

Richard F Mott

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

179
papers

28,691
citations

66
h-index

169
g-index

199
ext. papers

32,827
ext. citations

12.8
avg, IF

6.99
L-index

#	Paper	IF	Citations
179	Epigenetic interactions.. <i>EBioMedicine</i> , 2022 , 75, 103804	8.8	1
178	Limited haplotype diversity underlies polygenic trait architecture across 70 years of wheat breeding. <i>Genome Biology</i> , 2021 , 22, 137	18.3	9
177	Genome-wide association coupled gene to gene interaction studies unveil novel epistatic targets among major effect loci impacting rice grain chalkiness. <i>Plant Biotechnology Journal</i> , 2021 , 19, 910-925	11.6	9
176	Genetic mapping of novel modifiers for Apc induced intestinal polyps development using the genetic architecture power of the collaborative cross mice. <i>BMC Genomics</i> , 2021 , 22, 566	4.5	0
175	Container-aided integrative QTL and RNA-seq analysis of Collaborative Cross mice supports distinct sex-oriented molecular modes of response in obesity. <i>BMC Genomics</i> , 2020 , 21, 761	4.5	3
174	Collaborative Cross Mice Yield Genetic Modifiers for Pseudomonas aeruginosa Infection in Human Lung Disease. <i>MBio</i> , 2020 , 11,	7.8	6
173	Private Genomes and Public SNPs: Homomorphic Encryption of Genotypes and Phenotypes for Shared Quantitative Genetics. <i>Genetics</i> , 2020 , 215, 359-372	4	2
172	Multi-parent populations in crops: a toolbox integrating genomics and genetic mapping with breeding. <i>Heredity</i> , 2020 , 125, 396-416	3.6	53
171	A genome-wide association study in mice reveals a role for Rhbdf2 in skeletal homeostasis. <i>Scientific Reports</i> , 2020 , 10, 3286	4.9	5
170	ADDO: a comprehensive toolkit to detect, classify and visualize additive and non-additive quantitative trait loci. <i>Bioinformatics</i> , 2020 , 36, 1517-1521	7.2	0
169	Retraction Note: 11,670 whole-genome sequences representative of the Han Chinese population from the CONVERGE project. <i>Scientific Data</i> , 2020 , 7, 123	8.2	1
168	Conserved properties of genetic architecture of renal and fat transcriptomes in rat models of insulin resistance. <i>DMM Disease Models and Mechanisms</i> , 2019 , 12,	4.1	2
167	Genome-wide sexually antagonistic variants reveal long-standing constraints on sexual dimorphism in fruit flies. <i>PLoS Biology</i> , 2019 , 17, e3000244	9.7	38
166	Hepatic gene expression variations in response to high-fat diet-induced impaired glucose tolerance using RNAseq analysis in collaborative cross mouse population. <i>Mammalian Genome</i> , 2019 , 30, 260-275	3.2	8
165	A 3,000-year-old Egyptian emmer wheat genome reveals dispersal and domestication history. <i>Nature Plants</i> , 2019 , 5, 1120-1128	11.5	25
164	Toppar: an interactive browser for viewing association study results. <i>Bioinformatics</i> , 2018 , 34, 1922-1924	7.2	5
163	Integration of Murine and Human Studies for Mapping Periodontitis Susceptibility. <i>Journal of Dental Research</i> , 2018 , 97, 537-546	8.1	15

