10, 1568-1578.	2.4	155
47	Quantitative trait loci for bone density in C57BL/6J and CAST/Ej inbred mice. <i>Mammalian Genome</i> , 1999, 10, 1043-1049.	1.0	153
48	Structural Model Analysis of Multiple Quantitative Traits. <i>PLoS Genetics</i> , 2006, 2, e114.	1.5	152
49	The impact of reduced frequency of cage changes on the health of mice housed in ventilated cages. <i>Laboratory Animals</i> , 2001, 35, 58-73.	0.5	141
50	Genetic Analysis of a New Mouse Model for Non-Insulin-Dependent Diabetes. <i>Genomics</i> , 2001, 74, 273-286.	1.3	138
51	Using ANOVA to Analyze Microarray Data. <i>BioTechniques</i> , 2004, 37, 173-177.	0.8	138
52	Genome Wide Identification of SARS-CoV Susceptibility Loci Using the Collaborative Cross. <i>PLoS Genetics</i> , 2015, 11, e1005504.	1.5	137
53	Sex- and lineage-specific inheritance of depression-like behavior in the rat. <i>Mammalian Genome</i> , 2004, 15, 648-662.	1.0	129
54	Ten Years of the Collaborative Cross. <i>Genetics</i> , 2012, 190, 291-294.	1.2	128

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55	FXR and ABCG5/ABCG8 as determinants of cholesterol gallstone formation from quantitative trait locus mapping in mice. <i>Gastroenterology</i> , 2003, 125, 868-881.	0.6	122
56	Bayesian Model Selection for Genome-Wide Epistatic Quantitative Trait Loci Analysis. <i>Genetics</i> , 2005, 170, 1333-1344.	1.2	120
57	The Role of Subjectivity in Reconstructing Ancestral Character States: A Bayesian Approach to Unknown Rates, States, and Transformation Asymmetries. <i>Systematic Biology</i> , 1999, 48, 651-664.	2.7	115
58	The Collaborative Cross, developing a resource for mammalian systems genetics: A status report of the Wellcome Trust cohort. <i>Mammalian Genome</i> , 2008, 19, 379-381.	1.0	111
59	Diversity Outbred Mice Identify Population-Based Exposure Thresholds and Genetic Factors that Influence Benzene-Induced Genotoxicity. <i>Environmental Health Perspectives</i> , 2015, 123, 237-245.	2.8	111
60	High-precision genetic mapping of behavioral traits in the diversity outbred mouse population. <i>Genes, Brain and Behavior</i> , 2013, 12, 424-437.	1.1	110
61	Crossover Interference in the Mouse. <i>Genetics</i> , 2002, 160, 1123-1131.	1.2	109
62	A major quantitative trait locus on chromosome 3 controls colitis severity in IL-10-deficient mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 13820-13825.	3.3	103
63	Hierarchical analysis of RNA-seq reads improves the accuracy of allele-specific expression. <i>Bioinformatics</i> , 2018, 34, 2177-2184.	1.8	101
64	Hidden Markov chains and the analysis of genome structure. <i>Computers &amp; Chemistry</i> , 1992, 16, 107-115.	1.2	100
65	Mapping Quantitative Trait Loci for Vertebral Trabecular Bone Volume Fraction and Microarchitecture in Mice. <i>Journal of Bone and Mineral Research</i> , 2003, 19, 587-599.	3.1	98
66	Multiple mechanisms limit the duration of wakefulness in <i>Drosophila</i> brain. <i>Physiological Genomics</i> , 2006, 27, 337-350.	1.0	97
67	Combining Data From Multiple Inbred Line Crosses Improves the Power and Resolution of Quantitative Trait Loci Mapping. <i>Genetics</i> , 2005, 169, 1699-1709.	1.2	96
68	Statistical aspects of genetic mapping in autopolyploids. <i>Gene</i> , 1999, 235, 31-41.	1.0	95
69	Genetic Analysis of Susceptibility to Dextran Sulfate Sodium-Induced Colitis in Mice. <i>Genomics</i> , 1999, 55, 147-156.	1.3	94
