Richard F Mott

List of Publications by Year
in descending order

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179 papers	35,352 citations	11608 70 h-index	3815 178 g-index
199 all docs	199 docs citations	199 times ranked	37634 citing authors

#	ARTICLE	IF	CITATIONS
1	A novel gene containing a trinucleotide repeat that is expanded and unstable on Huntington's disease chromosomes. Cell, 1993, 72, 971-983.	13.5	7,960
2	Initial sequencing and comparative analysis of the mouse genome. Nature, 2002, 420, 520-562.	13.7	6,319
3	Mouse genomic variation and its effect on phenotypes and gene regulation. Nature, 2011, 477, 289-294.	13.7	1,461
4	1,135 Genomes Reveal the Global Pattern of Polymorphism in Arabidopsis thaliana. Cell, 2016, 166, 481-491.	13.5	1,107
5	The Collaborative Cross, a community resource for the genetic analysis of complex traits. Nature Genetics, 2004, 36, 1133-1137.	9.4	1,034
6	Chromatin accessibility pre-determines glucocorticoid receptor binding patterns. Nature Genetics, 2011, 43, 264-268.	9.4	854
7	Recent improvements to the SMART domain-based sequence annotation resource. Nucleic Acids Research, 2002, 30, 242-244.	6.5	613
8	Epigenomic Diversity in a Global Collection of Arabidopsis thaliana Accessions. Cell, 2016, 166, 492-505.	13.5	594
9	Multiple reference genomes and transcriptomes for Arabidopsis thaliana. Nature, 2011, 477, 419-423.	13.7	593
10	A Multiparent Advanced Generation Inter-Cross to Fine-Map Quantitative Traits in Arabidopsis thaliana. PLoS Genetics, 2009, 5, e1000551.	1.5	554
11	Genome-wide genetic association of complex traits in heterogeneous stock mice. Nature Genetics, 2006, 38, 879-887.	9.4	508
12	Strategies for mapping and cloning quantitative trait genes in rodents. Nature Reviews Genetics, 2005, 6, 271-286.	7.7	462
13	Subspecific origin and haplotype diversity in the laboratory mouse. Nature Genetics, 2011, 43, 648-655.	9.4	439
14	The 1001 Genomes Project for Arabidopsis thaliana. Genome Biology, 2009, 10, 107.	13.9	420
15	A first-generation linkage disequilibrium map of human chromosome 22. Nature, 2002, 418, 544-548.	13.7	376
16	Modularly assembled designer TAL effector nucleases for targeted gene knockout and gene replacement in eukaryotes. Nucleic Acids Research, 2011, 39, 6315-6325.	6.5	368
17	Genetic analysis of complex traits in the emerging Collaborative Cross. Genome Research, 2011, 21, 1213-1222.	2.4	327
18	Genome-wide analysis reveals novel molecular features of mouse recombination hotspots. Nature, 2011, 472, 375-378.	13.7	325

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19	Instability of highly expanded CAG repeats in mice transgenic for the Huntington's disease mutation. Nature Genetics, 1997, 15, 197-200.	9.4	302
20	Positional cloning of a quantitative trait locus on chromosome 13q14 that influences immunoglobulin E levels and asthma. Nature Genetics, 2003, 34, 181-186.	9.4	300
21	Sequence-based characterization of structural variation in the mouse genome. Nature, 2011, 477, 326-329.	13.7	299
22	Replication timing of the human genome. Human Molecular Genetics, 2004, 13, 191-202.	1.4	295
23	Adaptive Introgression of Anticoagulant Rodent Poison Resistance by Hybridization between Old World Mice. Current Biology, 2011, 21, 1296-1301.	1.8	282
24	Finding the molecular basis of quatitative traits: successes and pitfalls. Nature Reviews Genetics, 2001, 2, 437-445.	7.7	280
25	High resolution cosmid and P1 maps spanning the 14 Mb genome of the fission yeast S. pombe. Cell, 1993, 73, 109-120.	13.5	271
26	Genetic dissection of a behavioral quantitative trait locus shows that Rgs2 modulates anxiety in mice. Nature Genetics, 2004, 36, 1197-1202.	9.4	268
27	A High-Resolution Single Nucleotide Polymorphism Genetic Map of the Mouse Genome. PLoS Biology, 2006, 4, e395.	2.6	243