162	Weighted Burden Analysis of Exome-Sequenced Case-Control Sample Implicates Synaptic Genes in Schizophrenia Aetiology. <i>Behavior Genetics</i> , 2018 , 48, 198-208	3.2	16
161	Functional Mapping of Quantitative Trait Loci (QTLs) Associated With Plant Performance in a Wheat MAGIC Mapping Population. <i>Frontiers in Plant Science</i> , 2018 , 9, 887	6.2	24
160	Identification of new loci involved in the host susceptibility to Salmonella Typhimurium in collaborative cross mice. <i>BMC Genomics</i> , 2018 , 19, 303	4.5	14
159	Genetic Fine-Mapping and Identification of Candidate Genes and Variants for Adiposity Traits in Outbred Rats. <i>Obesity</i> , 2018 , 26, 213-222	8	33
158	Modeling the quantitative nature of neurodevelopmental disorders using Collaborative Cross mice. <i>Molecular Autism</i> , 2018 , 9, 63	6.5	12
157	Coping-Style Behavior Identified by a Survey of Parent-of-Origin Effects in the Rat. <i>G3: Genes, Genomes, Genetics</i> , 2018 , 8, 3283-3291	3.2	1
156	Mapping novel genetic loci associated with female liver weight variations using Collaborative Cross mice. <i>Animal Models and Experimental Medicine</i> , 2018 , 1, 212-220	4.2	4
155	Sixteen diverse laboratory mouse reference genomes define strain-specific haplotypes and novel functional loci. <i>Nature Genetics</i> , 2018 , 50, 1574-1583	36.3	91
154	Recovery of novel association loci in Arabidopsis thaliana and Drosophila melanogaster through leveraging INDELs association and integrated burden test. <i>PLoS Genetics</i> , 2018 , 14, e1007699	6	3
153	Unstable Inheritance of 45S rRNA Genes in. <i>G3: Genes, Genomes, Genetics</i> , 2017 , 7, 1201-1209	3.2	32
152	Genomic Rearrangements in Considered as Quantitative Traits. <i>Genetics</i> , 2017 , 205, 1425-1441	4	15
151	11,670 whole-genome sequences representative of the Han Chinese population from the CONVERGE project. <i>Scientific Data</i> , 2017 , 4, 170011	8.2	29
150	Structural Variation Shapes the Landscape of Recombination in Mouse. <i>Genetics</i> , 2017 , 206, 603-619	4	27
149	Heterogeneous Stock Populations for Analysis of Complex Traits. <i>Methods in Molecular Biology</i> , 2017 , 1488, 31-44	1.4	25
148	Epistatic and allelic interactions control expression of ribosomal RNA gene clusters in Arabidopsis thaliana. <i>Genome Biology</i> , 2017 , 18, 75	18.3	21
147	Prevalence of sexual dimorphism in mammalian phenotypic traits. <i>Nature Communications</i> , 2017 , 8, 15475	7.4	130
146	Selective breeding and selection mapping using a novel wild-derived heterogeneous stock of mice revealed two closely-linked loci for tameness. <i>Scientific Reports</i> , 2017 , 7, 4607	4.9	8
145	Glucose tolerance female-specific QTL mapped in collaborative cross mice. <i>Mammalian Genome</i> , 2017 , 28, 20-30	3.2	23

144	Epigenomic Diversity in a Global Collection of Arabidopsis thaliana Accessions. <i>Cell</i> , 2016 , 166, 492-505	56.2	353
143	Transcriptome Profiling in Rat Inbred Strains and Experimental Cross Reveals Discrepant Genetic Architecture of Genome-Wide Gene Expression. <i>G3: Genes, Genomes, Genetics</i> , 2016 , 6, 3671-3683	3.2	5
142	The Cardamine <i>hirsuta</i> genome offers insight into the evolution of morphological diversity. <i>Nature Plants</i> , 2016 , 2, 16167	11.5	56
141	A Genome-Wide Association Study for Regulators of Micronucleus Formation in Mice. <i>G3: Genes, Genomes, Genetics</i> , 2016 , 6, 2343-54	3.2	6
140	Genetic analysis of intestinal polyp development in Collaborative Cross mice carrying the Apc (Min/+) mutation. <i>BMC Genetics</i> , 2016 , 17, 46	2.6	13
139	1,135 Genomes Reveal the Global Pattern of Polymorphism in Arabidopsis thaliana. <i>Cell</i> , 2016 , 166, 481-491	62.0	
138	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. <i>BMC Genetics</i> , 2016 , 17, 10	2.6	37
137	A multiple-phenotype imputation method for genetic studies. <i>Nature Genetics</i> , 2016 , 48, 466-72	36.3	52
136	The Amount of Mitochondrial DNA in Blood Reflects the Course of a Depressive Episode. <i>Biological Psychiatry</i> , 2016 , 80, e41-e42	7.9	17
135	Dissecting the Effect of Genetic Variation on the Hepatic Expression of Drug Disposition Genes across the Collaborative Cross Mouse Strains. <i>Frontiers in Genetics</i> , 2016 , 7, 172	4.5	11
134	Determining Phenological Patterns Associated with the Onset of Senescence in a Wheat MAGIC Mapping Population. <i>Frontiers in Plant Science</i> , 2016 , 7, 1540	6.2	23
133	Rapid genotype imputation from sequence without reference panels. <i>Nature Genetics</i> , 2016 , 48, 965-969	36.3	79
132	Genome-wide association of multiple complex traits in outbred mice by ultra-low-coverage sequencing. <i>Nature Genetics</i> , 2016 , 48, 912-8	36.3	81
131	Mapping liver fat female-dependent quantitative trait loci in collaborative cross mice. <i>Mammalian Genome</i> , 2016 , 27, 565-573	3.2	16
130	Applying the ARRIVE Guidelines to an In Vivo Database. <i>PLoS Biology</i> , 2015 , 13, e1002151	9.7	56
129	Genetic differential calculus. <i>Nature Genetics</i> , 2015 , 47, 965-6	36.3	1
128	Collaborative cross mice in a genetic association study reveal new candidate genes for bone microarchitecture. <i>BMC Genomics</i> , 2015 , 16, 1013	4.5	29
127	Molecular signatures of major depression. <i>Current Biology</i> , 2015 , 25, 1146-56	6.3	162