70	A collaborative database of inbred mouse strain characteristics. <i>Bioinformatics</i> , 2004, 20, 2857-2859.	1.8	94
71	Aging Research Using Mouse Models. <i>Current Protocols in Mouse Biology</i> , 2015, 5, 95-133.	1.2	92
72	Transformations for cDNA Microarray Data. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2003, 2, Article4.	0.2	90

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73	Evidence of a Large-Scale Functional Organization of Mammalian Chromosomes. <i>PLoS Genetics</i> , 2005, 1, e33.	1.5	88
74	Gonadal sex reversal in mutant <i>Dax1</i> XY mice: a failure to upregulate <i>Sox9</i> in pre-Sertoli cells. <i>Development (Cambridge)</i> , 2005, 132, 3045-3054.	1.2	86
75	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
76	Pooled-sampling makes high-resolution mapping practical with DNA markers.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1993, 90, 16-20.	3.3	83
77	Discovery of blood transcriptomic markers for depression in animal models and pilot validation in subjects with early-onset major depression. <i>Translational Psychiatry</i> , 2012, 2, e101-e101.	2.4	83
78	A comparison of cDNA, oligonucleotide, and Affymetrix GeneChip gene expression microarray platforms. <i>Journal of Biomolecular Techniques</i> , 2004, 15, 276-84.	0.8	83
79	Clinicopathologic features and prognosis for wilms' tumor patients with metastases at diagnosis. <i>Cancer</i> , 1986, 58, 2501-2511.	2.0	82
80	Overexpression of innate immune response genes in a model of recessive polycystic kidney disease. <i>Kidney International</i> , 2008, 73, 63-76.	2.6	82
81	RNA-Seq Alignment to Individualized Genomes Improves Transcript Abundance Estimates in Multiparent Populations. <i>Genetics</i> , 2014, 198, 59-73.	1.2	82
82	Using Advanced Intercross Lines for High-Resolution Mapping of HDL Cholesterol Quantitative Trait Loci. <i>Genome Research</i> , 2003, 13, 1654-1664.	2.4	81
83	Heterogeneity in Rates of Recombination Across the Mouse Genome. <i>Genetics</i> , 1996, 142, 537-548.	1.2	81
84	Genetic Modulation of Tau Phosphorylation in the Mouse. <i>Journal of Neuroscience</i> , 2003, 23, 187-192.	1.7	80
85	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
86	Sensitivity to hepatotoxicity due to epigallocatechin gallate is affected by genetic background in diversity outbred mice. <i>Food and Chemical Toxicology</i> , 2015, 76, 19-26.	1.8	80
87	An imputed genotype resource for the laboratory mouse. <i>Mammalian Genome</i> , 2008, 19, 199-208.	1.0	79
88	Influence of sex and diet on quantitative trait loci for HDL cholesterol levels in an SM/J by NZB/BINJ intercross population. <i>Journal of Lipid Research</i> , 2004, 45, 881-888.	2.0	78
89	Ten Years of the Collaborative Cross. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 153-156.	0.8	78
90	Strain-Specific Effects of Rosiglitazone on Bone Mass, Body Composition, and Serum Insulin-Like Growth Factor-I. <i>Endocrinology</i> , 2009, 150, 1330-1340.	1.4	77

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91	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
92	Genetic determinants of gut microbiota composition and bile acid profiles in mice. <i>PLoS Genetics</i> , 2019, 15, e1008073.	1.5	75
93	Mapping quantitative trait loci for serum insulin-like growth factor-1 levels in mice. <i>Bone</i> , 2000, 27, 521-528.	1.4	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. <i>Journal of Bone and Mineral Research</i> , 2002, 17, 570-579.	3.1	73
