

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 | Genetic mechanisms of critical illness in COVID-19. <i>Nature</i> , 2021, 591, 92-98. | 13.7 | 1,014 |
| 2 | Epistasis: too often neglected in complex trait studies?. <i>Nature Reviews Genetics</i> , 2004, 5, 618-625. | 7.7 | 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. | 13.7 | 791 |
| 4 | Genetic mapping of quantitative trait loci for growth and fatness in pigs. <i>Science</i> , 1994, 263, 1771-1774. | 6.0 | 636 |
| 5 | Confidence Intervals in QTL Mapping by Bootstrapping. <i>Genetics</i> , 1996, 143, 1013-1020. | 1.2 | 540 |
| 6 | QTL Express: mapping quantitative trait loci in simple and complex pedigrees. <i>Bioinformatics</i> , 2002, 18, 339-340. | 1.8 | 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. | 5.8 | 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. | 1.2 | 411 |
| 9 | Detecting epistasis in human complex traits. <i>Nature Reviews Genetics</i> , 2014, 15, 722-733. | 7.7 | 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. | 1.2 | 361 |
| 11 | Genomic and drug target evaluation of 90 cardiovascular proteins in 30,931 individuals. <i>Nature Metabolism</i> , 2020, 2, 1135-1148. | 5.1 | 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. | 1.2 | 262 |
| 13 | The heritability of human disease: estimation, uses and abuses. <i>Nature Reviews Genetics</i> , 2013, 14, 139-149. | 7.7 | 231 |
| 14 | Signatures of Diversifying Selection in European Pig Breeds. <i>PLoS Genetics</i> , 2013, 9, e1003453. | 1.5 | 228 |
| 15 | Multitrait Least Squares for Quantitative Trait Loci Detection. <i>Genetics</i> , 2000, 156, 899-911. | 1.2 | 223 |
| 16 | Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , 2021, 53, 1311-1321. | 9.4 | 218 |
| 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 | Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , 2015, 523, 459-462. | 13.7 | 173 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 19 | Mapping Quantitative Trait Loci in Complex Pedigrees: A Two-Step Variance Component Approach. <i>Genetics</i> , 2000, 156, 2081-2092. | 1.2 | 153 |
| 20 | Epigenetic prediction of complex traits and death. <i>Genome Biology</i> , 2018, 19, 136. | 3.8 | 146 |
| 21 | Genomic analysis of family data reveals additional genetic effects on intelligence and personality. <i>Molecular Psychiatry</i> , 2018, 23, 2347-2362. | 4.1 | 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. | 1.2 | 128 |
| 23 | Genetical genomics in humans and model organisms. <i>Trends in Genetics</i> , 2005, 21, 377-381. | 2.9 | 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. | 2.2 | 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. | 1.2 | 113 |
| 26 | Localising Loci underlying Complex Trait Variation Using Regional Genomic Relationship Mapping. <i>PLoS ONE</i> , 2012, 7, e46501. | 1.1 | 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. | 3.6 | 110 |
| 28 | An Evolutionary Perspective on Epistasis and the Missing Heritability. <i>PLoS Genetics</i> , 2013, 9, e1003295. | 1.5 | 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. | 9.4 | 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. | 1.1 | 101 |
| 31 | Genetic Determination of Cardiac Mass in Normotensive Rats. <i>Hypertension</i> , 1999, 33, 949-953. | 1.3 | 93 |
| 32 | Mapping Quantitative Trait Loci Affecting Female Reproductive Traits on Porcine Chromosome 81. <i>Biology of Reproduction</i> , 2003, 68, 2172-2179. | 1.2 | 87 |
| 33 | Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019, 10, 4957. | 5.8 | 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. | 0.3 | 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. | 1.2 | 78 |
| 36 | EpiGPU: exhaustive pairwise epistasis scans parallelized on consumer level graphics cards. <i>Bioinformatics</i> , 2011, 27, 1462-1465. | 1.8 | 77 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 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. | 3.6 | 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. | 1.5 | 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. | 0.9 | 66 |
