Karl W Broman

List of Publications by Year
in descending order

151 papers	16,332 citations	36203 51 h-index	19136 118 g-index
168 all docs	168 docs citations	168 times ranked	17919 citing authors

#	ARTICLE	IF	CITATIONS
1	R/qtl: QTL mapping in experimental crosses. Bioinformatics, 2003, 19, 889-890.	1.8	3,197
2	Comprehensive Human Genetic Maps: Individual and Sex-Specific Variation in Recombination. American Journal of Human Genetics, 1998, 63, 861-869.	2.6	1,042
3	The Collaborative Cross, a community resource for the genetic analysis of complex traits. Nature Genetics, 2004, 36, 1133-1137.	9.4	1,034
4	A Guide to QTL Mapping with R/qtl. Statistics in the Health Sciences, 2009, , .	0.2	681
5	Perturbation of Nuclear Architecture by Long-Distance Chromosome Interactions. Cell, 1996, 85, 745-759.	13.5	444
6	R/qtl: high-throughput multiple QTL mapping. Bioinformatics, 2010, 26, 2990-2992.	1.8	419
7	A postgenomic method for predicting essential genes at subsaturation levels of mutagenesis: Application to Mycobacterium tuberculosis. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 7213-7218.	3.3	346
8	R/qtl2: Software for Mapping Quantitative Trait Loci with High-Dimensional Data and Multiparent Populations. Genetics, 2019, 211, 495-502.	1.2	333
9	Genetic analysis of complex traits in the emerging Collaborative Cross. Genome Research, 2011, 21, 1213-1222.	2.4	327
10	A model selection approach for the identification of quantitative trait loci in experimental crosses. Journal of the Royal Statistical Society Series B: Statistical Methodology, 2002, 64, 641-656.	1.1	289
11	Comparison of human genetic and sequence-based physical maps. Nature, 2001, 409, 951-953.	13.7	267
12	Genetic architecture of complex traits: Large phenotypic effects and pervasive epistasis. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 19910-19914.	3.3	254
13	Spectrum of heart disease associated with murine and human GATA4 mutation. Journal of Molecular and Cellular Cardiology, 2007, 43, 677-685.	0.9	218
14	A New Standard Genetic Map for the Laboratory Mouse. Genetics, 2009, 182, 1335-1344.	1.2	202
15	Genetic dissection of a model complex trait using the <i>Drosophila</i> Synthetic Population Resource. Genome Research, 2012, 22, 1558-1566.	2.4	199
16	Inheritance of a NovelCOL8A2Mutation Defines a Distinct Early-Onset Subtype of Fuchs Corneal Dystrophy. , 2005, 46, 1934.		195
17	Quantitative Trait Locus Mapping Methods for Diversity Outbred Mice. G3: Genes, Genomes, Genetics, 2014, 4, 1623-1633.	0.8	195
18	Genotypic Analysis of HIVâ€1 Drug Resistance at the Limit of Detection: Virus Production without Evolution in Treated Adults with Undetectable HIV Loads. Journal of Infectious Diseases, 2004, 189, 1452-1465.	1.9	186

