

Chris Haley

List of Publications by Year in descending order

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147
papers

12,664
citations

47006

47
h-index

30087

103
g-index

171
all docs

171
docs citations

171
times ranked

16717
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic mechanisms of critical illness in COVID-19. <i>Nature</i> , 2021, 591, 92-98.	27.8	1,014
2	Epistasis: too often neglected in complex trait studies?. <i>Nature Reviews Genetics</i> , 2004, 5, 618-625.	16.3	820
3	A regulatory mutation in IGF2 causes a major QTL effect on muscle growth in the pig. <i>Nature</i> , 2003, 425, 832-836.	27.8	791
4	Genetic Mapping of Quantitative Trait Loci for Growth and Fatness in Pigs. <i>Science</i> , 1994, 263, 1771-1774.	12.6	636
5	Confidence Intervals in QTL Mapping by Bootstrapping. <i>Genetics</i> , 1996, 143, 1013-1020.	2.9	540
6	QTL Express: mapping quantitative trait loci in simple and complex pedigrees. <i>Bioinformatics</i> , 2002, 18, 339-340.	4.1	434
7	Genome-wide association study of depression phenotypes in UK Biobank identifies variants in excitatory synaptic pathways. <i>Nature Communications</i> , 2018, 9, 1470.	12.8	415
8	Genomewide Rapid Association Using Mixed Model and Regression: A Fast and Simple Method For Genomewide Pedigree-Based Quantitative Trait Loci Association Analysis. <i>Genetics</i> , 2007, 177, 577-585.	2.9	411
9	Detecting epistasis in human complex traits. <i>Nature Reviews Genetics</i> , 2014, 15, 722-733.	16.3	372
10	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.	2.9	361
11	Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. <i>Nature Metabolism</i> , 2020, 2, 1135-1148.	11.9	327
12	Major Quantitative Trait Loci Affect Resistance to Infectious Pancreatic Necrosis in Atlantic Salmon (<i>Salmo salar</i>). <i>Genetics</i> , 2008, 178, 1109-1115.	2.9	262
13	The heritability of human disease: estimation, uses and abuses. <i>Nature Reviews Genetics</i> , 2013, 14, 139-149.	16.3	231
14	Signatures of Diversifying Selection in European Pig Breeds. <i>PLoS Genetics</i> , 2013, 9, e1003453.	3.5	228
15	Multitrait Least Squares for Quantitative Trait Loci Detection. <i>Genetics</i> , 2000, 156, 899-911.	2.9	223
16	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , 2021, 53, 1311-1321.	21.4	218
17	Improved precision of epigenetic clock estimates across tissues and its implication for biological ageing. <i>Genome Medicine</i> , 2019, 11, 54.	8.2	191
18	Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , 2015, 523, 459-462.	27.8	173

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19	Mapping Quantitative Trait Loci in Complex Pedigrees: A Two-Step Variance Component Approach. <i>Genetics</i> , 2000, 156, 2081-2092.	2.9	153
20	Epigenetic prediction of complex traits and death. <i>Genome Biology</i> , 2018, 19, 136.	8.8	146
21	Genomic analysis of family data reveals additional genetic effects on intelligence and personality. <i>Molecular Psychiatry</i> , 2018, 23, 2347-2362.	7.9	131
22	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.	2.9	128
23	Genetical genomics in humans and model organisms. <i>Trends in Genetics</i> , 2005, 21, 377-381.	6.7	126
24	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.	2.9	118
25	Quantitative Trait Loci Affecting Body Weight and Fatness From a Mouse Line Selected for Extreme High Growth. <i>Genetics</i> , 1998, 150, 369-381.	2.9	113
26	Localising Loci underlying Complex Trait Variation Using Regional Genomic Relationship Mapping. <i>PLoS ONE</i> , 2012, 7, e46501.	2.5	111
27	Exploration of haplotype research consortium imputation for genome-wide association studies in 20,032 Generation Scotland participants. <i>Genome Medicine</i> , 2017, 9, 23.	8.2	110
28	An Evolutionary Perspective on Epistasis and the Missing Heritability. <i>PLoS Genetics</i> , 2013, 9, e1003295.	3.5	107
29	Evaluating the contribution of genetics and familial shared environment to common disease using the UK Biobank. <i>Nature Genetics</i> , 2016, 48, 980-983.	21.4	105
30	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.	2.5	101
31	Genetic Determination of Cardiac Mass in Normotensive Rats. <i>Hypertension</i> , 1999, 33, 949-953.	2.7	93
32	Mapping Quantitative Trait Loci Affecting Female Reproductive Traits on Porcine Chromosome 81. <i>Biology of Reproduction</i> , 2003, 68, 2172-2179.	2.7	87
33	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019, 10, 4957.	12.8	84
34	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.	0.9	82
35	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.	2.8	78
36	EpiGPU: exhaustive pairwise epistasis scans parallelized on consumer level graphics cards. <i>Bioinformatics</i> , 2011, 27, 1462-1465.	4.1	77