126	Genetic Control over mtDNA and Its Relationship to Major Depressive Disorder. <i>Current Biology</i> , 2015 , 25, 3170-7	6.3	59
125	The architecture of parent-of-origin effects in mice. <i>Cell</i> , 2014 , 156, 332-42	56.2	59
124	Environmentally responsive genome-wide accumulation of de novo <i>Arabidopsis thaliana</i> mutations and epimutations. <i>Genome Research</i> , 2014 , 24, 1821-9	9.7	145
123	Microarray-based ultra-high resolution discovery of genomic deletion mutations. <i>BMC Genomics</i> , 2014 , 15, 224	4.5	4
122	Microarray-based optimization to detect genomic deletion mutations. <i>Genomics Data</i> , 2014 , 2, 53-54		4
121	Genetic interactions with sex make a relatively small contribution to the heritability of complex traits in mice. <i>PLoS ONE</i> , 2014 , 9, e96450	3.7	8
120	Susceptibility to <i>Klebsiella pneumoniae</i> infection in collaborative cross mice is a complex trait controlled by at least three loci acting at different time points. <i>BMC Genomics</i> , 2014 , 15, 865	4.5	46
119	Natural polymorphisms in <i>Tap2</i> influence negative selection and CD4:CD8 lineage commitment in the rat. <i>PLoS Genetics</i> , 2014 , 10, e1004151	6	14
118	<i>Cardamine hirsuta</i> : a versatile genetic system for comparative studies. <i>Plant Journal</i> , 2014 , 78, 1-15	6.9	61
117	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. <i>Mammalian Genome</i> , 2014 , 25, 109-19	3.2	32
116	Genetic control of differential acetylation in diabetic rats. <i>PLoS ONE</i> , 2014 , 9, e94555	3.7	4
115	Impact of temporal variation on design and analysis of mouse knockout phenotyping studies. <i>PLoS ONE</i> , 2014 , 9, e111239	3.7	32
114	ROS-mediated vascular homeostatic control of root-to-shoot soil Na delivery in <i>Arabidopsis</i> . <i>EMBO Journal</i> , 2013 , 32, 914-914	13	5
113	Dissecting quantitative traits in mice. <i>Annual Review of Genomics and Human Genetics</i> , 2013 , 14, 421-39	9.7	24
112	Genotype is an important determinant factor of host susceptibility to periodontitis in the Collaborative Cross and inbred mouse populations. <i>BMC Genetics</i> , 2013 , 14, 68	2.6	39
111	Combined sequence-based and genetic mapping analysis of complex traits in outbred rats. <i>Nature Genetics</i> , 2013 , 45, 767-75	36.3	131
110	Causes and consequences of chromatin variation between inbred mice. <i>PLoS Genetics</i> , 2013 , 9, e1003570		16
109	Ablating adult neurogenesis in the rat has no effect on spatial processing: evidence from a novel pharmacogenetic model. <i>PLoS Genetics</i> , 2013 , 9, e1003718	6	91