28	Genomic clusters, putative pathogen recognition molecules, and antimicrobial genes are induced by infection of C. elegans with M. nematophilum. Genome Research, 2006, 16, 1005-1016.	2.4	225
29	Molecular Signatures of Major Depression. Current Biology, 2015, 25, 1146-1156.	1.8	224
30	Prevalence of sexual dimorphism in mammalian phenotypic traits. Nature Communications, 2017, 8, 15475.	5.8	200
31	Environmentally responsive genome-wide accumulation of de novo <i>Arabidopsis thaliana</i> mutations and epimutations. Genome Research, 2014, 24, 1821-1829.	2.4	194
32	Linkage Analysis of Extremely Discordant and Concordant Sibling Pairs Identifies Quantitative-Trait Loci That Influence Variation in the Human Personality Trait Neuroticism. American Journal of Human Genetics, 2003, 72, 879-890.	2.6	180
33	ROS-mediated vascular homeostatic control of root-to-shoot soil Na delivery in<i>Arabidopsis</i>. EMBO Journal, 2012, 31, 4359-4370.	3.5	178
34	Combined sequence-based and genetic mapping analysis of complex traits in outbred rats. Nature Genetics, 2013, 45, 767-775.	9.4	176
35	SNP and haplotype mapping for genetic analysis in the rat. Nature Genetics, 2008, 40, 560-566.	9.4	172
36	Rapid genotype imputation from sequence without reference panels. Nature Genetics, 2016, 48, 965-969.	9.4	172

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37	Sixteen diverse laboratory mouse reference genomes define strain-specific haplotypes and novel functional loci. Nature Genetics, 2018, 50, 1574-1583.	9.4	169
38	Simulating the Collaborative Cross: Power of Quantitative Trait Loci Detection and Mapping Resolution in Large Sets of Recombinant Inbred Strains of Mice. Genetics, 2006, 172, 1783-1797.	1.2	168
39	Candidate-Gene Screening and Association Analysis at the Autism-Susceptibility Locus on Chromosome 16p: Evidence of Association at GRIN2A and ABAT. American Journal of Human Genetics, 2005, 76, 950-966.	2.6	165
40	Genetic and Environmental Effects on Complex Traits in Mice. Genetics, 2006, 174, 959-984.	1.2	161
41	Genetic Architecture of Flowering-Time Variation in <i>Arabidopsis thaliana</i>. Genetics, 2011, 188, 421-433.	1.2	160
42	Collaborative Cross mice and their power to map host susceptibility to<i>Aspergillus fumigatus</i>infection. Genome Research, 2011, 21, 1239-1248.	2.4	138
43	Status and access to the Collaborative Cross population. Mammalian Genome, 2012, 23, 706-712.	1.0	134
44	A Quantitative Trait Locus Influencing Anxiety in the Laboratory Rat. Genome Research, 2002, 12, 618-626.	2.4	133
45	Quantifying the Similarities within Fold Space. Journal of Molecular Biology, 2002, 323, 909-926.	2.0	133
46	Mapping in Structured Populations by Resample Model Averaging. Genetics, 2009, 182, 1263-1277.	1.2	133
47	Genome-wide association of multiple complex traits in outbred mice by ultra-low-coverage sequencing. Nature Genetics, 2016, 48, 912-918.	9.4	124
48	Multi-parent populations in crops: a toolbox integrating genomics and genetic mapping with breeding. Heredity, 2020, 125, 396-416.	1.2	124
49	Commercially Available Outbred Mice for Genome-Wide Association Studies. PLoS Genetics, 2010, 6, e1001085.	1.5	122
50	Genome-wide analysis of mutations in mutant lineages selected following fast-neutron irradiation mutagenesis of <i>Arabidopsis thaliana</i>. Genome Research, 2012, 22, 1306-1315.	2.4	119
51	Accurate formula for P-values of gapped local sequence and profile alignments. Journal of Molecular Biology, 2000, 300, 649-659.	2.0	115
52	Genomewide Analysis of the Host Response to Malaria in Kenyan Children. Journal of Infectious Diseases, 2005, 191, 1599-1611.	1.9	111