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37	Identification of epigenome-wide DNA methylation differences between carriers of APOE ϵ 4 and APOE ϵ 2 alleles. <i>Genome Medicine</i> , 2021, 13, 1.	8.2	76
38	Linkage Analysis of the Genetic Loci for High Myopia on 18p, 12q, and 17q in 51 U.K. Families. , 2004, 45, 2879.		72
39	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.	3.5	72
40	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.	1.9	66
41	Genome-wide meta-analyses of stratified depression in Generation Scotland and UK Biobank. <i>Translational Psychiatry</i> , 2018, 8, 9.	4.8	66
42	Modulation of Genetic Associations with Serum Urate Levels by Body-Mass-Index in Humans. <i>PLoS ONE</i> , 2015, 10, e0119752.	2.5	64
43	A Genetic and Cytogenetic Map for the Duck (<i>Anas platyrhynchos</i>). <i>Genetics</i> , 2006, 173, 287-296.	2.9	61
44	Uncovering Networks from Genome-Wide Association Studies via Circular Genomic Permutation. G3: Genes, Genomes, <i>Genetics</i> , 2012, 2, 1067-1075.	1.8	61
45	A linkage map of the porcine genome from a large-scale White Duroc \times Erhualian resource population and evaluation of factors affecting recombination rates. <i>Animal Genetics</i> , 2009, 40, 47-52.	1.7	60
46	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.	8.4	60
47	QTL for body weight, morphometric traits and stress response in European sea bass <i>Dicentrarchus labrax</i> . <i>Animal Genetics</i> , 2010, 41, 337-345.	1.7	59
48	BoLA-DR peptide binding pockets are fundamental for foot-and-mouth disease virus vaccine design in cattle. <i>Vaccine</i> , 2009, 28, 28-37.	3.8	56
49	Quantitative Trait Loci Variation for Growth and Obesity Between and Within Lines of Pigs (<i>Sus</i>) Tj ETQq1 1 0.784314 rgBT /Overl 2.9 56	2.9	56
50	QTL mapping designs for aquaculture. <i>Aquaculture</i> , 2008, 285, 23-29.	3.5	50
51	Estimates of heritability and genetic correlation for body length and resistance to fish pasteurellosis in the gilthead sea bream (<i>Sparus aurata</i> L.). <i>Aquaculture</i> , 2009, 298, 29-35.	3.5	49
52	High-throughput analysis of epistasis in genome-wide association studies with BiForce. <i>Bioinformatics</i> , 2012, 28, 1957-1964.	4.1	49
53	Quantitative trait loci for resistance to fish pasteurellosis in gilthead sea bream (<i>Sparus aurata</i>). <i>Animal Genetics</i> , 2011, 42, 191-203.	1.7	47
54	Recent genomic heritage in Scotland. <i>BMC Genomics</i> , 2015, 16, 437.	2.8	46