108	Host susceptibility to periodontitis: mapping murine genomic regions. <i>Journal of Dental Research</i> , 2013 , 92, 438-43	8.1	18
107	Mapping the genetic basis of ecologically and evolutionarily relevant traits in <i>Arabidopsis thaliana</i> . <i>Current Opinion in Plant Biology</i> , 2012 , 15, 212-7	9.9	13
106	ROS-mediated vascular homeostatic control of root-to-shoot soil Na delivery in <i>Arabidopsis</i> . <i>EMBO Journal</i> , 2012 , 31, 4359-70	13	120
105	Sequencing and characterization of the FVB/NJ mouse genome. <i>Genome Biology</i> , 2012 , 13, R72	18.3	65
104	Status and access to the Collaborative Cross population. <i>Mammalian Genome</i> , 2012 , 23, 706-12	3.2	103
103	Cofilin-1: a modulator of anxiety in mice. <i>PLoS Genetics</i> , 2012 , 8, e1002970	6	25
102	Bioinformatics tools and database resources for systems genetics analysis in mice--a short review and an evaluation of future needs. <i>Briefings in Bioinformatics</i> , 2012 , 13, 135-42	13.4	9
101	Genome-wide analysis of mutations in mutant lineages selected following fast-neutron irradiation mutagenesis of <i>Arabidopsis thaliana</i> . <i>Genome Research</i> , 2012 , 22, 1306-15	9.7	87
100	Robust and sensitive analysis of mouse knockout phenotypes. <i>PLoS ONE</i> , 2012 , 7, e52410	3.7	38
99	Mouse genomic variation and its effect on phenotypes and gene regulation. <i>Nature</i> , 2011 , 477, 289-94	50.4	1087
98	Modularly assembled designer TAL effector nucleases for targeted gene knockout and gene replacement in eukaryotes. <i>Nucleic Acids Research</i> , 2011 , 39, 6315-25	20.1	324
97	Chromatin accessibility pre-determines glucocorticoid receptor binding patterns. <i>Nature Genetics</i> , 2011 , 43, 264-8	36.3	711
96	Subspecific origin and haplotype diversity in the laboratory mouse. <i>Nature Genetics</i> , 2011 , 43, 648-55	36.3	332
95	Genome-wide analysis reveals novel molecular features of mouse recombination hotspots. <i>Nature</i> , 2011 , 472, 375-8	50.4	257
94	Adaptive introgression of anticoagulant rodent poison resistance by hybridization between old world mice. <i>Current Biology</i> , 2011 , 21, 1296-301	6.3	221
93	Regenerant <i>Arabidopsis</i> lineages display a distinct genome-wide spectrum of mutations conferring variant phenotypes. <i>Current Biology</i> , 2011 , 21, 1385-90	6.3	65
92	Sequence-based characterization of structural variation in the mouse genome. <i>Nature</i> , 2011 , 477, 326-9	50.4	230
91	Genetic architecture of flowering-time variation in <i>Arabidopsis thaliana</i> . <i>Genetics</i> , 2011 , 188, 421-33	4	128

90	Genetic analysis of complex traits in the emerging Collaborative Cross. <i>Genome Research</i> , 2011 , 21, 1213-22	9.7	263
89	Multiple reference genomes and transcriptomes for <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2011 , 477, 419-23	50.4	495
88	Collaborative Cross mice and their power to map host susceptibility to <i>Aspergillus fumigatus</i> infection. <i>Genome Research</i> , 2011 , 21, 1239-48	9.7	116
87	Commercially available outbred mice for genome-wide association studies. <i>PLoS Genetics</i> , 2010 , 6, e1001085	10.85	102
86	Elusive copy number variation in the mouse genome. <i>PLoS ONE</i> , 2010 , 5, e12839	3.7	22
85	Distribution Factors for Short-Haul Vehicular Loads on Prestressed Concrete Open Box Beam (U-Beam) Bridges. <i>Practice Periodical on Structural Design and Construction</i> , 2010 , 15, 101-108	1.2	2
84	A genetic and functional relationship between T cells and cellular proliferation in the adult hippocampus. <i>PLoS Biology</i> , 2010 , 8, e1000561	9.7	27
83	Bayesian quantitative trait locus mapping using inferred haplotypes. <i>Genetics</i> , 2010 , 184, 839-52	4	19
82	Dynamic and physical clustering of gene expression during epidermal barrier formation in differentiating keratinocytes. <i>PLoS ONE</i> , 2009 , 4, e7651	3.7	23
81	A Multiparent Advanced Generation Inter-Cross to fine-map quantitative traits in <i>Arabidopsis thaliana</i> . <i>PLoS Genetics</i> , 2009 , 5, e1000551	6	421
80	High resolution mapping of expression QTLs in heterogeneous stock mice in multiple tissues. <i>Genome Research</i> , 2009 , 19, 1133-40	9.7	60
79	Mapping in structured populations by resample model averaging. <i>Genetics</i> , 2009 , 182, 1263-77	4	110
78	GLIDERS--a web-based search engine for genome-wide linkage disequilibrium between HapMap SNPs. <i>BMC Bioinformatics</i> , 2009 , 10, 367	3.6	23
77	Failed gene conversion leads to extensive end processing and chromosomal rearrangements in fission yeast. <i>EMBO Journal</i> , 2009 , 28, 3400-12	13	34
76	The 1001 genomes project for <i>Arabidopsis thaliana</i> . <i>Genome Biology</i> , 2009 , 10, 107	18.3	325
75	A resource for the simultaneous high-resolution mapping of multiple quantitative trait loci in rats: the NIH heterogeneous stock. <i>Genome Research</i> , 2009 , 19, 150-8	9.7	63
74	Applying mouse complex-trait resources to behavioural genetics. <i>Nature</i> , 2008 , 456, 724-7	50.4	34
73	SNP and haplotype mapping for genetic analysis in the rat. <i>Nature Genetics</i> , 2008 , 40, 560-6	36.3	150