53	The Collaborative Cross, developing a resource for mammalian systems genetics: A status report of the Wellcome Trust cohort. Mammalian Genome, 2008, 19, 379-381.	1.0	111
54	Novel Protein Domains and Repeats in Drosophila melanogaster: Insights into Structure, Function, and Evolution. Genome Research, 2001, 11, 1996-2008.	2.4	109

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55	Ablating Adult Neurogenesis in the Rat Has No Effect on Spatial Processing: Evidence from a Novel Pharmacogenetic Model. PLoS Genetics, 2013, 9, e1003718.	1.5	107
56	A cosmid contig and high resolution restriction map of the 2 megabase region containing the Huntington's disease gene. Nature Genetics, 1993, 4, 181-186.	9.4	102
57	Quantitative prediction of NF-ÂB DNA- protein interactions. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 8167-8172.	3.3	102
58	The Architecture of Parent-of-Origin Effects in Mice. Cell, 2014, 156, 332-342.	13.5	100
59	Complete coverage of the Schizosaccharomyces pombe genome in yeast artificial chromosomes. Nature Genetics, 1992, 1, 273-277.	9.4	99
60	A protocol for high-throughput phenotyping, suitable for quantitative trait analysis in mice. Mammalian Genome, 2006, 17, 129-146.	1.0	99
61	Predicting Protein Cellular Localization Using a Domain Projection Method. Genome Research, 2002, 12, 1168-1174.	2.4	97
62	A multiple-phenotype imputation method for genetic studies. Nature Genetics, 2016, 48, 466-472.	9.4	93
63	The Cardamine hirsuta genome offers insight into the evolution of morphological diversity. Nature Plants, 2016, 2, 16167.	4.7	90
64	SW-ARRAY: a dynamic programming solution for the identification of copy-number changes in genomic DNA using array comparative genome hybridization data. Nucleic Acids Research, 2005, 33, 3455-3464.	6.5	87
65	Genetic Control over mtDNA and Its Relationship to Major Depressive Disorder. Current Biology, 2015, 25, 3170-3177.	1.8	84
66	Maximum-likelihood estimation of the statistical distribution of Smith-Waterman local sequence similarity scores. Bulletin of Mathematical Biology, 1992, 54, 59-75.	0.9	82
67	Regenerant Arabidopsis Lineages Display a Distinct Genome-Wide Spectrum of Mutations Conferring Variant Phenotypes. Current Biology, 2011, 21, 1385-1390.	1.8	82
68	Genome-wide sexually antagonistic variants reveal long-standing constraints on sexual dimorphism in fruit flies. PLoS Biology, 2019, 17, e3000244.	2.6	82
69	Algorithms and software tools for ordering clone libraries: application to the mapping of the genome ofSchizosaccharomyces pombe. Nucleic Acids Research, 1993, 21, 1965-1974.	6.5	80
70	An integrated YAC-overlap and â€˜cosmid-pocketâ€™ map of the human chromosome 21. Human Molecular Genetics, 1994, 3, 759-770.	1.4	79
71	Recognizing the fold of a protein structure. Bioinformatics, 2003, 19, 1748-1759.	1.8	79
72	<i>Cardamine hirsuta</i>: a versatile genetic system for comparative studies. Plant Journal, 2014, 78, 1-15.	2.8	78

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73	Simultaneous Detection and Fine Mapping of Quantitative Trait Loci in Mice Using Heterogeneous Stocks. Genetics, 2002, 160, 1609-1618.	1.2	78
74	Sequencing and characterization of the FVB/NJ mouse genome. Genome Biology, 2012, 13, R72.	13.9	76
75	Applying the ARRIVE Guidelines to an In Vivo Database. PLoS Biology, 2015, 13, e1002151.	2.6	75
76	Approximate Statistics of Gapped Alignments. Journal of Computational Biology, 1999, 6, 91-112.	0.8	74
77	A resource for the simultaneous high-resolution mapping of multiple quantitative trait loci in rats: The NIH heterogeneous stock. Genome Research, 2009, 19, 150-158.	2.4	72
78	Quantitative high-throughput analysis of transcription factor binding specificities. Nucleic Acids Research, 2004, 32, 44e-44.	6.5	70