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55	Mapping quantitative trait loci in European sea bass (<i>Dicentrarchus labrax</i>): The BASSMAP pilot study. <i>Aquaculture</i> , 2007, 272, S172-S182.	3.5	45
56	The genomic signature of trait-associated variants. <i>BMC Genomics</i> , 2013, 14, 108.	2.8	45
57	DNA microsatellite analysis of Dolly. <i>Nature</i> , 1998, 394, 329-329.	27.8	44
58	Genetic mapping of modifier loci affecting malignant hypertension in TGRmRen2 rats. <i>Kidney International</i> , 1999, 56, 414-420.	5.2	44
59	Mapping of Multiple Quantitative Trait Loci Affecting Bovine Spongiform Encephalopathy. <i>Genetics</i> , 2004, 167, 1863-1872.	2.9	44
60	Bayesian reassessment of the epigenetic architecture of complex traits. <i>Nature Communications</i> , 2020, 11, 2865.	12.8	43
61	QTL affecting morphometric traits and stress response in the gilthead seabream (<i>Sparus aurata</i>). <i>Aquaculture</i> , 2011, 319, 58-66.	3.5	42
62	An assessment of European pig diversity using molecular markers: Partitioning of diversity among breeds. <i>Conservation Genetics</i> , 2005, 6, 729-741.	1.5	40
63	Genetical genomics in livestock: potentials and pitfalls. <i>Animal Genetics</i> , 2006, 37, 10-12.	1.7	39
64	An empirical assessment of individual-based population genetic statistical techniques: application to British pig breeds. <i>Heredity</i> , 2011, 106, 261-269.	2.6	38
65	Correlations in refractive errors between siblings in the Singapore Cohort Study of Risk factors for Myopia. <i>British Journal of Ophthalmology</i> , 2007, 91, 781-784.	3.9	37
66	Genome-wide QTL mapping for three traits related to teat number in a White Duroc × Erhualian pig resource population. <i>BMC Genomics</i> , 2009, 10, 6.	2.7	37
67	Parent of origin genetic effects on methylation in humans are common and influence complex trait variation. <i>Nature Communications</i> , 2019, 10, 1383.	12.8	37
68	Livestock QTLs “bringing home the bacon?”. <i>Trends in Genetics</i> , 1995, 11, 488-492.	6.7	36
69	Simultaneous mapping of epistatic QTL in DU6i × DBA/2 mice. <i>Mammalian Genome</i> , 2005, 16, 481-494.	2.2	36
70	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.	2.3	36
71	Development of a genetic tool for product regulation in the diverse British pig breed market. <i>BMC Genomics</i> , 2012, 13, 580.	2.8	35
72	The genetic dissection of immune response using gene-expression studies and genome mapping. <i>Veterinary Immunology and Immunopathology</i> , 2005, 105, 343-352.	1.2	34

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73	QTLs for pre- and postweaning body weight and body composition in selected mice. <i>Mammalian Genome</i> , 2004, 15, 593-609.	2.2	33
74	Genome-wide analysis of epistasis in body mass index using multiple human populations. <i>European Journal of Human Genetics</i> , 2012, 20, 857-862.	2.8	33
75	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.	6.1	32
76	A Combined Pathway and Regional Heritability Analysis Indicates NETRIN1 Pathway Is Associated With Major Depressive Disorder. <i>Biological Psychiatry</i> , 2017, 81, 336-346.	1.3	32
77	Genome-wide search for markers associated with bovine spongiform encephalopathy. <i>Mammalian Genome</i> , 2002, 13, 164-168.	2.2	31
78	A QTL affecting daily feed intake maps to Chromosome 2 in pigs. <i>Mammalian Genome</i> , 2005, 16, 464-470.	2.2	31
79	Genetic diversity in European pigs utilizing amplified fragment length polymorphism markers. <i>Animal Genetics</i> , 2006, 37, 232-238.	1.7	31
80	Genome-wide search for markers associated with bovine spongiform encephalopathy. <i>Mammalian Genome</i> , 2002, 13, 164-168.	2.2	30
81	Analysis of the genetics of boar taint reveals both single SNPs and regional effects. <i>BMC Genomics</i> , 2014, 15, 424.	2.8	30
82	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.	2.0	29
83	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.	2.9	29
84	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.	3.5	29
85	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.	2.0	28
86	Heritability of cortisol response to confinement stress in European sea bass <i>dicentrarchus labrax</i> . <i>Genetics Selection Evolution</i> , 2012, 44, 15.	3.0	27
87	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.	1.8	27
88	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.	1.3	26
89	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.	14.5	25
90	Genomic prediction of complex human traits: relatedness, trait architecture and predictive meta-models. <i>Human Molecular Genetics</i> , 2015, 24, 4167-4182.	2.9	24