72	Human-mouse quantitative trait locus concordance and the dissection of a human neuroticism locus. <i>Biological Psychiatry</i> , 2008 , 63, 874-83	7.9	16
71	Differential sensitivity of mouse strains to an N-alkylated imino sugar: glycosphingolipid metabolism and acrosome formation. <i>Pharmacogenomics</i> , 2008 , 9, 717-31	2.6	7
70	Prospects for complex trait analysis in the mouse. <i>Mammalian Genome</i> , 2008 , 19, 306-8	3.2	10
69	The Collaborative Cross, developing a resource for mammalian systems genetics: a status report of the Wellcome Trust cohort. <i>Mammalian Genome</i> , 2008 , 19, 379-81	3.2	89
68	Genetic variants in major depression. <i>Novartis Foundation Symposium</i> , 2008 , 289, 23-32; discussion 33-42, 87-93		7
67	Replication profile of PCDH11X and PCDH11Y, a gene pair located in the non-pseudoautosomal homologous region Xq21.3/Yp11.2. <i>Chromosome Research</i> , 2007 , 15, 485-98	4.4	7
66	Management, presentation and interpretation of genome scans using GSCANDB. <i>Bioinformatics</i> , 2007 , 23, 1545-9	7.2	3
65	Evidence of a Large-Scale Functional Organization of Mammalian Chromosomes: AuthorsRReply. <i>PLoS Biology</i> , 2007 , 5, e128	9.7	1
64	An integrated system for genetic analysis. <i>BMC Bioinformatics</i> , 2006 , 7, 210	3.6	14
63	A high-resolution single nucleotide polymorphism genetic map of the mouse genome. <i>PLoS Biology</i> , 2006 , 4, e395	9.7	218
62	Genomic clusters, putative pathogen recognition molecules, and antimicrobial genes are induced by infection of <i>C. elegans</i> with <i>M. nematophilum</i> . <i>Genome Research</i> , 2006 , 16, 1005-16	9.7	193
61	Finding the molecular basis of complex genetic variation in humans and mice. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2006 , 361, 393-401	5.8	13
60	Genetic and environmental effects on complex traits in mice. <i>Genetics</i> , 2006 , 174, 959-84	4	134
59	Simulating the collaborative cross: power of quantitative trait loci detection and mapping resolution in large sets of recombinant inbred strains of mice. <i>Genetics</i> , 2006 , 172, 1783-97	4	136
58	Screening for recently selected alleles by analysis of human haplotype similarity. <i>American Journal of Human Genetics</i> , 2006 , 78, 153-9	11	41
57	Genome-wide genetic association of complex traits in heterogeneous stock mice. <i>Nature Genetics</i> , 2006 , 38, 879-87	36.3	442
56	A protocol for high-throughput phenotyping, suitable for quantitative trait analysis in mice. <i>Mammalian Genome</i> , 2006 , 17, 129-46	3.2	88
55	SW-ARRAY: a dynamic programming solution for the identification of copy-number changes in genomic DNA using array comparative genome hybridization data. <i>Nucleic Acids Research</i> , 2005 , 33, 3455-64	20.1	79