79	Model for a transcript map of human chromosome 21: isolation of new coding sequences from exon and enriched cDNA libraries. Human Molecular Genetics, 1995, 4, 1291-1304.	1.4	69
80	High resolution mapping of expression QTLs in heterogeneous stock mice in multiple tissues. Genome Research, 2009, 19, 1133-1140.	2.4	69
81	Genetic Fineâ€Mapping and Identification of Candidate Genes and Variants for Adiposity Traits in Outbred Rats. Obesity, 2018, 26, 213-222.	1.5	64
82	Comparative gene expression profiling by oligonucleotide fingerprinting. Nucleic Acids Research, 1998, 26, 2216-2223.	6.5	60
83	Haplotypic analysis of the TNF locus by association efficiency and entropy. Genome Biology, 2003, 4, R24.	13.9	59
84	Susceptibility to klebsiella pneumonaie infection in collaborative cross mice is a complex trait controlled by at least three loci acting at different time points. BMC Genomics, 2014, 15, 865.	1.2	55
85	High-fat-diet induced development of increased fasting glucose levels and impaired response to intraperitoneal glucose challenge in the collaborative cross mouse genetic reference population. BMC Genetics, 2016, 17, 10.	2.7	51
86	Structural Variation Shapes the Landscape of Recombination in Mouse. Genetics, 2017, 206, 603-619.	1.2	51
87	Screening for Recently Selected Alleles by Analysis of Human Haplotype Similarity. American Journal of Human Genetics, 2006, 78, 153-159.	2.6	47
88	Heterogeneous Stock Populations for Analysis of Complex Traits. Methods in Molecular Biology, 2017, 1488, 31-44.	0.4	47
89	LD mapping of maternally and non-maternally derived alleles and atopy in FcÎµRI-Î². Human Molecular Genetics, 2003, 12, 2577-2585.	1.4	46
90	Failed gene conversion leads to extensive end processing and chromosomal rearrangements in fission yeast. EMBO Journal, 2009, 28, 3400-3412.	3.5	46

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91	A 3,000-year-old Egyptian emmer wheat genome reveals dispersal and domestication history. Nature Plants, 2019, 5, 1120-1128.	4.7	46
92	Impact of Temporal Variation on Design and Analysis of Mouse Knockout Phenotyping Studies. PLoS ONE, 2014, 9, e111239.	1.1	46
93	Unstable Inheritance of 45S rRNA Genes in<i>Arabidopsis thaliana</i>. G3: Genes, Genomes, Genetics, 2017, 7, 1201-1209.	0.8	43
94	Genotype is an important determinant factor of host susceptibility to periodontitis in the Collaborative Cross and inbred mouse populations. BMC Genetics, 2013, 14, 68.	2.7	42
95	Heritability and coefficient of genetic variation analyses of phenotypic traits provide strong basis for high-resolution QTL mapping in the Collaborative Cross mouse genetic reference population. Mammalian Genome, 2014, 25, 109-119.	1.0	40
96	Collaborative cross mice in a genetic association study reveal new candidate genes for bone microarchitecture. BMC Genomics, 2015, 16, 1013.	1.2	39
97	Limited haplotype diversity underlies polygenic trait architecture across 70â€‰years of wheat breeding. Genome Biology, 2021, 22, 137.	3.8	39
98	Robust and Sensitive Analysis of Mouse Knockout Phenotypes. PLoS ONE, 2012, 7, e52410.	1.1	39
99	Applying mouse complex-trait resources to behavioural genetics. Nature, 2008, 456, 724-727.	13.7	37
100	Functional Mapping of Quantitative Trait Loci (QTLs) Associated With Plant Performance in a Wheat MAGIC Mapping Population. Frontiers in Plant Science, 2018, 9, 887.	1.7	37
101	Efficient high-resolution genetic mapping of mouse interspersed repetitive sequence PCR products, toward integrated genetic and physical mapping of the mouse genome.. Proceedings of the National Academy of Sciences of the United States of America, 1995, 92, 5302-5306.	3.3	36
102	Determining Phenological Patterns Associated with the Onset of Senescence in a Wheat MAGIC Mapping Population. Frontiers in Plant Science, 2016, 7, 1540.	1.7	36