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91	The genetic landscape of Scotland and the Isles. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 19064-19070.	7.1	24
92	Genome-wide haplotype-based association analysis of major depressive disorder in Generation Scotland and UK Biobank. Translational Psychiatry, 2017, 7, 1263.	4.8	23
93	Single QTL Effects, Epistasis, and Pleiotropy Account for Two-thirds of the Phenotypic $F_{2\text{}}$ Variance of Growth and Obesity in DU6i x DBA/2 Mice. Genome Research, 2000, 10, 1941-1957.	5.5	23
94	A catalogue of omics biological ageing clocks reveals substantial commonality and associations with disease risk. Aging, 2022, 14, 623-659.	3.1	22
95	Genomic regions influencing intramuscular fat in divergently selected rabbit lines. Animal Genetics, 2020, 51, 58-69.	1.7	21
96	Secreted Phosphoprotein 1 Expression in Endometrium and Placental Tissues of Hyperproliferic Large White and Meishan Gilts1. Biology of Reproduction, 2013, 88, 120.	2.7	20
97	Detecting signatures of selection in nine distinct lines of broiler chickens. Animal Genetics, 2015, 46, 37-49.	1.7	20
98	Detecting parent of origin and dominant QTL in a two-generation commercial poultry pedigree using variance component methodology. Genetics Selection Evolution, 2009, 41, 6.	3.0	19
99	Genetic and environmental determinants of stressful life events and their overlap with depression and neuroticism. Wellcome Open Research, 2018, 3, 11.	1.8	19
100	Livestock genomics: bridging the gap between mice and men. Trends in Biotechnology, 2007, 25, 483-489.	9.3	17
101	An actionable KCNH2 Long QT Syndrome variant detected by sequence and haplotype analysis in a population research cohort. Scientific Reports, 2019, 9, 10964.	3.3	17
102	Increased ultra-rare variant load in an isolated Scottish population impacts exonic and regulatory regions. PLoS Genetics, 2019, 15, e1008480.	3.5	17
103	Shared activity patterns arising at genetic susceptibility loci reveal underlying genomic and cellular architecture of human disease. PLoS Computational Biology, 2018, 14, e1005934.	3.2	17
104	QTL detection and allelic effects for growth and fat traits in outbred pig populations. Genetics Selection Evolution, 2004, 36, 83-96.	3.0	16
105	Addendum: Genome-wide association study of depression phenotypes in UK Biobank identifies variants in excitatory synaptic pathways. Nature Communications, 2018, 9, 3578.	12.8	16
106	Association of Whole-Genome and NETRIN1 Signaling Pathway-Derived Polygenic Risk Scores for Major Depressive Disorder and White Matter Microstructure in the UK Biobank. Biological Psychiatry: Cognitive Neuroscience and Neuroimaging, 2019, 4, 91-100.	1.5	16
107	Rapid and robust association mapping of expression quantitative trait loci. BMC Proceedings, 2007, 1, S144.	1.6	15
108	Properties of Local Interactions and Their Potential Value in Complementing Genome-Wide Association Studies. PLoS ONE, 2013, 8, e71203.	2.5	15