#	ARTICLE	IF	CITATIONS
19	A Second-Generation Genetic Linkage Map of the Domestic Dog, Canis familiaris. Genetics, 1999, 151, 803-820.	1.2	186
20	Poor Performance of Bootstrap Confidence Intervals for the Location of a Quantitative Trait Locus. Genetics, 2006, 174, 481-489.	1.2	184
21	Breed distribution and history of canine mdr1-1Â, a pharmacogenetic mutation that marks the emergence of breeds from the collie lineage. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 11725-11730.	3.3	172
22	Extreme hyperopia is the result of null mutations in MFRP, which encodes a Frizzled-related protein. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 9553-9558.	3.3	172
23	The Genomes of Recombinant Inbred Lines. Genetics, 2005, 169, 1133-1146.	1.2	166
24	The Paternal-Age Effect in Apert Syndrome Is Due, in Part, to the Increased Frequency of Mutations in Sperm. American Journal of Human Genetics, 2003, 73, 939-947.	2.6	164
25	Characterization of Human Crossover Interference. American Journal of Human Genetics, 2000, 66, 1911-1926.	2.6	153
26	A Model Selection Approach for the Identification of Quantitative Trait Loci in Experimental Crosses, Allowing Epistasis. Genetics, 2009, 181, 1077-1086.	1.2	149
27	A Genome Screen of Multiplex Sibships with Prostate Cancer. American Journal of Human Genetics, 2000, 66, 933-944.	2.6	147
28	An SNP-Based Linkage Map for Zebrafish Reveals Sex Determination Loci. G3: Genes, Genomes, Genetics, 2011, 1, 3-9.	0.8	145
29	Genomewide Scan for Prostate Cancerâ€"Aggressiveness Loci. American Journal of Human Genetics, 2000, 67, 92-99.	2.6	138
30	Cross-Reactive T Cells Are Involved in Rapid Clearance of 2009 Pandemic H1N1 Influenza Virus in Nonhuman Primates. PLoS Pathogens, 2011, 7, e1002381.	2.1	136
31	The Recombinational Anatomy of a Mouse Chromosome. PLoS Genetics, 2008, 4, e1000119.	1.5	135
32	Mapping Quantitative Trait Loci in the Case of a Spike in the Phenotype Distribution. Genetics, 2003, 163, 1169-1175.	1.2	122
33	Crossover Interference in the Mouse. Genetics, 2002, 160, 1123-1131.	1.2	109
34	Estimation of Pairwise Relationships in the Presence of Genotyping Errors. American Journal of Human Genetics, 1998, 63, 1563.	2.6	108
35	Linkage of Late-Onset Fuchs Corneal Dystrophy to a Novel Locus at 13pTel-13q12.13. , 2006, 47, 140.		107
36	Broad-Scale Recombination Patterns Underlying Proper Disjunction in Humans. PLoS Genetics, 2009, 5, e1000658.	1.5	107

#	ARTICLE	IF	CITATIONS
37	Meiotic Recombination in Human Oocytes. PLoS Genetics, 2009, 5, e1000661.	1.5	100
38	Cytological Studies of Human Meiosis: Sex-Specific Differences in Recombination Originate at, or Prior to, Establishment of Double-Strand Breaks. PLoS ONE, 2013, 8, e85075.	1.1	100
39	A Common Locus for Late-Onset Fuchs Corneal Dystrophy Maps to 18q21.2-q21.32. , 2006, 47, 3919.		98
40	Crossover interference underlies sex differences in recombination rates. Trends in Genetics, 2007, 23, 539-542.	2.9	95
41	A Comprehensive Linkage Map of the Dog Genome. Genetics, 2010, 184, 595-605.	1.2	92
42	Multigenic control of Listeria monocytogenes susceptibility in mice. Nature Genetics, 2001, 27, 259-260.	9.4	79
43	Mapping Quantitative Trait Loci by an Extension of the Haleyâ€"Knott Regression Method Using Estimating Equations. Genetics, 2006, 173, 2269-2282.	1.2	78
44	Genetic determinants of gut microbiota composition and bile acid profiles in mice. PLoS Genetics, 2019, 15, e1008073.	1.5	75
45	BayesMendel: an R Environment for Mendelian Risk Prediction. Statistical Applications in Genetics and Molecular Biology, 2004, 3, 1-19.	0.2	74
46	Data Organization in Spreadsheets. American Statistician, 2018, 72, 2-10.	0.9	74
47	Clinical and molecular characterization of the bladder exstrophy-epispadias complex: analysis of 232 families. BJU International, 2004, 94, 1337-1343.	1.3	73
48	High-Throughput Computer Vision Introduces the Time Axis to a Quantitative Trait Map of a Plant Growth Response. Genetics, 2013, 195, 1077-1086.	1.2	72
49	The X Chromosome in Quantitative Trait Locus Mapping. Genetics, 2006, 174, 2151-2158.	1.2	66
50	Quantitative Trait Loci Ã— Maternal Cytoplasmic Environment Interaction for Development Rate in Oncorhynchus mykiss. Genetics, 2007, 175, 335-347.	1.2	64
51	Î²A3/A1-crystallin in astroglial cells regulates retinal vascular remodeling during development. Molecular and Cellular Neurosciences, 2008, 37, 85-95.	1.0	64
52	Genetic Fineâ€Mapping and Identification of Candidate Genes and Variants for Adiposity Traits in Outbred Rats. Obesity, 2018, 26, 213-222.	1.5	64
53	<i>FMR1</i> CGG expansions: Prevalence and sex ratios. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2013, 162, 466-473.	1.1	62
54	Variation in Genomic Recombination Rates Among Heterogeneous Stock Mice. Genetics, 2009, 182, 1345-1349.	1.2	61