103	Epistatic and allelic interactions control expression of ribosomal RNA gene clusters in Arabidopsis thaliana. Genome Biology, 2017, 18, 75.	3.8	36
104	A Genetic and Functional Relationship between T Cells and Cellular Proliferation in the Adult Hippocampus. PLoS Biology, 2010, 8, e1000561.	2.6	32
105	GLIDERS - A web-based search engine for genome-wide linkage disequilibrium between HapMap SNPs. BMC Bioinformatics, 2009, 10, 367.	1.2	31
106	Glucose tolerance female-specific QTL mapped in collaborative cross mice. Mammalian Genome, 2017, 28, 20-30.	1.0	31
107	Cofilin-1: A Modulator of Anxiety in Mice. PLoS Genetics, 2012, 8, e1002970.	1.5	28
108	Dissecting Quantitative Traits in Mice. Annual Review of Genomics and Human Genetics, 2013, 14, 421-439.	2.5	28

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109	Construction of Genetic Maps Using Distance Geometry. Genomics, 1995, 30, 59-70.	1.3	27
110	Dynamic and Physical Clustering of Gene Expression during Epidermal Barrier Formation in Differentiating Keratinocytes. PLoS ONE, 2009, 4, e7651.	1.1	26
111	Identification of new loci involved in the host susceptibility to Salmonella Typhimurium in collaborative cross mice. BMC Genomics, 2018, 19, 303.	1.2	26
112	Genomeâ€wide association coupled gene to gene interaction studies unveil novel epistatic targets among major effect loci impacting rice grain chalkiness. Plant Biotechnology Journal, 2021, 19, 910-925.	4.1	26
113	Complex haplotypic structure of the central MHC region flanking TNF in a West African population. Genes and Immunity, 2003, 4, 476-486.	2.2	24
114	Elusive Copy Number Variation in the Mouse Genome. PLoS ONE, 2010, 5, e12839.	1.1	24
115	The Amount of Mitochondrial DNA in Blood Reflects the Course of a Depressive Episode. Biological Psychiatry, 2016, 80, e41-e42.	0.7	24
116	Host Susceptibility to Periodontitis. Journal of Dental Research, 2013, 92, 438-443.	2.5	23
117	Weighted Burden Analysis of Exome-Sequenced Case-Control Sample Implicates Synaptic Genes in Schizophrenia Aetiology. Behavior Genetics, 2018, 48, 198-208.	1.4	23
118	Modeling the quantitative nature of neurodevelopmental disorders using Collaborative Cross mice. Molecular Autism, 2018, 9, 63.	2.6	22
119	Comparing the fine specificity of DNA binding by NF-kappaB p50 and p52 using principal coordinates analysis. Nucleic Acids Research, 2003, 31, 1497-1501.	6.5	21
120	Bayesian Quantitative Trait Locus Mapping Using Inferred Haplotypes. Genetics, 2010, 184, 839-852.	1.2	21
121	Genomic Rearrangements in<i>Arabidopsis</i>Considered as Quantitative Traits. Genetics, 2017, 205, 1425-1441.	1.2	21
122	Integration of Murine and Human Studies for Mapping Periodontitis Susceptibility. Journal of Dental Research, 2018, 97, 537-546.	2.5	21
123	QTL fine-mapping with recombinant-inbred heterogeneous stocks and in vitro heterogeneous stocks. Mammalian Genome, 2003, 14, 830-838.	1.0	20
124	Mapping liver fat female-dependent quantitative trait loci in collaborative cross mice. Mammalian Genome, 2016, 27, 565-573.	1.0	20
125	Causes and Consequences of Chromatin Variation between Inbred Mice. PLoS Genetics, 2013, 9, e1003570.	1.5	18
126	Genetic analysis of intestinal polyp development in Collaborative Cross mice carrying the Apc Min/+ mutation. BMC Genetics, 2016, 17, 46.	2.7	18

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127	Human-Mouse Quantitative Trait Locus Concordance and the Dissection of a Human Neuroticism Locus. Biological Psychiatry, 2008, 63, 874-883.	0.7	17
128	Collaborative Cross Mice Yield Genetic Modifiers for Pseudomonas aeruginosa Infection in Human Lung Disease. MBio, 2020, 11, .	1.8	17
129	Sequence Assembly withâ€‰CAFTOOLS. Genome Research, 1998, 8, 260-267.	2.4	16