95	Adaptive Evolution and Effective Population Size in Wild House Mice. <i>Molecular Biology and Evolution</i> , 2012, 29, 2949-2955.	3.5	73
96	Quantitative Trait Loci Analysis for Plasma HDL-Cholesterol Concentrations and Atherosclerosis Susceptibility Between Inbred Mouse Strains C57BL/6J and 129S1/SvImJ. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2004, 24, 161-166.	1.1	72
97	What are microarrays teaching us about sleep?. <i>Trends in Molecular Medicine</i> , 2009, 15, 79-87.	3.5	70
98	Spontaneous voiding by mice reveals strain-specific lower urinary tract function to be a quantitative genetic trait. <i>American Journal of Physiology - Renal Physiology</i> , 2014, 306, F1296-F1307.	1.3	68
99	Pleiotropy, Homeostasis, and Functional Networks Based on Assays of Cardiovascular Traits in Genetically Randomized Populations. <i>Genome Research</i> , 2003, 13, 2082-2091.	2.4	67
100	Quantitative trait locus analysis for obesity reveals multiple networks of interacting loci. <i>Mammalian Genome</i> , 2006, 17, 22-36.	1.0	67
101	The accuracy of DNA sequences: Estimating sequence quality. <i>Genomics</i> , 1992, 14, 89-98.	1.3	66
102	The X Chromosome in Quantitative Trait Locus Mapping. <i>Genetics</i> , 2006, 174, 2151-2158.	1.2	66
103	The future of model organisms in human disease research. <i>Nature Reviews Genetics</i> , 2011, 12, 575-582.	7.7	66
104	Collaborative Cross and Diversity Outbred data resources in the Mouse Phenome Database. <i>Mammalian Genome</i> , 2015, 26, 511-520.	1.0	66
105	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
106	Estimating p-values in small microarray experiments. <i>Bioinformatics</i> , 2007, 23, 38-43.	1.8	65
107	Identification of quantitative trait loci associated with acylsugar accumulation using intraspecific populations of the wild tomato, <i>Lycopersicon pennellii</i> . <i>Theoretical and Applied Genetics</i> , 1998, 96, 458-467.	1.8	63
108	QTL analysis of self-selected macronutrient diet intake: fat, carbohydrate, and total kilocalories. <i>Physiological Genomics</i> , 2002, 11, 205-217.	1.0	62

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109	Proteomic and transcriptomic profiling reveal different aspects of aging in the kidney. <i>ELife</i> , 2021, 10, .	2.8	62
110	Discovery of novel variants in genotyping arrays improves genotype retention and reduces ascertainment bias. <i>BMC Genomics</i> , 2012, 13, 34.	1.2	61
111	Gene loci associated with insulin secretion in islets from nondiabetic mice. <i>Journal of Clinical Investigation</i> , 2019, 129, 4419-4432.	3.9	60
112	Naive Application of Permutation Testing Leads to Inflated Type I Error Rates. <i>Genetics</i> , 2008, 178, 609-610.	1.2	59
113	Critical reasoning on causal inference in genome-wide linkage and association studies. <i>Trends in Genetics</i> , 2010, 26, 493-498.	2.9	59
114	Selective Phenotyping for Increased Efficiency in Genetic Mapping Studies. <i>Genetics</i> , 2004, 168, 2285-2293.	1.2	58
115	R/qtDesign: inbred line cross experimental design. <i>Mammalian Genome</i> , 2007, 18, 87-93.	1.0	58
116	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
117	Report of the National Heart, Lung, and Blood Institute Working Group on Sex Differences Research in Cardiovascular Disease. <i>Hypertension</i> , 2016, 67, 802-807.	1.3	58
118	A Markov Chain Model of Coalescence with Recombination. <i>Theoretical Population Biology</i> , 1997, 52, 43-59.	0.5	57
