

# Gary A Churchill

## List of Publications by Year in descending order

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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	Intermittent fasting and caloric restriction interact with genetics to shape physiological health in mice. <i>Genetics</i> , 2022, 220, .	2.9	3
2	Prediction performance of linear models and gradient boosting machine on complex phenotypes in outbred mice. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	7
3	A Bayesian model selection approach to mediation analysis. <i>PLoS Genetics</i> , 2022, 18, e1010184.	3.5	8
4	QTLViewer: an interactive webtool for genetic analysis in the Collaborative Cross and Diversity Outbred mouse populations. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	8
5	Life-long dietary restrictions have negligible or damaging effects on late-life cognitive performance: A key role for genetics in outcomes. <i>Neurobiology of Aging</i> , 2022, 118, 108-116.	3.1	2
6	Strain-Specific Peptide (SSP) Interference Reference Sample: A Genetically Encoded Quality Control for Isobaric Tagging Strategies. <i>Analytical Chemistry</i> , 2021, 93, 5241-5247.	6.5	8
7	Proteomic and transcriptomic profiling reveal different aspects of aging in the kidney. <i>ELife</i> , 2021, 10, .	6.0	62
8	Heritability of fat distributions in male mice from the founder strains of the Diversity Outbred mouse population. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	2
9	The Jackson Laboratory Nathan Shock Center: impact of genetic diversity on aging. <i>GeroScience</i> , 2021, 43, 2129-2137.	4.6	4
10	INFIMA leverages multi-omics model organism data to identify effector genes of human GWAS variants. <i>Genome Biology</i> , 2021, 22, 241.	8.8	3
11	Sex-specific phenotypic effects and evolutionary history of an ancient polymorphic deletion of the human growth hormone receptor. <i>Science Advances</i> , 2021, 7, eabi4476.	10.3	11
12	Regulation of protein abundance in genetically diverse mouse populations. <i>Cell Genomics</i> , 2021, 1, 100003.	6.5	27
13	A systems approach using Diversity Outbred mice distinguishes the cardiovascular effects and genetics of circulating GDF11 from those of its homolog, myostatin. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	1.8	1
14	Fasting blood glucose as a predictor of mortality: Lost in translation. <i>Cell Metabolism</i> , 2021, 33, 2189-2200.e3.	16.2	29
15	Quantitative trait mapping in Diversity Outbred mice identifies novel genomic regions associated with the hepatic glutathione redox system. <i>Redox Biology</i> , 2021, 46, 102093.	9.0	5
16	Genetic mapping of renal glutathione suggests a novel regulatory locus on the murine X chromosome and overlap with hepatic glutathione regulation. <i>Free Radical Biology and Medicine</i> , 2021, 174, 28-39.	2.9	1
17	The dihydropyrimidine dehydrogenase gene contributes to heritable differences in sleep in mice. <i>Current Biology</i> , 2021, 31, 5238-5248.e7.	3.9	5
18	Misexpression of genes lacking CpG islands drives degenerative changes during aging. <i>Science Advances</i> , 2021, 7, eabj9111.	10.3	8