| 41 | Genome-wide meta-analyses of stratified depression in Generation Scotland and UK Biobank. <i>Translational Psychiatry</i> , 2018, 8, 9. | 2.4 | 66 |
| 42 | Modulation of Genetic Associations with Serum Urate Levels by Body-Mass-Index in Humans. <i>PLoS ONE</i> , 2015, 10, e0119752. | 1.1 | 64 |
| 43 | A Genetic and Cytogenetic Map for the Duck (<i>Anas platyrhynchos</i>). <i>Genetics</i> , 2006, 173, 287-296. | 1.2 | 61 |
| 44 | Uncovering Networks from Genome-Wide Association Studies via Circular Genomic Permutation. G3: Genes, Genomes, <i>Genetics</i> , 2012, 2, 1067-1075. | 0.8 | 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. | 0.6 | 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. | 3.9 | 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. | 0.6 | 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. | 1.7 | 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 | 1.2 | 56 |
| 50 | QTL mapping designs for aquaculture. <i>Aquaculture</i> , 2008, 285, 23-29. | 1.7 | 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. | 1.7 | 49 |
| 52 | High-throughput analysis of epistasis in genome-wide association studies with BiForce. <i>Bioinformatics</i> , 2012, 28, 1957-1964. | 1.8 | 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. | 0.6 | 47 |
| 54 | Recent genomic heritage in Scotland. <i>BMC Genomics</i> , 2015, 16, 437. | 1.2 | 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. | 1.7 | 45 |
| 56 | The genomic signature of trait-associated variants. <i>BMC Genomics</i> , 2013, 14, 108. | 1.2 | 45 |
| 57 | DNA microsatellite analysis of Dolly. <i>Nature</i> , 1998, 394, 329-329. | 13.7 | 44 |
| 58 | Genetic mapping of modifier loci affecting malignant hypertension in TGRmRen2 rats. <i>Kidney International</i> , 1999, 56, 414-420. | 2.6 | 44 |
| 59 | Mapping of Multiple Quantitative Trait Loci Affecting Bovine Spongiform Encephalopathy. <i>Genetics</i> , 2004, 167, 1863-1872. | 1.2 | 44 |
| 60 | Bayesian reassessment of the epigenetic architecture of complex traits. <i>Nature Communications</i> , 2020, 11, 2865. | 5.8 | 43 |
| 61 | QTL affecting morphometric traits and stress response in the gilthead seabream (<i>Sparus aurata</i>). <i>Aquaculture</i> , 2011, 319, 58-66. | 1.7 | 42 |
| 62 | 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 |
| 63 | Genetical genomics in livestock: potentials and pitfalls. <i>Animal Genetics</i> , 2006, 37, 10-12. | 0.6 | 39 |
| 64 | An empirical assessment of individual-based population genetic statistical techniques: application to British pig breeds. <i>Heredity</i> , 2011, 106, 261-269. | 1.2 | 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. | 2.1 | 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. | 5.8 | 37 |
| 68 | Livestock QTLs “bringing home the bacon?”. <i>Trends in Genetics</i> , 1995, 11, 488-492. | 2.9 | 36 |
| 69 | Simultaneous mapping of epistatic QTL in DU6i × DBA/2 mice. <i>Mammalian Genome</i> , 2005, 16, 481-494. | 1.0 | 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. | 1.1 | 36 |
| 71 | Development of a genetic tool for product regulation in the diverse British pig breed market. <i>BMC Genomics</i> , 2012, 13, 580. | 1.2 | 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. | 0.5 | 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. | 1.0 | 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. | 1.4 | 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. | 2.7 | 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. | 0.7 | 32 |
| 77 | Genome-wide search for markers associated with bovine spongiform encephalopathy. <i>Mammalian Genome</i> , 2002, 13, 164-168. | 1.0 | 31 |
