

# Chris Haley

## List of Publications by Year in descending order

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Version: 2024-02-01

147  
papers

12,664  
citations

46918

47  
h-index

30010

103  
g-index

171  
all docs

171  
docs citations

171  
times ranked

16717  
citing authors

#	ARTICLE	IF	CITATIONS
1	A catalogue of omics biological ageing clocks reveals substantial commonality and associations with disease risk. <i>Aging</i> , 2022, 14, 623-659.	1.4	22
2	Nontrivial Replication of Loci Detected by Multi-Trait Methods. <i>Frontiers in Genetics</i> , 2021, 12, 627989.	1.1	4
3	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , 2021, 53, 1311-1321.	9.4	218
4	Genome-wide methylation data improves dissection of the effect of smoking on body mass index. <i>PLoS Genetics</i> , 2021, 17, e1009750.	1.5	7
5	Identification of epigenome-wide DNA methylation differences between carriers of APOE $\epsilon$ 4 and APOE $\epsilon$ 2 alleles. <i>Genome Medicine</i> , 2021, 13, 1.	3.6	76
6	Genetic mechanisms of critical illness in COVID-19. <i>Nature</i> , 2021, 591, 92-98.	13.7	1,014
7	SNP and Haplotype Regional Heritability Mapping (SNHap-RHM): Joint Mapping of Common and Rare Variation Affecting Complex Traits. <i>Frontiers in Genetics</i> , 2021, 12, 791712.	1.1	2
8	Lifestyle and Genetic Factors Modify Parent-of-Origin Effects on the Human Methylome. <i>EBioMedicine</i> , 2021, 74, 103730.	2.7	5
9	Genomic regions influencing intramuscular fat in divergently selected rabbit lines. <i>Animal Genetics</i> , 2020, 51, 58-69.	0.6	21
10	Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. <i>Nature Metabolism</i> , 2020, 2, 1135-1148.	5.1	327
11	Bayesian reassessment of the epigenetic architecture of complex traits. <i>Nature Communications</i> , 2020, 11, 2865.	5.8	43
12	Identifying epigenetic biomarkers of established prognostic factors and survival in a clinical cohort of individuals with oropharyngeal cancer. <i>Clinical Epigenetics</i> , 2020, 12, 95.	1.8	6
13	Linking protein to phenotype with Mendelian Randomization detects 38 proteins with causal roles in human diseases and traits. <i>PLoS Genetics</i> , 2020, 16, e1008785.	1.5	29
14	An actionable KCNH2 Long QT Syndrome variant detected by sequence and haplotype analysis in a population research cohort. <i>Scientific Reports</i> , 2019, 9, 10964.	1.6	17
15	“Arte et Labore” A Blackburn Rovers fan's legacy in human complex trait genetics. <i>Journal of Animal Breeding and Genetics</i> , 2019, 136, 273-278.	0.8	1
16	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019, 10, 4957.	5.8	84
17	Improved precision of epigenetic clock estimates across tissues and its implication for biological ageing. <i>Genome Medicine</i> , 2019, 11, 54.	3.6	191
18	The genetic landscape of Scotland and the Isles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 19064-19070.	3.3	24