54	Population-specific patterns of linkage disequilibrium in the human 5q31 region. <i>Genes and Immunity</i> , 2005 , 6, 723-7	4.4	5
53	Candidate-gene screening and association analysis at the autism-susceptibility locus on chromosome 16p: evidence of association at GRIN2A and ABAT. <i>American Journal of Human Genetics</i> , 2005 , 76, 950-66	11	143
52	Strategies for mapping and cloning quantitative trait genes in rodents. <i>Nature Reviews Genetics</i> , 2005 , 6, 271-86	30.1	418
51	Alignment: Statistical Significance 2005 ,		17
50	Genomewide analysis of the host response to malaria in Kenyan children. <i>Journal of Infectious Diseases</i> , 2005 , 191, 1599-611	7	100
49	Replication timing of the human genome. <i>Human Molecular Genetics</i> , 2004 , 13, 575-575	5.6	4
48	Quantitative high-throughput analysis of transcription factor binding specificities. <i>Nucleic Acids Research</i> , 2004 , 32, e44	20.1	67
47	The Collaborative Cross, a community resource for the genetic analysis of complex traits. <i>Nature Genetics</i> , 2004 , 36, 1133-7	36.3	822
46	Genetic dissection of a behavioral quantitative trait locus shows that Rgs2 modulates anxiety in mice. <i>Nature Genetics</i> , 2004 , 36, 1197-202	36.3	249
45	Replication timing of the human genome. <i>Human Molecular Genetics</i> , 2004 , 13, 191-202	5.6	259
44	LD mapping of maternally and non-maternally derived alleles and atopy in FcepsilonRI-beta. <i>Human Molecular Genetics</i> , 2003 , 12, 2577-85	5.6	40
43	Recognizing the fold of a protein structure. <i>Bioinformatics</i> , 2003 , 19, 1748-59	7.2	74
42	Comparing the fine specificity of DNA binding by NF-kappaB p50 and p52 using principal coordinates analysis. <i>Nucleic Acids Research</i> , 2003 , 31, 1497-501	20.1	18
41	QTL fine-mapping with recombinant-inbred heterogeneous stocks and in vitro heterogeneous stocks. <i>Mammalian Genome</i> , 2003 , 14, 830-8	3.2	18
40	Complex haplotypic structure of the central MHC region flanking TNF in a West African population. <i>Genes and Immunity</i> , 2003 , 4, 476-86	4.4	22
39	Positional cloning of a quantitative trait locus on chromosome 13q14 that influences immunoglobulin E levels and asthma. <i>Nature Genetics</i> , 2003 , 34, 181-6	36.3	263
38	Linkage analysis of extremely discordant and concordant sibling pairs identifies quantitative-trait loci that influence variation in the human personality trait neuroticism. <i>American Journal of Human Genetics</i> , 2003 , 72, 879-90	11	170
37	Haplotypic analysis of the TNF locus by association efficiency and entropy. <i>Genome Biology</i> , 2003 , 4, R2418.3		50

36	A first-generation linkage disequilibrium map of human chromosome 22. <i>Nature</i> , 2002 , 418, 544-8	50.4	342
35	Initial sequencing and comparative analysis of the mouse genome. <i>Nature</i> , 2002 , 420, 520-62	50.4	5376
34	A quantitative trait locus influencing anxiety in the laboratory rat. <i>Genome Research</i> , 2002 , 12, 618-26	9.7	64
33	Recent improvements to the SMART domain-based sequence annotation resource. <i>Nucleic Acids Research</i> , 2002 , 30, 242-4	20.1	535
32	Predicting protein cellular localization using a domain projection method. <i>Genome Research</i> , 2002 , 12, 1168-74	9.7	81
31	Quantifying the similarities within fold space. <i>Journal of Molecular Biology</i> , 2002 , 323, 909-26	6.5	121
30	Quantitative prediction of NF-kappa B DNA-protein interactions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 8167-72	11.5	90
29	Simultaneous detection and fine mapping of quantitative trait loci in mice using heterogeneous stocks. <i>Genetics</i> , 2002 , 160, 1609-18	4	70
28	Finding the molecular basis of quantitative traits: successes and pitfalls. <i>Nature Reviews Genetics</i> , 2001 , 2, 437-45	30.1	242
27	Novel protein domains and repeats in <i>Drosophila melanogaster</i> : insights into structure, function, and evolution. <i>Genome Research</i> , 2001 , 11, 1996-2008	9.7	89
26	Accurate formula for P-values of gapped local sequence and profile alignments. <i>Journal of Molecular Biology</i> , 2000 , 300, 649-59	6.5	103
25	Approximate statistics of gapped alignments. <i>Journal of Computational Biology</i> , 1999 , 6, 91-112	1.7	56
24	Sequence assembly with CAFTOOLS. <i>Genome Research</i> , 1998 , 8, 260-7	9.7	12
23	Comparative gene expression profiling by oligonucleotide fingerprinting. <i>Nucleic Acids Research</i> , 1998 , 26, 2216-23	20.1	42
22	Instability of highly expanded CAG repeats in mice transgenic for the Huntington's disease mutation. <i>Nature Genetics</i> , 1997 , 15, 197-200	36.3	275
21	Integrated Genome Mapping by Hybridization Techniques 1996 , 319-346		2
20	Model for a transcript map of human chromosome 21: isolation of new coding sequences from exon and enriched cDNA libraries. <i>Human Molecular Genetics</i> , 1995 , 4, 1291-304	5.6	68
19	Construction of genetic maps using distance geometry. <i>Genomics</i> , 1995 , 30, 59-70	4.3	22