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19	Cross-Species Analyses Identify Dlgap2 as a Regulator of Age-Related Cognitive Decline and Alzheimer's Dementia. <i>Cell Reports</i> , 2020, 32, 108091.	6.4	27
20	Nine quick tips for efficient bioinformatics curriculum development and training. <i>PLoS Computational Biology</i> , 2020, 16, e1008007.	3.2	4
21	Bayesian model selection reveals biological origins of zero inflation in single-cell transcriptomics. <i>Genome Biology</i> , 2020, 21, 183.	8.8	45
22	Naive Pluripotent Stem Cells Exhibit Phenotypic Variability that Is Driven by Genetic Variation. <i>Cell Stem Cell</i> , 2020, 27, 470-481.e6.	11.1	38
23	Mapping the Effects of Genetic Variation on Chromatin State and Gene Expression Reveals Loci That Control Ground State Pluripotency. <i>Cell Stem Cell</i> , 2020, 27, 459-469.e8.	11.1	31
24	A large-scale genome-wide lipid association map guides lipid identification. <i>Nature Metabolism</i> , 2020, 2, 1149-1162.	11.9	43
25	High-throughput sleep phenotyping produces robust and heritable traits in Diversity Outbred mice and their founder strains. <i>Sleep</i> , 2020, 43, .	1.1	21
26	Doxorubicin-Induced Cardiotoxicity in Collaborative Cross (CC) Mice Recapitulates Individual Cardiotoxicity in Humans. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 2637-2646.	1.8	41
27	A Bayesian mixture model for the analysis of allelic expression in single cells. <i>Nature Communications</i> , 2019, 10, 5188.	12.8	18
28	Genetic determinants of gut microbiota composition and bile acid profiles in mice. <i>PLoS Genetics</i> , 2019, 15, e1008073.	3.5	75
29	R/qtl2: Software for Mapping Quantitative Trait Loci with High-Dimensional Data and Multiparent Populations. <i>Genetics</i> , 2019, 211, 495-502.	2.9	333
30	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.	1.8	49
31	Mouse genome-wide association and systems genetics identifies Lhfp as a regulator of bone mass. <i>PLoS Genetics</i> , 2019, 15, e1008123.	3.5	22
32	Cleaning Genotype Data from Diversity Outbred Mice. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1571-1579.	1.8	21
33	Genetic mapping in Diversity Outbred mice identifies a Trpa1 variant influencing late-phase formalin response. <i>Pain</i> , 2019, 160, 1740-1753.	4.2	22
34	Gene loci associated with insulin secretion in islets from nondiabetic mice. <i>Journal of Clinical Investigation</i> , 2019, 129, 4419-4432.	8.2	60
35	Hierarchical analysis of RNA-seq reads improves the accuracy of allele-specific expression. <i>Bioinformatics</i> , 2018, 34, 2177-2184.	4.1	101
36	Genetic Drivers of Pancreatic Islet Function. <i>Genetics</i> , 2018, 209, 335-356.	2.9	54

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37	Genetic background influences susceptibility to chemotherapy-induced hematotoxicity. <i>Pharmacogenomics Journal</i> , 2018, 18, 319-330.	2.0	20
38	A multi-tissue full lifespan epigenetic clock for mice. <i>Aging</i> , 2018, 10, 2832-2854.	3.1	166
39	Structural Variation Shapes the Landscape of Recombination in Mouse. <i>Genetics</i> , 2017, 206, 603-619.	2.9	51
40	Epistatic Networks Jointly Influence Phenotypes Related to Metabolic Disease and Gene Expression in Diversity Outbred Mice. <i>Genetics</i> , 2017, 206, 621-639.	2.9	50
41	How mice are indispensable for understanding obesity and diabetes genetics. <i>Current Opinion in Endocrinology, Diabetes and Obesity</i> , 2017, 24, 83-91.	2.3	29
42	Genomes of the Mouse Collaborative Cross. <i>Genetics</i> , 2017, 206, 537-556.	2.9	189
43	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.	6.2	44
44	High-Resolution Maps of Mouse Reference Populations. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3427-3434.	1.8	27
45	The Mouse Universal Genotyping Array: From Substrains to Subspecies. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 263-279.	1.8	199
46	Diversity Outbred Mice at 21: Maintaining Allelic Variation in the Face of Selection. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3893-3902.	1.8	66
47	Accessing Data Resources in the Mouse Phenome Database for Genetic Analysis of Murine Life Span and Health Span. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2016, 71, 170-177.	3.6	32
48	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.	2.7	58
49	Eric Lander and David Botstein on Mapping Quantitative Traits. <i>Genetics</i> , 2016, 203, 1-3.	2.9	9
50	Genetic identification of thiosulfate sulfurtransferase as an adipocyte-expressed antidiabetic target in mice selected for leanness. <i>Nature Medicine</i> , 2016, 22, 771-779.	30.7	57
51	Defining the consequences of genetic variation on a proteome-wide scale. <i>Nature</i> , 2016, 534, 500-505.	27.8	335
52	Genetic Architectures of Quantitative Variation in RNA Editing Pathways. <i>Genetics</i> , 2016, 202, 787-798.	2.9	25
53	<i>Ucp1</i> Drives Selfish Sweeps in the House Mouse. <i>Molecular Biology and Evolution</i> , 2016, 33, 1381-1395.	8.9	55
54	Weak Epistasis Generally Stabilizes Phenotypes in a Mouse Intercross. <i>PLoS Genetics</i> , 2016, 12, e1005805.	3.5	28