130	A haplotype map for the laboratory mouse. Nature Genetics, 2007, 39, 1054-1056.	9.4	16
131	Mapping the genetic basis of ecologically and evolutionarily relevant traits in Arabidopsis thaliana. Current Opinion in Plant Biology, 2012, 15, 212-217.	3.5	16
132	Natural Polymorphisms in Tap2 Influence Negative Selection and CD4â^¶CD8 Lineage Commitment in the Rat. PLoS Genetics, 2014, 10, e1004151.	1.5	16
133	Selective breeding and selection mapping using a novel wild-derived heterogeneous stock of mice revealed two closely-linked loci for tameness. Scientific Reports, 2017, 7, 4607.	1.6	16
134	Recovery of novel association loci in Arabidopsis thaliana and Drosophila melanogaster through leveraging INDELs association and integrated burden test. PLoS Genetics, 2018, 14, e1007699.	1.5	16
135	An integrated system for genetic analysis. BMC Bioinformatics, 2006, 7, 210.	1.2	15
136	The transcriptional control proteins c-Myb and v-Myb contain a basic region DNA binding motif. FEBS Letters, 1991, 282, 293-294.	1.3	14
137	Finding the molecular basis of complex genetic variation in humans and mice. Philosophical Transactions of the Royal Society B: Biological Sciences, 2006, 361, 393-401.	1.8	13
138	Hepatic gene expression variations in response to high-fat diet-induced impaired glucose tolerance using RNAseq analysis in collaborative cross mouse population. Mammalian Genome, 2019, 30, 260-275.	1.0	13
139	Dissecting the Effect of Genetic Variation on the Hepatic Expression of Drug Disposition Genes across the Collaborative Cross Mouse Strains. Frontiers in Genetics, 2016, 7, 172.	1.1	12
140	Schistosoma mansoni: histological analysis of the synergistic interaction between vaccine immunity and praziquantel therapy in the lungs of mice. Parasite Immunology, 1990, 12, 367-387.	0.7	11
141	An Algorithm to Detect Chimeric Clones and Random Noise in Genomic Mapping. Genomics, 1994, 22, 482-486.	1.3	11
142	Prospects for complex trait analysis in the mouse. Mammalian Genome, 2008, 19, 306-308.	1.0	11
143	Bioinformatics tools and database resources for systems genetics analysis in mice--a short review and an evaluation of future needs. Briefings in Bioinformatics, 2012, 13, 135-142.	3.2	11
144	Dissociation of antibody responses during human schistosomiasis and evidence for enhancement of granuloma size by anti-carbohydrate IgM. Transactions of the Royal Society of Tropical Medicine and Hygiene, 1990, 84, 808-814.	0.7	10

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145	A genome-wide association study in mice reveals a role for Rhbdf2 in skeletal homeostasis. Scientific Reports, 2020, 10, 3286.	1.6	10
146	Genetic Interactions with Sex Make a Relatively Small Contribution to the Heritability of Complex Traits in Mice. PLoS ONE, 2014, 9, e96450.	1.1	9
147	Transcriptome Profiling in Rat Inbred Strains and Experimental Cross Reveals Discrepant Genetic Architecture of Genome-Wide Gene Expression. G3: Genes, Genomes, Genetics, 2016, 6, 3671-3683.	0.8	9
148	Toppar: an interactive browser for viewing association study results. Bioinformatics, 2018, 34, 1922-1924.	1.8	9
149	Private Genomes and Public SNPs: Homomorphic Encryption of Genotypes and Phenotypes for Shared Quantitative Genetics. Genetics, 2020, 215, 359-372.	1.2	9
150	Transcriptome-wide analyses of adipose tissue in outbred rats reveal genetic regulatory mechanisms relevant for human obesity. Physiological Genomics, 2022, 54, 206-219.	1.0	9
151	Replication profile of PCDH11X and PCDH11Y, a gene pair located in the non-pseudoautosomal homologous region Xq21.3/Yp11.2. Chromosome Research, 2007, 15, 485-498.	1.0	8
152	Differential sensitivity of mouse strains to an <i>N</i>-alkylated imino sugar: glycosphingolipid metabolism and acrosome formation. Pharmacogenomics, 2008, 9, 717-731.	0.6	8