| 78 | A QTL affecting daily feed intake maps to Chromosome 2 in pigs. <i>Mammalian Genome</i> , 2005, 16, 464-470. | 1.0 | 31 |
| 79 | Genetic diversity in European pigs utilizing amplified fragment length polymorphism markers. <i>Animal Genetics</i> , 2006, 37, 232-238. | 0.6 | 31 |
| 80 | Genome-wide search for markers associated with bovine spongiform encephalopathy. <i>Mammalian Genome</i> , 2002, 13, 164-168. | 1.0 | 30 |
| 81 | Analysis of the genetics of boar taint reveals both single SNPs and regional effects. <i>BMC Genomics</i> , 2014, 15, 424. | 1.2 | 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. | 0.9 | 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. | 1.4 | 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. | 1.5 | 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. | 0.9 | 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. | 1.2 | 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. | 0.9 | 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. | 0.7 | 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. | 6.5 | 25 |
| 90 | Genomic prediction of complex human traits: relatedness, trait architecture and predictive meta-models. <i>Human Molecular Genetics</i> , 2015, 24, 4167-4182. | 1.4 | 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. | 3.3 | 24 |
| 92 | Genome-wide haplotype-based association analysis of major depressive disorder in Generation Scotland and UK Biobank. Translational Psychiatry, 2017, 7, 1263. | 2.4 | 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. | 2.4 | 23 |
| 94 | A catalogue of omics biological ageing clocks reveals substantial commonality and associations with disease risk. Aging, 2022, 14, 623-659. | 1.4 | 22 |
| 95 | Genomic regions influencing intramuscular fat in divergently selected rabbit lines. Animal Genetics, 2020, 51, 58-69. | 0.6 | 21 |
| 96 | Secreted Phosphoprotein 1 Expression in Endometrium and Placental Tissues of Hyperproliferic Large White and Meishan Gilts1. Biology of Reproduction, 2013, 88, 120. | 1.2 | 20 |
| 97 | Detecting signatures of selection in nine distinct lines of broiler chickens. Animal Genetics, 2015, 46, 37-49. | 0.6 | 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. | 1.2 | 19 |
| 99 | Genetic and environmental determinants of stressful life events and their overlap with depression and neuroticism. Wellcome Open Research, 2018, 3, 11. | 0.9 | 19 |
| 100 | Livestock genomics: bridging the gap between mice and men. Trends in Biotechnology, 2007, 25, 483-489. | 4.9 | 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. | 1.6 | 17 |
| 102 | Increased ultra-rare variant load in an isolated Scottish population impacts exonic and regulatory regions. PLoS Genetics, 2019, 15, e1008480. | 1.5 | 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. | 1.5 | 17 |
| 104 | QTL detection and allelic effects for growth and fat traits in outbred pig populations. Genetics Selection Evolution, 2004, 36, 83-96. | 1.2 | 16 |
| 105 | Addendum: Genome-wide association study of depression phenotypes in UK Biobank identifies variants in excitatory synaptic pathways. Nature Communications, 2018, 9, 3578. | 5.8 | 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. | 1.1 | 16 |
| 107 | Rapid and robust association mapping of expression quantitative trait loci. BMC Proceedings, 2007, 1, S144. | 1.8 | 15 |
| 108 | Properties of Local Interactions and Their Potential Value in Complementing Genome-Wide Association Studies. PLoS ONE, 2013, 8, e71203. | 1.1 | 15 |

| # | ARTICLE | IF | CITATIONS |
|-----|---|-----|-----------|
| 109 | Regional variation in health is predominantly driven by lifestyle rather than genetics. <i>Nature Communications</i> , 2017, 8, 801. | 5.8 | 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. | 0.9 | 15 |
| 111 | Characterisation of Genome-Wide Association Epistasis Signals for Serum Uric Acid in Human Population Isolates. <i>PLoS ONE</i> , 2011, 6, e23836. | 1.1 | 15 |