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55	Aging Research Using Mouse Models. <i>Current Protocols in Mouse Biology</i> , 2015, 5, 95-133.	1.2	92
56	High-Density Genotypes of Inbred Mouse Strains: Improved Power and Precision of Association Mapping. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 2021-2026.	1.8	37
57	Genetic Analysis of Substrain Divergence in Non-Obese Diabetic (NOD) Mice. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 771-775.	1.8	19
58	Genome Wide Identification of SARS-CoV Susceptibility Loci Using the Collaborative Cross. <i>PLoS Genetics</i> , 2015, 11, e1005504.	3.5	137
59	A Multi-Megabase Copy Number Gain Causes Maternal Transmission Ratio Distortion on Mouse Chromosome 2. <i>PLoS Genetics</i> , 2015, 11, e1004850.	3.5	76
60	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.	3.6	80
61	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.	6.0	111
62	Identification of microRNAs associated with allergic airway disease using a genetically diverse mouse population. <i>BMC Genomics</i> , 2015, 16, 633.	2.8	22
63	Collaborative Cross and Diversity Outbred data resources in the Mouse Phenome Database. <i>Mammalian Genome</i> , 2015, 26, 511-520.	2.2	66
64	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.	8.8	225
65	Genetic Regulation of Female Sexual Maturation and Longevity Through Circulating IGF1. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2015, 70, 817-826.	3.6	8
66	Genetic Regulation of <i>Zfp30</i> , <i>CXCL1</i> , and Neutrophilic Inflammation in Murine Lung. <i>Genetics</i> , 2014, 198, 735-745.	2.9	44
67	Integrative Genetic Analysis of Allergic Inflammation in the Murine Lung. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2014, 51, 436-445.	2.9	37
68	Quantitative Trait Locus Mapping Methods for Diversity Outbred Mice. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 1623-1633.	1.8	195
69	High-Resolution Sex-Specific Linkage Maps of the Mouse Reveal Polarized Distribution of Crossovers in Male Germline. <i>Genetics</i> , 2014, 197, 91-106.	2.9	85
70	RNA-Seq Alignment to Individualized Genomes Improves Transcript Abundance Estimates in Multiparent Populations. <i>Genetics</i> , 2014, 198, 59-73.	2.9	82
71	Misleading Results: Don't Blame the Mice. <i>Science</i> , 2014, 343, 370-370.	12.6	5
72	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.	2.7	68