119	Genetic identification of thiosulfate sulfurtransferase as an adipocyte-expressed antidiabetic target in mice selected for leanness. <i>Nature Medicine</i> , 2016, 22, 771-779.	15.2	57
120	Genetics of Colitis Susceptibility in IL-10-Deficient Mice: Backcross versus F2 Results Contrasted by Principal Component Analysis. <i>Genomics</i> , 2002, 80, 274-282.	1.3	56
121	<i>PPARG</i> by Dietary Fat Interaction Influences Bone Mass in Mice and Humans. <i>Journal of Bone and Mineral Research</i> , 2008, 23, 1398-1408.	3.1	56
122	QTL associated with blood pressure, heart rate, and heart weight in CBA/CAJ and BALB/c mice. <i>Physiological Genomics</i> , 2002, 10, 5-12.	1.0	55
123	Kinesin Family Member 12 Is a Candidate Polycystic Kidney Disease Modifier in the cpk Mouse. <i>Journal of the American Society of Nephrology: JASN</i> , 2005, 16, 905-916.	3.0	55
124	<i>R2d2</i> Drives Selfish Sweeps in the House Mouse. <i>Molecular Biology and Evolution</i> , 2016, 33, 1381-1395.	3.5	55
125	Precise genetic mapping and integrative bioinformatics in Diversity Outbred mice reveals Hydin as a novel pain gene. <i>Mammalian Genome</i> , 2014, 25, 211-222.	1.0	54
126	Genetic Drivers of Pancreatic Islet Function. <i>Genetics</i> , 2018, 209, 335-356.	1.2	54



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127	Test- and behavior-specific genetic factors affect WKY hypoactivity in tests of emotionality. <i>Behavioural Brain Research</i> , 2006, 169, 220-230.	1.2	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. <i>Journal of Bone and Mineral Research</i> , 2010, 25, 1808-1820.	3.1	53
129	Exploration of Low-Dose Estrogen Effects: Identification of No Observed Transcriptional Effect Level (NOTEL). <i>Toxicologic Pathology</i> , 2004, 32, 482-492.	0.9	53
130	Effects of atherogenic diet on hepatic gene expression across mouse strains. <i>Physiological Genomics</i> , 2009, 39, 172-182.	1.0	52
131	Structural Variation Shapes the Landscape of Recombination in Mouse. <i>Genetics</i> , 2017, 206, 603-619.	1.2	51
132	Quantitative trait loci that determine plasma lipids and obesity in C57BL/6J and 129S1/SvImJ inbred mice. <i>Journal of Lipid Research</i> , 2004, 45, 1624-1632.	2.0	50
133	Genetic analysis of the stress-responsive adrenocortical axis. <i>Physiological Genomics</i> , 2006, 27, 362-369.	1.0	50
134	Epistatic Networks Jointly Influence Phenotypes Related to Metabolic Disease and Gene Expression in Diversity Outbred Mice. <i>Genetics</i> , 2017, 206, 621-639.	1.2	50
135	Sex, flies and microarrays. <i>Nature Genetics</i> , 2001, 29, 355-356.	9.4	49
136	Genetic analysis of blood pressure in C3H/HeJ and SWR/J mice. <i>Physiological Genomics</i> , 2004, 17, 215-220.	1.0	49
137	The Genome of C57BL/6J "Eve", the Mother of the Laboratory Mouse Genome Reference Strain. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1795-1805.	0.8	49
138	A General Bayesian Approach to Analyzing Diallel Crosses of Inbred Strains. <i>Genetics</i> , 2012, 190, 413-435.	1.2	47
139	Major Locus on Mouse Chromosome 17 and Minor Locus on Chromosome 9 are Linked with Alopecia Areata in C3H/HeJ Mice. <i>Journal of Investigative Dermatology</i> , 2003, 120, 771-775.	0.3	46
140	Quantitative trait loci that determine lipoprotein cholesterol levels in DBA/2J and CAST/Ei inbred mice. <i>Journal of Lipid Research</i> , 2003, 44, 953-967.	2.0	46