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19	Parent of origin genetic effects on methylation in humans are common and influence complex trait variation. <i>Nature Communications</i> , 2019, 10, 1383.	5.8	37
20	Insulin resistance: Genetic associations with depression and cognition in population based cohorts. <i>Experimental Neurology</i> , 2019, 316, 20-26.	2.0	10
21	Increased ultra-rare variant load in an isolated Scottish population impacts exonic and regulatory regions. <i>PLoS Genetics</i> , 2019, 15, e1008480.	1.5	17
22	Association of Whole-Genome and NETRIN1 Signaling Pathwayâ€‘Derived Polygenic Risk Scores for Major Depressive Disorder and White Matter Microstructure in the UK Biobank. <i>Biological Psychiatry: Cognitive Neuroscience and Neuroimaging</i> , 2019, 4, 91-100.	1.1	16
23	Cohort profile for the STRatifying Resilience and Depression Longitudinally (STRADL) study: A depression-focused investigation of Generation Scotland, using detailed clinical, cognitive, and neuroimaging assessments. <i>Wellcome Open Research</i> , 2019, 4, 185.	0.9	27
24	Cohort Profile: Stratifying Resilience and Depression Longitudinally (STRADL): a questionnaire follow-up of Generation Scotland: Scottish Family Health Study (GS:SFHS). <i>International Journal of Epidemiology</i> , 2018, 47, 13-14g.	0.9	66
25	Genome-wide association study of depression phenotypes in UK Biobank identifies variants in excitatory synaptic pathways. <i>Nature Communications</i> , 2018, 9, 1470.	5.8	415
26	Genome-wide meta-analyses of stratified depression in Generation Scotland and UK Biobank. <i>Translational Psychiatry</i> , 2018, 8, 9.	2.4	66
27	Genomic analysis of family data reveals additional genetic effects on intelligence and personality. <i>Molecular Psychiatry</i> , 2018, 23, 2347-2362.	4.1	131
28	Haplotype Heritability Mapping Method Uncovers Missing Heritability of Complex Traits. <i>Scientific Reports</i> , 2018, 8, 4982.	1.6	14
29	Epigenetic prediction of complex traits and death. <i>Genome Biology</i> , 2018, 19, 136.	3.8	146
30	Addendum: Genome-wide association study of depression phenotypes in UK Biobank identifies variants in excitatory synaptic pathways. <i>Nature Communications</i> , 2018, 9, 3578.	5.8	16
31	Genome-wide pleiotropy and shared biological pathways for resistance to bovine pathogens. <i>PLoS ONE</i> , 2018, 13, e0194374.	1.1	4
32	Genetic and environmental determinants of stressful life events and their overlap with depression and neuroticism. <i>Wellcome Open Research</i> , 2018, 3, 11.	0.9	15
33	Genetic and environmental determinants of stressful life events and their overlap with depression and neuroticism. <i>Wellcome Open Research</i> , 2018, 3, 11.	0.9	19
34	Shared activity patterns arising at genetic susceptibility loci reveal underlying genomic and cellular architecture of human disease. <i>PLoS Computational Biology</i> , 2018, 14, e1005934.	1.5	17
35	A Combined Pathway and Regional Heritability Analysis Indicates NETRIN1 Pathway Is Associated With Major Depressive Disorder. <i>Biological Psychiatry</i> , 2017, 81, 336-346.	0.7	32
36	Exploration of haplotype research consortium imputation for genome-wide association studies in 20,032 Generation Scotland participants. <i>Genome Medicine</i> , 2017, 9, 23.	3.6	110

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37	Genome-wide Regional Heritability Mapping Identifies a Locus Within the TOX2 Gene Associated With Major Depressive Disorder. <i>Biological Psychiatry</i> , 2017, 82, 312-321.	0.7	26
38	Regional variation in health is predominantly driven by lifestyle rather than genetics. <i>Nature Communications</i> , 2017, 8, 801.	5.8	15
39	Genome-wide haplotype-based association analysis of major depressive disorder in Generation Scotland and UK Biobank. <i>Translational Psychiatry</i> , 2017, 7, 1263.	2.4	23
40	Haplotype-based association analysis of general cognitive ability in Generation Scotland, the English Longitudinal Study of Ageing, and UK Biobank. <i>Wellcome Open Research</i> , 2017, 2, 61.	0.9	4
41	Antagonistic genetic correlations for milking traits within the genome of dairy cattle. <i>PLoS ONE</i> , 2017, 12, e0175105.	1.1	4
42	Evaluating the contribution of genetics and familial shared environment to common disease using the UK Biobank. <i>Nature Genetics</i> , 2016, 48, 980-983.	9.4	105
43	Shared Genetics and Couple-Associated Environment Are Major Contributors to the Risk of Both Clinical and Self-Declared Depression. <i>EBioMedicine</i> , 2016, 14, 161-167.	2.7	32
44	Gene expression comparison of resistant and susceptible Atlantic salmon fry challenged with Infectious Pancreatic Necrosis virus reveals a marked contrast in immune response. <i>BMC Genomics</i> , 2016, 17, 279.	1.2	78
45	The heritability and patterns of DNA methylation in normal human colorectum. <i>Human Molecular Genetics</i> , 2016, 25, ddw072.	1.4	11
46	Pedigree- and SNP-Associated Genetics and Recent Environment are the Major Contributors to Anthropometric and Cardiometabolic Trait Variation. <i>PLoS Genetics</i> , 2016, 12, e1005804.	1.5	72
47	Genetic and Environmental Risk for Chronic Pain and the Contribution of Risk Variants for Major Depressive Disorder: A Family-Based Mixed-Model Analysis. <i>PLoS Medicine</i> , 2016, 13, e1002090.	3.9	60
48	Epidemiology and Heritability of Major Depressive Disorder, Stratified by Age of Onset, Sex, and Illness Course in Generation Scotland: Scottish Family Health Study (GS:SFHS). <i>PLoS ONE</i> , 2015, 10, e0142197.	1.1	101
49	Genomic prediction of complex human traits: relatedness, trait architecture and predictive meta-models. <i>Human Molecular Genetics</i> , 2015, 24, 4167-4182.	1.4	24
50	Genetic loci inherited from hens lacking maternal behaviour both inhibit and paradoxically promote this behaviour. <i>Genetics Selection Evolution</i> , 2015, 47, 100.	1.2	10
51	Detecting signatures of selection in nine distinct lines of broiler chickens. <i>Animal Genetics</i> , 2015, 46, 37-49.	0.6	20
52	Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , 2015, 523, 459-462.	18.7	173
53	Recent genomic heritage in Scotland. <i>BMC Genomics</i> , 2015, 16, 437.	1.2	46
54	Modulation of Genetic Associations with Serum Urate Levels by Body-Mass-Index in Humans. <i>PLoS ONE</i> , 2015, 10, e0119752.	1.1	64