| 112 | Genome-wide search for loci controlling serum IGF binding protein levels of mice. <i>FASEB Journal</i> , 2001, 15, 978-987. | 0.2 | 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. | 1.4 | 14 |
| 114 | Haplotype Heritability Mapping Method Uncovers Missing Heritability of Complex Traits. <i>Scientific Reports</i> , 2018, 8, 4982. | 1.6 | 14 |
| 115 | Prediction of IBD based on population history for fine gene mapping. <i>Genetics Selection Evolution</i> , 2006, 38, 231. | 1.2 | 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. | 1.1 | 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. | 0.9 | 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. | 1.4 | 11 |
| 120 | On the prediction of simultaneous inbreeding coefficients at multiple loci. <i>Genetical Research</i> , 2004, 83, 113-120. | 0.3 | 10 |
| 121 | Linkage mapping of the locus for inherited ovine arthrogyrosis (IOA) to sheep Chromosome 5. <i>Mammalian Genome</i> , 2007, 18, 43-52. | 1.0 | 10 |
| 122 | A combined strategy for quantitative trait loci detection by genome-wide association. <i>BMC Proceedings</i> , 2009, 3, S6. | 1.8 | 10 |
| 123 | A cornucopia of maize genes. <i>Nature Genetics</i> , 2011, 43, 87-88. | 9.4 | 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. | 1.2 | 10 |
| 125 | Insulin resistance: Genetic associations with depression and cognition in population based cohorts. <i>Experimental Neurology</i> , 2019, 316, 20-26. | 2.0 | 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. | 0.6 | 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. | 1.2 | 8 |
| 128 | What Can the Genetics Revolution Offer the Meat Industry?. <i>Outlook on Agriculture</i> , 2003, 32, 219-226. | 1.8 | 7 |
| 129 | Genetic comparison of a Croatian isolate and CEPH European founders. <i>Genetic Epidemiology</i> , 2010, 34, 140-145. | 0.6 | 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. | 1.8 | 7 |
| 131 | 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 |
| 132 | Genetic control of lipids in the mouse cross DU6i \times DBA/2. <i>Mammalian Genome</i> , 2007, 18, 757-766. | 1.0 | 6 |
| 133 | Detection of multiple quantitative trait loci and their pleiotropic effects in outbred pig populations. <i>Genetics Selection Evolution</i> , 2009, 41, 44. | 1.2 | 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. | 1.8 | 6 |
| 135 | Towards in vitro genetics. <i>Trends in Genetics</i> , 2007, 23, 382-386. | 2.9 | 5 |
| 136 | Detecting dominant QTL with variance component analysis in simulated pedigrees. <i>Genetical Research</i> , 2008, 90, 363-374. | 0.3 | 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. | 1.3 | 5 |
| 138 | Lifestyle and Genetic Factors Modify Parent-of-Origin Effects on the Human Methylome. <i>EBioMedicine</i> , 2021, 74, 103730. | 2.7 | 5 |
| 139 | Power of QTL detection using association tests with family controls. <i>European Journal of Human Genetics</i> , 2003, 11, 819-827. | 1.4 | 4 |
| 140 | Genome-wide pleiotropy and shared biological pathways for resistance to bovine pathogens. <i>PLoS ONE</i> , 2018, 13, e0194374. | 1.1 | 4 |
| 141 | Nontrivial Replication of Loci Detected by Multi-Trait Methods. <i>Frontiers in Genetics</i> , 2021, 12, 627989. | 1.1 | 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. | 0.9 | 4 |
| 143 | Antagonistic genetic correlations for milking traits within the genome of dairy cattle. <i>PLoS ONE</i> , 2017, 12, e0175105. | 1.1 | 4 |
| 144 | Optimal Design of Genetic Studies of Gene Expression With Two-Color Microarrays in Outbred Crosses. <i>Genetics</i> , 2008, 180, 1691-1698. | 1.2 | 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. | 1.1 | 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. | 0.8 | 1 |
| 147 | QTL (Quantitative Trait Locus). , 2013, , 4-7. | | 0 |