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73	When Are Results Too Good to Be True?. <i>Genetics</i> , 2014, 198, 447-448.	2.9	10
74	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.	2.2	54
75	38 MOUSE VOIDING PATTERNS ARE STRAIN-SPECIFIC: A NOVEL ASSAY FOR AGE-RELATED DEVELOPMENT OF LOWER URINARY TRACT SYMPTOMS (LUTS). <i>Journal of Urology</i> , 2013, 189, .	0.4	0
76	C57BL/6N Mutation in <i>Cytoplasmic FMRP interacting protein 2</i> Regulates Cocaine Response. <i>Science</i> , 2013, 342, 1508-1512.	12.6	198
77	Relationship between obesity phenotypes and genetic determinants in a mouse model for juvenile obesity. <i>Physiological Genomics</i> , 2013, 45, 817-826.	2.3	2
78	Modeling Host Genetic Regulation of Influenza Pathogenesis in the Collaborative Cross. <i>PLoS Pathogens</i> , 2013, 9, e1003196.	4.7	183
79	High-precision genetic mapping of behavioral traits in the diversity outbred mouse population. <i>Genes, Brain and Behavior</i> , 2013, 12, 424-437.	2.2	110
80	Students as Collaborators in Systems Biology Research. <i>Science</i> , 2013, 340, 1061-1062.	12.6	1
81	Integration of Mouse and Human Genome-Wide Association Data Identifies KCNIP4 as an Asthma Gene. <i>PLoS ONE</i> , 2013, 8, e56179.	2.5	28
82	Genetic analysis of albuminuria in collaborative cross and multiple mouse intercross populations. <i>American Journal of Physiology - Renal Physiology</i> , 2012, 303, F972-F981.	2.7	19
83	What Can Causal Networks Tell Us about Metabolic Pathways?. <i>PLoS Computational Biology</i> , 2012, 8, e1002458.	3.2	20
84	Using bioinformatics and systems genetics to dissect HDL-cholesterol genetics in an MRL/MpJ $\times$ SM/J intercross. <i>Journal of Lipid Research</i> , 2012, 53, 1163-1175.	4.2	13
85	Ten Years of the Collaborative Cross. G3: Genes, Genomes, <i>Genetics</i> , 2012, 2, 153-156.	1.8	78
86	Adaptive Evolution and Effective Population Size in Wild House Mice. <i>Molecular Biology and Evolution</i> , 2012, 29, 2949-2955.	8.9	73
87	Genome-Wide Association Mapping of Quantitative Traits in Outbred Mice. G3: Genes, Genomes, <i>Genetics</i> , 2012, 2, 167-174.	1.8	42
88	Ten Years of the Collaborative Cross. <i>Genetics</i> , 2012, 190, 291-294.	2.9	128
89	Genetic Analysis of Hematological Parameters in Incipient Lines of the Collaborative Cross. G3: Genes, Genomes, <i>Genetics</i> , 2012, 2, 157-165.	1.8	80
90	Imputation of Single-Nucleotide Polymorphisms in Inbred Mice Using Local Phylogeny. <i>Genetics</i> , 2012, 190, 449-458.	2.9	42

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91	High-Resolution Genetic Mapping Using the Mouse Diversity Outbred Population. <i>Genetics</i> , 2012, 190, 437-447.	2.9	437
92	A General Bayesian Approach to Analyzing Diallel Crosses of Inbred Strains. <i>Genetics</i> , 2012, 190, 413-435.	2.9	47
93	The diversity outbred mouse population. <i>Mammalian Genome</i> , 2012, 23, 713-718.	2.2	406
94	Discovery of novel variants in genotyping arrays improves genotype retention and reduces ascertainment bias. <i>BMC Genomics</i> , 2012, 13, 34.	2.8	61
95	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.	4.8	83
96	Gene expression patterns in the hippocampus and amygdala of endogenous depression and chronic stress models. <i>Molecular Psychiatry</i> , 2012, 17, 49-61.	7.9	165
97	Pla2g12b and Hpn Are Genes Identified by Mouse ENU Mutagenesis That Affect HDL Cholesterol. <i>PLoS ONE</i> , 2012, 7, e43139.	2.5	29
98	Genetic Susceptibility To Allergen-Induced Airway Inflammation In Mice. , 2011, , .		0
99	Subspecific origin and haplotype diversity in the laboratory mouse. <i>Nature Genetics</i> , 2011, 43, 648-655.	21.4	439
100	The future of model organisms in human disease research. <i>Nature Reviews Genetics</i> , 2011, 12, 575-582.	16.3	66
101	Stochastic variation of transcript abundance in C57BL/6J mice. <i>BMC Genomics</i> , 2011, 12, 167.	2.8	25
102	Integration of QTL and bioinformatic tools to identify candidate genes for triglycerides in mice. <i>Journal of Lipid Research</i> , 2011, 52, 1672-1682.	4.2	26
103	Uncovering Genes and Regulatory Pathways Related to Urinary Albumin Excretion. <i>Journal of the American Society of Nephrology: JASN</i> , 2011, 22, 73-81.	6.1	11
104	A Bayesian Framework for Inference of the Genotype-Phenotype Map for Segregating Populations. <i>Genetics</i> , 2011, 187, 1163-1170.	2.9	36
105	Genetic analysis of complex traits in the emerging Collaborative Cross. <i>Genome Research</i> , 2011, 21, 1213-1222.	5.5	327
106	Genetic analysis in the Collaborative Cross breeding population. <i>Genome Research</i> , 2011, 21, 1223-1238.	5.5	158
107	The Collaborative Cross: A Recombinant Inbred Mouse Population for the Systems Genetic Era. <i>ILAR Journal</i> , 2011, 52, 24-31.	1.8	183
108	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.	3.5	58