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109	Regional variation in health is predominantly driven by lifestyle rather than genetics. <i>Nature Communications</i> , 2017, 8, 801.	12.8	15
110	Genetic and environmental determinants of stressful life events and their overlap with depression and neuroticism. <i>Wellcome Open Research</i> , 2018, 3, 11.	1.8	15
111	Characterisation of Genome-Wide Association Epistasis Signals for Serum Uric Acid in Human Population Isolates. <i>PLoS ONE</i> , 2011, 6, e23836.	2.5	15
112	Genome-wide search for loci controlling serum IGF binding protein levels of mice. <i>FASEB Journal</i> , 2001, 15, 978-987.	0.5	14
113	Inference of identity by descent in population isolates and optimal sequencing studies. <i>European Journal of Human Genetics</i> , 2013, 21, 1140-1145.	2.8	14
114	Haplotype Heritability Mapping Method Uncovers Missing Heritability of Complex Traits. <i>Scientific Reports</i> , 2018, 8, 4982.	3.3	14
115	Prediction of IBD based on population history for fine gene mapping. <i>Genetics Selection Evolution</i> , 2006, 38, 231.	3.0	13
116	Local Exome Sequences Facilitate Imputation of Less Common Variants and Increase Power of Genome Wide Association Studies. <i>PLoS ONE</i> , 2013, 8, e68604.	2.5	13
117	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> , 0, 4, 185.	1.8	12
118	European Sea Bass. , 2008, , 117-133.		11
119	The heritability and patterns of DNA methylation in normal human colorectum. <i>Human Molecular Genetics</i> , 2016, 25, ddw072.	2.9	11
120	On the prediction of simultaneous inbreeding coefficients at multiple loci. <i>Genetical Research</i> , 2004, 83, 113-120.	0.9	10
121	Linkage mapping of the locus for inherited ovine arthrogyrosis (IOA) to sheep Chromosome 5. <i>Mammalian Genome</i> , 2007, 18, 43-52.	2.2	10
122	A combined strategy for quantitative trait loci detection by genome-wide association. <i>BMC Proceedings</i> , 2009, 3, S6.	1.6	10
123	A cornucopia of maize genes. <i>Nature Genetics</i> , 2011, 43, 87-88.	21.4	10
124	Genetic loci inherited from hens lacking maternal behaviour both inhibit and paradoxically promote this behaviour. <i>Genetics Selection Evolution</i> , 2015, 47, 100.	3.0	10
125	Insulin resistance: Genetic associations with depression and cognition in population based cohorts. <i>Experimental Neurology</i> , 2019, 316, 20-26.	4.1	10
126	True and false positive peaks in genomewide scans: The long and the short of it. <i>Genetic Epidemiology</i> , 2001, 20, 409-414.	1.3	8

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127	The Impact of Using Related Individuals for Haplotype Reconstruction in Population Studies. <i>Genetics</i> , 2005, 171, 1321-1330.	2.9	8
128	What Can the Genetics Revolution Offer the Meat Industry?. <i>Outlook on Agriculture</i> , 2003, 32, 219-226.	3.4	7
129	Genetic comparison of a Croatian isolate and CEPH European founders. <i>Genetic Epidemiology</i> , 2010, 34, 140-145.	1.3	7
130	Association analyses of the MAS-QTL data set using grammar, principal components and Bayesian network methodologies. <i>BMC Proceedings</i> , 2011, 5, S8.	1.6	7
131	Genome-wide methylation data improves dissection of the effect of smoking on body mass index. <i>PLoS Genetics</i> , 2021, 17, e1009750.	3.5	7
132	Genetic control of lipids in the mouse cross DU6i \times DBA/2. <i>Mammalian Genome</i> , 2007, 18, 757-766.	2.2	6
133	Detection of multiple quantitative trait loci and their pleiotropic effects in outbred pig populations. <i>Genetics Selection Evolution</i> , 2009, 41, 44.	3.0	6
134	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.	4.1	6
135	Towards in vitro genetics. <i>Trends in Genetics</i> , 2007, 23, 382-386.	6.7	5
136	Detecting dominant QTL with variance component analysis in simulated pedigrees. <i>Genetical Research</i> , 2008, 90, 363-374.	0.9	5
137	Mapping of quantitative trait loci affecting classical scrapie incubation time in a population comprising several generations of scrapie-infected sheep. <i>Journal of General Virology</i> , 2010, 91, 575-579.	2.9	5
138	Lifestyle and Genetic Factors Modify Parent-of-Origin Effects on the Human Methylome. <i>EBioMedicine</i> , 2021, 74, 103730.	6.1	5
139	Power of QTL detection using association tests with family controls. <i>European Journal of Human Genetics</i> , 2003, 11, 819-827.	2.8	4
140	Genome-wide pleiotropy and shared biological pathways for resistance to bovine pathogens. <i>PLoS ONE</i> , 2018, 13, e0194374.	2.5	4
141	Nontrivial Replication of Loci Detected by Multi-Trait Methods. <i>Frontiers in Genetics</i> , 2021, 12, 627989.	2.3	4
142	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.	1.8	4
143	Antagonistic genetic correlations for milking traits within the genome of dairy cattle. <i>PLoS ONE</i> , 2017, 12, e0175105.	2.5	4
144	Optimal Design of Genetic Studies of Gene Expression With Two-Color Microarrays in Outbred Crosses. <i>Genetics</i> , 2008, 180, 1691-1698.	2.9	3

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145	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.	2.3	2
146	“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.	2.0	1
147	QTL (Quantitative Trait Locus). , 2013, , 4-7.		0