18	Efficient high-resolution genetic mapping of mouse interspersed repetitive sequence PCR products, toward integrated genetic and physical mapping of the mouse genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1995 , 92, 5302-6	11.5	30
17	An integrated YAC-overlap and Rosmid-pocketRmap of the human chromosome 21. <i>Human Molecular Genetics</i> , 1994 , 3, 759-70	5.6	70
16	An algorithm to detect chimeric clones and random noise in genomic mapping. <i>Genomics</i> , 1994 , 22, 482-4.3	4.3	8
15	Informatics and Experiments for the Human Genome Project 1994 , 19-24		
14	High resolution cosmid and P1 maps spanning the 14 Mb genome of the fission yeast <i>S. pombe</i> . <i>Cell</i> , 1993 , 73, 109-20	56.2	237
13	A novel gene containing a trinucleotide repeat that is expanded and unstable on Huntington's disease chromosomes. The Huntington's Disease Collaborative Research Group. <i>Cell</i> , 1993 , 72, 971-83	56.2	6854
12	Algorithms and software tools for ordering clone libraries: application to the mapping of the genome of <i>Schizosaccharomyces pombe</i> . <i>Nucleic Acids Research</i> , 1993 , 21, 1965-74	20.1	66
11	A cosmid contig and high resolution restriction map of the 2 megabase region containing the Huntington's disease gene. <i>Nature Genetics</i> , 1993 , 4, 181-6	36.3	93
10	Complete coverage of the <i>Schizosaccharomyces pombe</i> genome in yeast artificial chromosomes. <i>Nature Genetics</i> , 1992 , 1, 273-7	36.3	90
9	Maximum-likelihood estimation of the statistical distribution of Smith-Waterman local sequence similarity scores. <i>Bulletin of Mathematical Biology</i> , 1992 , 54, 59-75	2.1	70
8	The transcriptional control proteins c-Myb and v-Myb contain a basic region DNA binding motif. <i>FEBS Letters</i> , 1991 , 282, 293-4	3.8	10
7	Dissociation of antibody responses during human schistosomiasis and evidence for enhancement of granuloma size by anti-carbohydrate IgM. <i>Transactions of the Royal Society of Tropical Medicine and Hygiene</i> , 1990 , 84, 808-14	2	7
6	An accurate approximation to the distribution of the length of the longest matching word between two random DNA sequences. <i>Bulletin of Mathematical Biology</i> , 1990 , 52, 773-784	2.1	5
5	Tests for the statistical significance of protein sequence similarities in data-bank searches. <i>Protein Engineering, Design and Selection</i> , 1990 , 4, 149-54	1.9	5
4	<i>Schistosoma mansoni</i> : histological analysis of the synergistic interaction between vaccine immunity and praziquantel therapy in the lungs of mice. <i>Parasite Immunology</i> , 1990 , 12, 367-87	2.2	11
3	Limited haplotype diversity underlies polygenic trait architecture across 70 years of wheat breeding		3
2	Multiple laboratory mouse reference genomes define strain specific haplotypes and novel functional loci		7
1	Analysis of independent cohorts of outbred CFW mice reveals novel loci for behavioral and physiological traits and identifies factors determining reproducibility		1