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109	Abstract 4387: Diversity Outbred: a new, highly diverse mouse stock for toxicology and cancer. , 2011, , .		0
110	CGDSNPdb: a database resource for error-checked and imputed mouse SNPs. Database: the Journal of Biological Databases and Curation, 2010, 2010, baq008.	3.0	8
111	Sequence variation at multiple loci influences red cell hemoglobin concentration. Blood, 2010, 116, e139-e149.	1.4	13
112	Critical reasoning on causal inference in genome-wide linkage and association studies. Trends in Genetics, 2010, 26, 493-498.	6.7	59
113	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
114	Identification of genetic determinants of IGFâ€1 levels and longevity among mouse inbred strains. Aging Cell, 2010, 9, 823-836.	6.7	32
115	INNATE IMMUNE GENE DISCOVERY USING MACROPHAGE RESPONSE TO PATHOGEN-ASSOCIATED MOLECULAR PATTERNS (PAMPS). , 2010, , .		0
116	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
117	Epistasis contributes to the genetic buffering of plasma HDL cholesterol in mice. Physiological Genomics, 2010, 42A, 228-234.	2.3	6
118	Coordinated Expression Domains in Mammalian Genomes. PLoS ONE, 2010, 5, e12158.	2.5	29
119	A New Standard Genetic Map for the Laboratory Mouse. Genetics, 2009, 182, 1335-1344.	2.9	202
120	Importance of randomization in microarray experimental designs with Illumina platforms. Nucleic Acids Research, 2009, 37, 5610-5618.	14.5	29
121	Effects of atherogenic diet on hepatic gene expression across mouse strains. Physiological Genomics, 2009, 39, 172-182.	2.3	52
122	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
123	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
124	Genetic Analysis of Blood Pressure in 8 Mouse Intercross Populations. Hypertension, 2009, 54, 802-809.	2.7	33
125	Chromosome Y variants from different inbred mouse strains are linked to differences in the morphologic and molecular responses of cardiac cells to postpubertal testosterone. BMC Genomics, 2009, 10, 150.	2.8	15
126	PPARÎ² 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



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127	A Cmv2 QTL on chromosome X affects MCMV resistance in New Zealand male mice. <i>Mammalian Genome</i> , 2009, 20, 414-423.	2.2	4
128	Identification of genetic loci involved in diabetes using a rat model of depression. <i>Mammalian Genome</i> , 2009, 20, 486-497.	2.2	14
129	A customized and versatile high-density genotyping array for the mouse. <i>Nature Methods</i> , 2009, 6, 663-666.	19.0	236
130	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.	6.7	359
131	What are microarrays teaching us about sleep?. <i>Trends in Molecular Medicine</i> , 2009, 15, 79-87.	6.7	70
132	Genetic factors contributing to obesity and body weight can act through mechanisms affecting muscle weight, fat weight, or both. <i>Physiological Genomics</i> , 2009, 36, 114-126.	2.3	21
133	Quantitative Trait Locus Analysis Using J/qtl. <i>Methods in Molecular Biology</i> , 2009, 573, 175-188.	0.9	31
134	An imputed genotype resource for the laboratory mouse. <i>Mammalian Genome</i> , 2008, 19, 199-208.	2.2	79
135	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.	2.2	111
136	The Collaborative Cross at Oak Ridge National Laboratory: developing a powerful resource for systems genetics. <i>Mammalian Genome</i> , 2008, 19, 382-389.	2.2	245
137	Quantitative Trait Loci for BMD in an SM/J by NZB/BINJ Intercross Population and Identification of <i>Trps1</i> as a Probable Candidate Gene. <i>Journal of Bone and Mineral Research</i> , 2008, 23, 1529-1537.	2.8	27
138	<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.	2.8	56
139	Identification of quantitative trait loci for locomotor activation and anxiety using closely related inbred strains. <i>Genes, Brain and Behavior</i> , 2008, 7, 761-769.	2.2	23
140	Naive Application of Permutation Testing Leads to Inflated Type I Error Rates. <i>Genetics</i> , 2008, 178, 609-610.	2.9	59
141	Relationships of dietary fat, body composition, and bone mineral density in inbred mouse strain panels. <i>Physiological Genomics</i> , 2008, 33, 26-32.	2.3	19
142	Genetic variation in <i>Glp1r</i> expression influences the rate of gastric emptying in mice. <i>American Journal of Physiology - Regulatory Integrative and Comparative Physiology</i> , 2008, 294, R362-R371.	1.8	14
143	Applying Gene Expression, Proteomics and Single-Nucleotide Polymorphism Analysis for Complex Trait Gene Identification. <i>Genetics</i> , 2008, 178, 1795-1805.	2.9	42
144	Quantitative Trait Loci for Urinary Albumin in Crosses Between C57BL/6J and A/J Inbred Mice in the Presence and Absence of <i>Apoe</i> . <i>Genetics</i> , 2008, 179, 693-699.	2.9	15