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55	Abundant local interactions in the 4p16.1 region suggest functional mechanisms underlying SLC2A9 associations with human serum uric acid. <i>Human Molecular Genetics</i> , 2014, 23, 5061-5068.	1.4	29
56	Detecting epistasis in human complex traits. <i>Nature Reviews Genetics</i> , 2014, 15, 722-733.	7.7	372
57	Analysis of the genetics of boar taint reveals both single SNPs and regional effects. <i>BMC Genomics</i> , 2014, 15, 424.	1.2	30
58	The genomic signature of trait-associated variants. <i>BMC Genomics</i> , 2013, 14, 108.	1.2	45
59	The heritability of human disease: estimation, uses and abuses. <i>Nature Reviews Genetics</i> , 2013, 14, 139-149.	7.7	231
60	Signatures of Diversifying Selection in European Pig Breeds. <i>PLoS Genetics</i> , 2013, 9, e1003453.	1.5	228
61	An Evolutionary Perspective on Epistasis and the Missing Heritability. <i>PLoS Genetics</i> , 2013, 9, e1003295.	1.5	107
62	QTL (Quantitative Trait Locus). , 2013, , 4-7.		0
63	Inference of identity by descent in population isolates and optimal sequencing studies. <i>European Journal of Human Genetics</i> , 2013, 21, 1140-1145.	1.4	14
64	Secreted Phosphoprotein 1 Expression in Endometrium and Placental Tissues of Hyperproliferic Large White and Meishan Gilts1. <i>Biology of Reproduction</i> , 2013, 88, 120.	1.2	20
65	Properties of Local Interactions and Their Potential Value in Complementing Genome-Wide Association Studies. <i>PLoS ONE</i> , 2013, 8, e71203.	1.1	15
66	The power of regional heritability analysis for rare and common variant detection: simulations and application to eye biometrical traits. <i>Frontiers in Genetics</i> , 2013, 4, 232.	1.1	36
67	Local Exome Sequences Facilitate Imputation of Less Common Variants and Increase Power of Genome Wide Association Studies. <i>PLoS ONE</i> , 2013, 8, e68604.	1.1	13
68	High-throughput analysis of epistasis in genome-wide association studies with BiForce. <i>Bioinformatics</i> , 2012, 28, 1957-1964.	1.8	49
69	Uncovering Networks from Genome-Wide Association Studies via Circular Genomic Permutation. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 1067-1075.	0.8	61
70	BiForce Toolbox: powerful high-throughput computational analysis of gene-gene interactions in genome-wide association studies. <i>Nucleic Acids Research</i> , 2012, 40, W628-W632.	6.5	25
71	Genome-wide analysis of epistasis in body mass index using multiple human populations. <i>European Journal of Human Genetics</i> , 2012, 20, 857-862.	1.4	33
72	Heritability of cortisol response to confinement stress in European sea bass <i>dicentrarchus labrax</i> . <i>Genetics Selection Evolution</i> , 2012, 44, 15.	1.2	27