#	Article	IF	Citations
55	SNP-specific array-based allele-specific expression analysis. Genome Research, 2008, 18, 771-779.	2.4	60
56	Gene loci associated with insulin secretion in islets from nondiabetic mice. Journal of Clinical Investigation, 2019, 129, 4419-4432.	3.9	60
57	Novel autoantigens in autoimmune hypophysitis. Clinical Endocrinology, 2008, 69, 269-278.	1.2	59
58	Quantitative trait locus mapping identifies candidate alleles involved in adaptive introgression and range expansion in a wild sunflower. Molecular Ecology, 2015, 24, 2194-2211.	2.0	59
59	R/qtlDesign: inbred line cross experimental design. Mammalian Genome, 2007, 18, 87-93.	1.0	58
60	Genetic Drivers of Pancreatic Islet Function. Genetics, 2018, 209, 335-356.	1.2	54
61	Genetic Control of X Chromosome Inactivation in Mice: Definition of the Xce Candidate Interval. Genetics, 2006, 173, 2103-2110.	1.2	52
62	GeneNetwork: framework for web-based genetics. Journal of Open Source Software, 2016, 1, 25.	2.0	51
63	Particle Effects on Heart-Rate Regulation in Senescent Mice. Inhalation Toxicology, 2004, 16, 381-390.	0.8	50
64	High-Resolution Quantitative Trait Locus Mapping Reveals Sign Epistasis Controlling Ovariole Number Between Two Drosophila Species. Genetics, 2006, 173, 197-205.	1.2	50
65	Quantitative trait linkage analysis by generalized estimating equations: Unification of variance components and Haseman-Elston regression. Genetic Epidemiology, 2004, 26, 265-272.	0.6	48
66	Variation in Genome-Wide Levels of Meiotic Recombination Is Established at the Onset of Prophase in Mammalian Males. PLoS Genetics, 2014, 10, e1004125.	1.5	48
67	Characterization of killer immunoglobulin-like receptor genetics and comprehensive genotyping by pyrosequencing in rhesus macaques. BMC Genomics, 2011, 12, 295.	1.2	45
68	Genetics of Rapid and Extreme Size Evolution in Island Mice. Genetics, 2015, 201, 213-228.	1.2	44
69	Two Autoimmune Diabetes Loci Influencing T Cell Apoptosis Control Susceptibility to Experimental Autoimmune Myocarditis. Journal of Immunology, 2005, 174, 2167-2173.	0.4	43
70	A large-scale genome–lipid association map guides lipid identification. Nature Metabolism, 2020, 2, 1149-1162.	5.1	43
71	An Imprinted Locus Epistatically Influences Nstr1 and Nstr2 to Control Resistance to Nerve Sheath Tumors in a Neurofibromatosis Type 1 Mouse Model. Cancer Research, 2006, 66, 62-68.	0.4	42
72	Discrete Gene Loci Regulate Neurodegeneration, Lymphocyte Infiltration, and Major Histocompatibility Complex Class II Expression in the CNS. Journal of Neuroscience, 2003, 23, 9817-9823.	1.7	40