153	A Genome-Wide Association Study for Regulators of Micronucleus Formation in Mice. G3: Genes, Genomes, Genetics, 2016, 6, 2343-2354.	0.8	8
154	Genetic mapping of novel modifiers for ApcMin induced intestinal polypsâ€™ development using the genetic architecture power of the collaborative cross mice. BMC Genomics, 2021, 22, 566.	1.2	8
155	A Quantitative Trait Locus Influencing Anxiety in the Laboratory Rat. Genome Research, 2002, 12, 618-626.	2.4	8
156	Container-aided integrative QTL and RNA-seq analysis of Collaborative Cross mice supports distinct sex-oriented molecular modes of response in obesity. BMC Genomics, 2020, 21, 761.	1.2	7
157	Genetic Variants in Major Depression. Novartis Foundation Symposium, 2008, 289, 23-42.	1.2	7
158	Genetic Control of Differential Acetylation in Diabetic Rats. PLoS ONE, 2014, 9, e94555.	1.1	7
159	An accurate approximation to the distribution of the length of the longest matching word between two random DNA sequences. Bulletin of Mathematical Biology, 1990, 52, 773-784.	0.9	6
160	Tests for the statistical significance of protein sequence similarities in data-bank searches. Protein Engineering, Design and Selection, 1990, 4, 149-154.	1.0	6
161	ROS-mediated vascular homeostatic control of root-to-shoot soil Na delivery in Arabidopsis. EMBO Journal, 2013, 32, 914-914.	3.5	6
162	Mapping novel genetic loci associated with female liver weight variations using Collaborative Cross mice. Animal Models and Experimental Medicine, 2018, 1, 212-220.	1.3	6

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163	Conserved properties of genetic architecture of renal and fat transcriptomes in rat models of insulin resistance. DMM Disease Models and Mechanisms, 2019, 12, .	1.2	6
164	Replication timing of the human genome. Human Molecular Genetics, 2004, 13, 575-575.	1.4	5
165	Population-specific patterns of linkage disequilibrium in the human 5q31 region. Genes and Immunity, 2005, 6, 723-727.	2.2	5
166	Analysis of independent cohorts of outbred CFW mice reveals novel loci for behavioral and physiological traits and identifies factors determining reproducibility. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	5
167	Management, presentation and interpretation of genome scans using GSCANDB. Bioinformatics, 2007, 23, 1545-1549.	1.8	4
168	Distribution Factors for Short-Haul Vehicular Loads on Prestressed Concrete Open Box Beam (U-Beam) Bridges. Practice Periodical on Structural Design and Construction, 2010, 15, 101-108.	0.7	4
169	Microarray-based ultra-high resolution discovery of genomic deletion mutations. BMC Genomics, 2014, 15, 224.	1.2	4
170	Microarray-based optimization to detect genomic deletion mutations. Genomics Data, 2014, 2, 53-54.	1.3	4
171	Coping-Style Behavior Identified by a Survey of Parent-of-Origin Effects in the Rat. G3: Genes, Genomes, Genetics, 2018, 8, 3283-3291.	0.8	4
172	Integrated Genome Mapping by Hybridization Techniques. , 1996, , 319-346.		4
173	ADDO: a comprehensive toolkit to detect, classify and visualize additive and non-additive quantitative trait loci. Bioinformatics, 2020, 36, 1517-1521.	1.8	2
174	Genetic differential calculus. Nature Genetics, 2015, 47, 965-966.	9.4	1
175	Evidence of a Large-Scale Functional Organization of Mammalian Chromosomes: Authors' Reply. PLoS Biology, 2007, 5, e128.	2.6	1
176	Epigenetic interactions. EBioMedicine, 2022, 75, 103804.	2.7	1
177	Construction of Genetic Maps Using Distance Geometry. Genomics, 1996, 34, 283.	1.3	0
178	Construction of Genetic Maps Using Distance GeometryVolume30,Number 1 (1995), pages 59â€“70. Genomics, 1996, 34, 283.	1.3	0
179	CONVERGE dataset: 12,000 whole-genome sequences representative of the Han Chinese population. GigaScience, 2016, 5, .	3.3	0