141	Quantitative Trait Loci Modulate Renal Cystic Disease Severity in the Mouse bpk Model. <i>Journal of the American Society of Nephrology: JASN</i> , 2000, 11, 1253-1260.	3.0	46
142	Bayesian model selection reveals biological origins of zero inflation in single-cell transcriptomics. <i>Genome Biology</i> , 2020, 21, 183.	3.8	45
143	Methods for inferring phylogenies from nucleic acid sequence data by using maximum likelihood and linear invariants. <i>Molecular Biology and Evolution</i> , 1991, 8, 128-43.	3.5	45
144	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

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145	Mapping Complex Traits in a Diversity Outbred F1 Mouse Population Identifies Germline Modifiers of Metastasis in Human Prostate Cancer. <i>Cell Systems</i> , 2017, 4, 31-45.e6.	2.9	44
146	A large-scale genome-wide lipid association map guides lipid identification. <i>Nature Metabolism</i> , 2020, 2, 1149-1162.	5.1	43
147	Applying Gene Expression, Proteomics and Single-Nucleotide Polymorphism Analysis for Complex Trait Gene Identification. <i>Genetics</i> , 2008, 178, 1795-1805.	1.2	42
148	Genome-Wide Association Mapping of Quantitative Traits in Outbred Mice. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 167-174.	0.8	42
149	Imputation of Single-Nucleotide Polymorphisms in Inbred Mice Using Local Phylogeny. <i>Genetics</i> , 2012, 190, 449-458.	1.2	42
150	The Reconstruction of Ancestral Character States. <i>Evolution; International Journal of Organic Evolution</i> , 1996, 50, 504.	1.1	41
151	Genetic Modifiers of Polycystic Kidney Disease in Intersubspecific KAT2J Mutants. <i>Genomics</i> , 1999, 58, 129-137.	1.3	41
152	Locating Ath8, a locus for murine atherosclerosis susceptibility and testing several of its candidate genes in mice and humans. <i>Atherosclerosis</i> , 2004, 177, 443-450.	0.4	41
153	Interacting genetic loci cause airway hyperresponsiveness. <i>Physiological Genomics</i> , 2005, 21, 105-111.	1.0	41
154	High-fat diet leads to tissue-specific changes reflecting risk factors for diseases in DBA/2J mice. <i>Physiological Genomics</i> , 2010, 42, 55-66.	1.0	41
155	Doxorubicin-Induced Cardiotoxicity in Collaborative Cross (CC) Mice Recapitulates Individual Cardiotoxicity in Humans. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2637-2646.	0.8	41
156	Network models for sequence evolution. <i>Journal of Molecular Evolution</i> , 1993, 37, 77-85.	0.8	39
157	Interacting QTLs for cholesterol gallstones and gallbladder mucin in AKR and SWR strains of mice. <i>Physiological Genomics</i> , 2002, 8, 67-77.	1.0	39
158	Quantitative Trait Loci That Determine BMD in C57BL/6J and 129S1/SvImJ Inbred Mice. <i>Journal of Bone and Mineral Research</i> , 2005, 21, 105-112.	3.1	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. <i>Immunogenetics</i> , 2003, 55, 491-496.	1.2	38
160	Association of a lithogenic Abcg5/Abcg8 allele on Chromosome 17 (Lith9) with cholesterol gallstone formation in PERA/Eij mice. <i>Mammalian Genome</i> , 2005, 16, 495-504.	1.0	38
161	Naive Pluripotent Stem Cells Exhibit Phenotypic Variability that Is Driven by Genetic Variation. <i>Cell Stem Cell</i> , 2020, 27, 470-481.e6.	5.2	38
162	Integrative Genetic Analysis of Allergic Inflammation in the Murine Lung. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2014, 51, 436-445.	1.4	37

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