#	ARTICLE	IF	CITATIONS
73	Nuclear Cataract Shows Significant Familial Aggregation in an Older Population after Adjustment for Possible Shared Environmental Factors. , 2004, 45, 2182.		40
74	Identification of X-linked quantitative trait loci affecting cold tolerance in Drosophila melanogaster and fine mapping by selective sweep analysis. Molecular Ecology, 2011, 20, 530-544.	2.0	40
75	The Transcription Factor Nfatc2 Regulates Î²-Cell Proliferation and Genes Associated with Type 2 Diabetes in Mouse and Human Islets. PLoS Genetics, 2016, 12, e1006466.	1.5	40
76	Modified Vaccinia Virus Ankara Encoding Influenza Virus Hemagglutinin Induces Heterosubtypic Immunity in Macaques. Journal of Virology, 2014, 88, 13418-13428.	1.5	39
77	Systems genetics of susceptibility to obesity-induced diabetes in mice. Physiological Genomics, 2012, 44, 1-13.	1.0	38
78	Genome-wide linkage identifies novel modifier loci of aganglionosis in the Sox10Dom model of Hirschsprung disease. Human Molecular Genetics, 2005, 14, 1549-1558.	1.4	37
79	Differential MHC class I expression in distinct leukocyte subsets. BMC Immunology, 2011, 12, 39.	0.9	36
80	Mapping expression in randomized rodent genomes. Nature Genetics, 2005, 37, 209-210.	9.4	35
81	Cortical, but not posterior subcapsular, cataract shows significant familial aggregation in an older population after adjustment for possible shared environmental factors. Ophthalmology, 2005, 112, 73-77.	2.5	35
82	Genome Reshuffling for Advanced Intercross Permutation (GRAIP): Simulation and Permutation for Advanced Intercross Population Analysis. PLoS ONE, 2008, 3, e1977.	1.1	35
83	A Simple Regression-Based Method to Map Quantitative Trait Loci Underlying Function-Valued Phenotypes. Genetics, 2014, 197, 1409-1416.	1.2	35
84	R/qtlcharts: Interactive Graphics for Quantitative Trait Locus Mapping. Genetics, 2015, 199, 359-361.	1.2	35
85	Mapping Quantitative Trait Loci Underlying Function-Valued Traits Using Functional Principal Component Analysis and Multi-Trait Mapping. G3: Genes, Genomes, Genetics, 2016, 6, 79-86.	0.8	34
86	Immunity-related GTPase induces lipophagy to prevent excess hepatic lipid accumulation. Journal of Hepatology, 2020, 73, 771-782.	1.8	34
87	An ADAMTSL2 Founder Mutation Causes Musladin-Lueke Syndrome, a Heritable Disorder of Beagle Dogs, Featuring Stiff Skin and Joint Contractures. PLoS ONE, 2010, 5, e12817.	1.1	32
88	Efficient Imputation of Missing Markers in Low-Coverage Genotyping-by-Sequencing Data from Multiparental Crosses. Genetics, 2014, 197, 401-404.	1.2	32
89	Estimation of allele frequencies with data on sibships. Genetic Epidemiology, 2001, 20, 307-315.	0.6	31
90	Genetic resistance to diet-induced obesity in chromosome substitution strains of mice. Mammalian Genome, 2010, 21, 115-129.	1.0	31

#	Article	IF	Citations
91	Haplotype Probabilities for Multiple-Strain Recombinant Inbred Lines. Genetics, 2007, 175, 1267-1274.	1.2	30
92	Genotype Probabilities at Intermediate Generations in the Construction of Recombinant Inbred Lines. Genetics, 2012, 190, 403-412.	1.2	30
93	A major locus conferring susceptibility to infection by Streptococcus pneumoniae in mice. Mammalian Genome, 2003, 14, 448-453.	1.0	29
94	The C. savignyi genetic map and its integration with the reference sequence facilitates insights into chordate genome evolution. Genome Research, 2008, 18, 1369-1379.	2.4	29
95	Selective Genotyping and Phenotyping Strategies in a Complex Trait Context. Genetics, 2009, 181, 1613-1626.	1.2	29
96	Extralymphoid CD8 ⁺ T Cells Resident in Tissue from Simian Immunodeficiency Virus SIVmac239Î"nef-Vaccinated Macaques Suppress SIVmac239 Replication <i>Ex Vivo</i>. Journal of Virology, 2010, 84, 3362-3372.	1.5	29
97	The Dissection of Expression Quantitative Trait Locus Hotspots. Genetics, 2016, 202, 1563-1574.	1.2	29
98	Correlations between Synaptic Initiation and Meiotic Recombination: A Study of Humans and Mice. American Journal of Human Genetics, 2016, 98, 102-115.	2.6	28
99	Patterns of Recombination Activity on Mouse Chromosome 11 Revealed by High Resolution Mapping. PLoS ONE, 2010, 5, e15340.	1.1	27
100	Failure to recombine is a common feature of human oogenesis. American Journal of Human Genetics, 2021, 108, 16-24.	2.6	27
101	Quantitative lymphatic vessel trait analysis suggests Vcam1 as candidate modifier gene of inflammatory bowel disease. Genes and Immunity, 2010, 11, 219-231.	2.2	26
102	Significance Thresholds for Quantitative Trait Locus Mapping Under Selective Genotyping. Genetics, 2007, 177, 1963-1966.	1.2	25
103	Haplotype Probabilities in Advanced Intercross Populations. G3: Genes, Genomes, Genetics, 2012, 2, 199-202.	0.8	25
104	Identification and Correction of Sample Mix-Ups in Expression Genetic Data: A Case Study. G3: Genes, Genomes, Genetics, 2015, 5, 2177-2186.	0.8	25
105	Multiple loci contribute to genome-wide recombination levels in male mice. Mammalian Genome, 2010, 21, 550-555.	1.0	24
106	Acute-Phase CD8 T Cell Responses That Select for Escape Variants Are Needed to Control Live Attenuated Simian Immunodeficiency Virus. Journal of Virology, 2013, 87, 9353-9364.	1.5	24
107	Examining Variation in Recombination Levels in the Human Female: A Test of the Production-Line Hypothesis. American Journal of Human Genetics, 2014, 95, 108-112.	2.6	22
108	Identification of the Bile Acid Transporter <i>Slco1a6</i> as a Candidate Gene That Broadly Affects Gene Expression in Mouse Pancreatic Islets. Genetics, 2015, 201, 1253-1262.	1.2	22