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145	Overexpression of innate immune response genes in a model of recessive polycystic kidney disease. <i>Kidney International</i> , 2008, 73, 63-76.	5.2	82
146	Response to $\beta$ -Overexpression of complement-component genes in Han:SPRD rats a model of polycystic kidney disease $\beta$ <sup>TM</sup> . <i>Kidney International</i> , 2008, 73, 1325.	5.2	0
147	Randomization in Laboratory Procedure Is Key to Obtaining Reproducible Microarray Results. <i>PLoS ONE</i> , 2008, 3, e3724.	2.5	33
148	Genetic Evidence That Sequence Variation at the $\beta$ -Globin Locus Underlies Differences in Cell Hemoglobin Concentration and Cell Hydration in Single (Hbbs) Vs. Diffuse (Hbbd) Inbred Mouse Strains: Implications for Inherited Anemias. <i>Blood</i> , 2008, 112, 419-419.	1.4	0
149	Genetic analysis of albuminuria in a cross between C57BL/6J and DBA/2J mice. <i>American Journal of Physiology - Renal Physiology</i> , 2007, 293, F1649-F1656.	2.7	35
150	Evidence of a Large-Scale Functional Organization of Mammalian Chromosomes. <i>PLoS Biology</i> , 2007, 5, e127.	5.6	16
151	Genetic Background Modifies Inner Ear and Eye Phenotypes of Jag1 Heterozygous Mice. <i>Genetics</i> , 2007, 177, 307-311.	2.9	23
152	Statistical design and the analysis of gene expression microarray data. <i>Genetical Research</i> , 2007, 89, 509-514.	0.9	195
153	Estimating $p$ -values in small microarray experiments. <i>Bioinformatics</i> , 2007, 23, 38-43.	4.1	65
154	Sequential Quantitative Trait Locus Mapping in Experimental Crosses. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2007, 6, Article12.	0.6	9
155	Identification of conserved gene expression features between murine mammary carcinoma models and human breast tumors. <i>Genome Biology</i> , 2007, 8, R76.	9.6	1,009
156	Macromolecule biosynthesis: a key function of sleep. <i>Physiological Genomics</i> , 2007, 31, 441-457.	2.3	322
157	Modifier locus for exencephaly in <i>Cecr2</i> mutant mice is syntenic to the 10q25.3 region associated with neural tube defects in humans. <i>Physiological Genomics</i> , 2007, 31, 244-251.	2.3	16
158	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.	2.5	160
159	Recombinant inbred strain panels: a tool for systems genetics. <i>Physiological Genomics</i> , 2007, 31, 174-175.	2.3	20
160	Characterization of human embryonic stem cell lines by the International Stem Cell Initiative. <i>Nature Biotechnology</i> , 2007, 25, 803-816.	17.5	983
161	On the subspecific origin of the laboratory mouse. <i>Nature Genetics</i> , 2007, 39, 1100-1107.	21.4	281
162	The mouse as a model for human biology: a resource guide for complex trait analysis. <i>Nature Reviews Genetics</i> , 2007, 8, 58-69.	16.3	270

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