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73	Development of a genetic tool for product regulation in the diverse British pig breed market. BMC Genomics, 2012, 13, 580.	1.2	35
74	Localising Loci underlying Complex Trait Variation Using Regional Genomic Relationship Mapping. PLoS ONE, 2012, 7, e46501.	1.1	111
75	QTL affecting morphometric traits and stress response in the gilthead seabream ( <i>Sparus aurata</i> ). Aquaculture, 2011, 319, 58-66.	1.7	42
76	Quantitative trait loci for resistance to fish pasteurellosis in gilthead sea bream ( <i>Sparus aurata</i> ). Animal Genetics, 2011, 42, 191-203.	0.6	47
77	A cornucopia of maize genes. Nature Genetics, 2011, 43, 87-88.	9.4	10
78	An empirical assessment of individual-based population genetic statistical techniques: application to British pig breeds. Heredity, 2011, 106, 261-269.	1.2	38
79	Association analyses of the MAS-QTL data set using grammar, principal components and Bayesian network methodologies. BMC Proceedings, 2011, 5, S8.	1.8	7
80	EpiGPU: exhaustive pairwise epistasis scans parallelized on consumer level graphics cards. Bioinformatics, 2011, 27, 1462-1465.	1.8	77
81	Characterisation of Genome-Wide Association Epistasis Signals for Serum Uric Acid in Human Population Isolates. PLoS ONE, 2011, 6, e23836.	1.1	15
82	QTL for body weight, morphometric traits and stress response in European sea bass <i>Dicentrarchus labrax</i> . Animal Genetics, 2010, 41, 337-345.	0.6	59
83	Genetic comparison of a Croatian isolate and CEPH European founders. Genetic Epidemiology, 2010, 34, 140-145.	0.6	7
84	Mapping of quantitative trait loci affecting classical scrapie incubation time in a population comprising several generations of scrapie-infected sheep. Journal of General Virology, 2010, 91, 575-579.	1.3	5
85	Detection of multiple quantitative trait loci and their pleiotropic effects in outbred pig populations. Genetics Selection Evolution, 2009, 41, 44.	1.2	6
86	Detecting parent of origin and dominant QTL in a two-generation commercial poultry pedigree using variance component methodology. Genetics Selection Evolution, 2009, 41, 6.	1.2	19
87	Genome-wide QTL mapping for three traits related to teat number in a White Duroc × Erhualian pig resource population. BMC Genetics, 2009, 10, 6.	2.7	37
88	A linkage map of the porcine genome from a large-scale White Duroc × Erhualian resource population and evaluation of factors affecting recombination rates. Animal Genetics, 2009, 40, 47-52.	0.6	60
89	BoLA-DR peptide binding pockets are fundamental for foot-and-mouth disease virus vaccine design in cattle. Vaccine, 2009, 28, 28-37.	1.7	56
90	Estimates of heritability and genetic correlation for body length and resistance to fish pasteurellosis in the gilthead sea bream ( <i>Sparus aurata</i> L.). Aquaculture, 2009, 298, 29-35.	1.7	49