#	Article	IF	Citations
109	Genetics of Skeletal Evolution in Unusually Large Mice from Gough Island. Genetics, 2016, 204, 1559-1572.	1.2	22
110	Arlm1 is a male-specific modifier of astrocytoma resistance on mouse Chr 12. Neuro-Oncology, 2012, 14, 160-174.	0.6	21
111	Cleaning Genotype Data from Diversity Outbred Mice. G3: Genes, Genomes, Genetics, 2019, 9, 1571-1579.	0.8	21
112	Endothelial dystrophy, iris hypoplasia, congenital cataract, and stromal thinning (edict) syndrome maps to chromosome 15q22.1â€"q25.3. American Journal of Ophthalmology, 2002, 134, 172-176.	1.7	20
113	Simulation-Based P Values: Response to North et al.. American Journal of Human Genetics, 2003, 72, 496.	2.6	20
114	Multiple polymorphic loci determine basal hepatic and splenic iron status in mice. Hepatology, 2006, 44, 174-185.	3.6	20
115	Modifiers of von Willebrand factor identified by natural variation in inbred strains of mice. Blood, 2009, 114, 5368-5374.	0.6	20
116	Interactions in hypoxic and hypercapnic breathing are genetically linked to mouse chromosomes 1 and 5. Journal of Applied Physiology, 2004, 97, 77-84.	1.2	19
117	Detecting single-nucleotide polymorphism by single-nucleotide polymorphism interactions in rheumatoid arthritis using a two-step approach with machine learning and a Bayesian threshold least absolute shrinkage and selection operator (LASSO) model. BMC Proceedings, 2009, 3, S63.	1.8	19
118	Multiperson Use of Syringes Among Injection Drug Users in a Needle Exchange Program. Journal of Acquired Immune Deficiency Syndromes (1999), 2006, 43, 335-343.	0.9	18
119	Quantile-Based Permutation Thresholds for Quantitative Trait Loci Hotspots. Genetics, 2012, 191, 1355-1365.	1.2	18
120	Recombination rate variation in mice from an isolated island. Molecular Ecology, 2017, 26, 457-470.	2.0	17
121	Genetic background modifies phenotypic severity and longevity in a mouse model of Niemann-Pick disease type C1. DMM Disease Models and Mechanisms, 2020, 13, .	1.2	17
122	Power and robustness of linkage tests for quantitative traits in general pedigrees. Genetic Epidemiology, 2005, 28, 11-23.	0.6	16
123	xQTL workbench: a scalable web environment for multi-level QTL analysis. Bioinformatics, 2012, 28, 1042-1044.	1.8	16
124	A Simple Method for Combining Genetic Mapping Data from Multiple Crosses and Experimental Designs. PLoS ONE, 2007, 2, e1036.	1.1	16
125	A Spontaneous Missense Mutation in Branched Chain Keto Acid Dehydrogenase Kinase in the Rat Affects Both the Central and Peripheral Nervous Systems. PLoS ONE, 2016, 11, e0160447.	1.1	16
126	Scram1 is a modifier of spinal cord resistance for astrocytoma on mouse Chr 5. Mammalian Genome, 2012, 23, 277-285.	1.0	14