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91	A combined strategy for quantitative trait loci detection by genome-wide association. BMC Proceedings, 2009, 3, S6.	1.8	10
92	QTL mapping designs for aquaculture. Aquaculture, 2008, 285, 23-29.	1.7	50
93	European Sea Bass. , 2008, , 117-133.		11
94	Major Quantitative Trait Loci Affect Resistance to Infectious Pancreatic Necrosis in Atlantic Salmon ( <i>Salmo salar</i> ). Genetics, 2008, 178, 1109-1115.	1.2	262
95	Optimal Design of Genetic Studies of Gene Expression With Two-Color Microarrays in Outbred Crosses. Genetics, 2008, 180, 1691-1698.	1.2	3
96	Detecting dominant QTL with variance component analysis in simulated pedigrees. Genetical Research, 2008, 90, 363-374.	0.3	5
97	Correlations in refractive errors between siblings in the Singapore Cohort Study of Risk factors for Myopia. British Journal of Ophthalmology, 2007, 91, 781-784.	2.1	37
98	Genomewide Rapid Association Using Mixed Model and Regression: A Fast and Simple Method For Genomewide Pedigree-Based Quantitative Trait Loci Association Analysis. Genetics, 2007, 177, 577-585.	1.2	411
99	Mapping quantitative trait loci in European sea bass ( <i>Dicentrarchus labrax</i> ): The BASSMAP pilot study. Aquaculture, 2007, 272, S172-S182.	1.7	45
100	Rapid and robust association mapping of expression quantitative trait loci. BMC Proceedings, 2007, 1, S144.	1.8	15
101	Livestock genomics: bridging the gap between mice and men. Trends in Biotechnology, 2007, 25, 483-489.	4.9	17
102	Towards in vitro genetics. Trends in Genetics, 2007, 23, 382-386.	2.9	5
103	Linkage mapping of the locus for inherited ovine arthrogyrosis (IOA) to sheep Chromosome 5. Mammalian Genome, 2007, 18, 43-52.	1.0	10
104	Genetic control of lipids in the mouse cross DU6i $\times$ DBA/2. Mammalian Genome, 2007, 18, 757-766.	1.0	6
105	A Genetic and Cytogenetic Map for the Duck ( <i>Anas platyrhynchos</i> ). Genetics, 2006, 173, 287-296.	1.2	61
106	Genetic diversity in European pigs utilizing amplified fragment length polymorphism markers. Animal Genetics, 2006, 37, 232-238.	0.6	31
107	Genetical genomics in livestock: potentials and pitfalls. Animal Genetics, 2006, 37, 10-12.	0.6	39
108	Prediction of IBD based on population history for fine gene mapping. Genetics Selection Evolution, 2006, 38, 231.	1.2	13

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109	Genetical genomics in humans and model organisms. <i>Trends in Genetics</i> , 2005, 21, 377-381.	2.9	126
110	Simultaneous mapping of epistatic QTL in DU6i $\times$ DBA/2 mice. <i>Mammalian Genome</i> , 2005, 16, 481-494.	1.0	36
111	A QTL affecting daily feed intake maps to Chromosome 2 in pigs. <i>Mammalian Genome</i> , 2005, 16, 464-470.	1.0	31
112	An assessment of European pig diversity using molecular markers: Partitioning of diversity among breeds. <i>Conservation Genetics</i> , 2005, 6, 729-741.	0.8	40
113	The Impact of Using Related Individuals for Haplotype Reconstruction in Population Studies. <i>Genetics</i> , 2005, 171, 1321-1330.	1.2	8
114	A Microsatellite Linkage Map of the European Sea Bass <i>Dicentrarchus labrax</i> L. Sequence data from this article have been deposited with the EMBL/GenBank Data Libraries under accession nos. AY383721â€“383728, AY387399â€“387406, AY430367â€“430377, AY453615â€“453617, AY453620â€“453628, AY523943â€“523968, AY529493â€“529497, AY604983â€“604992, AY628756â€“628762, AY636156â€“636161, AY639097â€“639109, AY639891â€“639899, AY694149â€“694154, and AY714324â€“714334.. <i>Genetics</i> , 2005, 170, 1821-1826.		118
115	The genetic dissection of immune response using gene-expression studies and genome mapping. <i>Veterinary Immunology and Immunopathology</i> , 2005, 105, 343-352.	0.5	34
116	Linkage Analysis of the Genetic Loci for High Myopia on 18p, 12q, and 17q in 51 U.K. Families. , 2004, 45, 2879.		72
117	Mapping of Multiple Quantitative Trait Loci Affecting Bovine Spongiform Encephalopathy. <i>Genetics</i> , 2004, 167, 1863-1872.	1.2	44
118	Epistasis: too often neglected in complex trait studies?. <i>Nature Reviews Genetics</i> , 2004, 5, 618-625.	7.7	820
119	QTL detection and allelic effects for growth and fat traits in outbred pig populations. <i>Genetics Selection Evolution</i> , 2004, 36, 83-96.	1.2	16
120	QTLs for pre- and postweaning body weight and body composition in selected mice. <i>Mammalian Genome</i> , 2004, 15, 593-609.	1.0	33
121	Simultaneous mapping of epistatic QTL in chickens reveals clusters of QTL pairs with similar genetic effects on growth. <i>Genetical Research</i> , 2004, 83, 197-209.	0.3	82
122	On the prediction of simultaneous inbreeding coefficients at multiple loci. <i>Genetical Research</i> , 2004, 83, 113-120.	0.3	10
123	A regulatory mutation in IGF2 causes a major QTL effect on muscle growth in the pig. <i>Nature</i> , 2003, 425, 832-836.	13.7	791
124	Power of QTL detection using association tests with family controls. <i>European Journal of Human Genetics</i> , 2003, 11, 819-827.	1.4	4
125	Mapping Quantitative Trait Loci Affecting Female Reproductive Traits on Porcine Chromosome 81. <i>Biology of Reproduction</i> , 2003, 68, 2172-2179.	1.2	87
126	What Can the Genetics Revolution Offer the Meat Industry?. <i>Outlook on Agriculture</i> , 2003, 32, 219-226.	1.8	7



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127	Quantitative Trait Loci Variation for Growth and Obesity Between and Within Lines of Pigs (<i>Sus Tj ETQq1 1 0.784314 rgBT <sub>56</sub> /Overloc	1.2	56
128	QTL Express: mapping quantitative trait loci in simple and complex pedigrees. <i>Bioinformatics</i> , 2002, 18, 339-340.	1.8	434
129	Genome-wide search for markers associated with bovine spongiform encephalopathy. <i>Mammalian Genome</i> , 2002, 13, 164-168.	1.0	30
130	Genome-wide search for markers associated with bovine spongiform encephalopathy. <i>Mammalian Genome</i> , 2002, 13, 164-168.	1.0	31
131	The porcine gonadotropin-releasing hormone receptor gene (GNRHR): Genomic organization, polymorphisms, and association with the number of corpora lutea. <i>Genome</i> , 2001, 44, 7-12.	0.9	29
132	True and false positive peaks in genomewide scans: The long and the short of it. <i>Genetic Epidemiology</i> , 2001, 20, 409-414.	0.6	8
133	Genome-wide search for loci controlling serum IGF binding protein levels of mice. <i>FASEB Journal</i> , 2001, 15, 978-987.	0.2	14
134	The porcine gonadotropin-releasing hormone receptor gene (<i>GNRHR</i>): Genomic organization, polymorphisms, and association with the number of corpora lutea. <i>Genome</i> , 2001, 44, 7-12.	0.9	28
135	Combined Analyses of Data From Quantitative Trait Loci Mapping Studies: Chromosome 4 Effects on Porcine Growth and Fatness. <i>Genetics</i> , 2000, 155, 1369-1378.	1.2	128
136	Multitrait Least Squares for Quantitative Trait Loci Detection. <i>Genetics</i> , 2000, 156, 899-911.	1.2	223
137	Mapping Quantitative Trait Loci in Complex Pedigrees: A Two-Step Variance Component Approach. <i>Genetics</i> , 2000, 156, 2081-2092.	1.2	153
138	Single QTL Effects, Epistasis, and Pleiotropy Account for Two-thirds of the Phenotypic F <sub>2</sub> Variance of Growth and Obesity in DU6i x DBA/2 Mice. <i>Genome Research</i> , 2000, 10, 1941-1957.	2.4	23
139	Genetic Determination of Cardiac Mass in Normotensive Rats. <i>Hypertension</i> , 1999, 33, 949-953.	1.3	93
140	Genetic mapping of modifier loci affecting malignant hypertension in TGRmRen2 rats. <i>Kidney International</i> , 1999, 56, 414-420.	2.6	44
141	DNA microsatellite analysis of Dolly. <i>Nature</i> , 1998, 394, 329-329.	13.7	44
142	Multiple Marker Mapping of Quantitative Trait Loci in a Cross Between Outbred Wild Boar and Large White Pigs. <i>Genetics</i> , 1998, 149, 1069-1080.	1.2	361
143	Quantitative Trait Loci Affecting Body Weight and Fatness From a Mouse Line Selected for Extreme High Growth. <i>Genetics</i> , 1998, 150, 369-381.	1.2	113
144	Confidence Intervals in QTL Mapping by Bootstrapping. <i>Genetics</i> , 1996, 143, 1013-1020.	1.2	540

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145	Livestock QTLs “bringing home the bacon?”. Trends in Genetics, 1995, 11, 488-492.	2.9	36
146	Genetic mapping of quantitative trait loci for growth and fatness in pigs. Science, 1994, 263, 1771-1774.	6.0	636
147	Cohort profile for the STRatifying Resilience and Depression Longitudinally (STRADL) study: A depression-focused investigation of Generation Scotland, using detailed clinical, cognitive, and neuroimaging assessments. Wellcome Open Research, 0, 4, 185.	0.9	12