#	ARTICLE	IF	CITATIONS
127	An initial linkage map of the West Nile Virus vector *Culex tarsalis*. Insect Molecular Biology, 2009, 18, 453-463.	1.0	12
128	Resistance to Noise-Induced Hearing Loss in 129S6 and MOLF Mice: Identification of Independent, Overlapping, and Interacting Chromosomal Regions. JARO - Journal of the Association for Research in Otolaryngology, 2014, 15, 721-738.	0.9	11
129	Testing Pleiotropy *vs.* Separate QTL in Multiparental Populations. G3: Genes, Genomes, Genetics, 2019, 9, 2317-2324.	0.8	11
130	Mapping genetic determinants of host susceptibility to Pseudomonas aeruginosa lung infection in mice. BMC Genomics, 2016, 17, 351.	1.2	10
131	Tsc2, a positional candidate gene underlying a quantitative trait locus for hepatic steatosis. Journal of Lipid Research, 2012, 53, 1493-1501.	2.0	9
132	A modified vaccinia Ankara vaccine vector expressing a mosaic H5 hemagglutinin reduces viral shedding in rhesus macaques. PLoS ONE, 2017, 12, e0181738.	1.1	9
133	Mapping Quantitative Trait Loci onto a Phylogenetic Tree. Genetics, 2012, 192, 267-279.	1.2	8
134	QTLViewer: an interactive webtool for genetic analysis in the Collaborative Cross and Diversity Outbred mouse populations. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	8
135	Identification of Susceptibility Loci for Skin Disease in a Murine Psoriasis Model. Journal of Immunology, 2006, 177, 4612-4619.	0.4	7
136	Fourteen Years of R/qtl: Just Barely Sustainable. Journal of Open Research Software, 2014, 2, e11.	2.7	7
137	SNPs made routine. Nature Methods, 2004, 1, 104-105.	9.0	6
138	Binary Trait Mapping in Experimental Crosses With Selective Genotyping. Genetics, 2009, 182, 863-874.	1.2	6
139	Quasi-linkage: a confounding factor in linkage analysis of complex diseases?. Human Genetics, 2004, 114, 588-593.	1.8	5
140	"Bias toward the Null" Means Reduced Power. American Journal of Human Genetics, 2004, 75, 720-722.	2.6	5
141	Ex Vivo SIV-Specific CD8 T Cell Responses in Heterozygous Animals Are Primarily Directed against Peptides Presented by a Single MHC Haplotype. PLoS ONE, 2012, 7, e43690.	1.1	5
142	Identification of a Novel Polymorphism in X-Linked Sterol-4-Alpha-Carboxylate 3-Dehydrogenase (*Nsdhl*) Associated with Reduced High-Density Lipoprotein Cholesterol Levels in I/LnJ Mice. G3: Genes, Genomes, Genetics, 2013, 3, 1819-1825.	0.8	5
143	Genetic mapping and prediction of flowering time and plant height in a maize Stiff Stalk MAGIC population. Genetics, 2022, 221, .	1.2	5
144	Unknown biological mixtures evaluation using STR analytical quantification. Electrophoresis, 2006, 27, 409-415.	1.3	3

#	Article	IF	Citations
145	The *Lsktm1* Locus Modulates Lung and Skin Tumorigenesis in the Mouse. G3: Genes, Genomes, Genetics, 2012, 2, 1041-1046.	0.8	3
146	Speeding up eQTL scans in the BXD population using GPUs. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	2
147	Identification of sample mix-ups and mixtures in microbiome data in Diversity Outbred mice. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	2
148	A generic hidden Markov model for multiparent populations. G3: Genes, Genomes, Genetics, 2022, 12, .	0.8	2
149	Treatment of the X chromosome in mapping multiple quantitative trait loci. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	0
150	Genetic determinants of lung architecture are linked to mouse chromosomes 12 and 18. FASEB Journal, 2011, 25, 862.4.	0.2	0
151	qtl2pleio: Testing pleiotropy vs. separate QTL in multiparental populations. Journal of Open Source Software, 2019, 4, 1435.	2.0	0