David M Evans

List of Publications by Year
in descending order

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240 papers	48,246 citations	3159 92 h-index	2078 204 g-index
249 all docs	249 docs citations	249 times ranked	51776 citing authors

#	Article	IF	Citations
1	A second generation human haplotype map of over 3.1 million SNPs. Nature, 2007, 449, 851-861.	27.8	4,137
2	The MR-Base platform supports systematic causal inference across the human phenome. ELife, 2018, 7, .	6.0	3,639
3	Genome-wide detection and characterization of positive selection in human populations. Nature, 2007, 449, 913-918.	27.8	1,788
4	Six new loci associated with body mass index highlight a neuronal influence on body weight regulation. Nature Genetics, 2009, 41, 25-34.	21.4	1,572
5	Association scan of 14,500 nonsynonymous SNPs in four diseases identifies autoimmunity variants. Nature Genetics, 2007, 39, 1329-1337.	21.4	1,298
6	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	27.8	1,204
7	Common variants near MC4R are associated with fat mass, weight and risk of obesity. Nature Genetics, 2008, 40, 768-775.	21.4	1,179
8	Genome-wide meta-analysis identifies 56 bone mineral density loci and reveals 14 loci associated with risk of fracture. Nature Genetics, 2012, 44, 491-501.	21.4	1,100
9	The UK10K project identifies rare variants in health and disease. Nature, 2015, 526, 82-90.	27.8	1,014
10	A genome-wide association study identifies new psoriasis susceptibility loci and an interaction between HLA-C and ERAP1. Nature Genetics, 2010, 42, 985-990.	21.4	918
11	LD Hub: a centralized database and web interface to perform LD score regression that maximizes the potential of summary level GWAS data for SNP heritability and genetic correlation analysis. Bioinformatics, 2017, 33, 272-279.	4.1	822
12	Interaction between ERAP1 and HLA-B27 in ankylosing spondylitis implicates peptide handling in the mechanism for HLA-B27 in disease susceptibility. Nature Genetics, 2011, 43, 761-767.	21.4	778
13	GWAS of 126,559 Individuals Identifies Genetic Variants Associated with Educational Attainment. Science, 2013, 340, 1467-1471.	12.6	750
14	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. Nature Genetics, 2012, 44, 991-1005.	21.4	746
15	Genome-wide association analysis identifies 20 loci that influence adult height. Nature Genetics, 2008, 40, 575-583.	21.4	742
16	Genome-wide association study of CNVs in 16,000 cases of eight common diseases and 3,000 shared controls. Nature, 2010, 464, 713-720.	27.8	737
17	Identification of multiple risk variants for ankylosing spondylitis through high-density genotyping of immune-related loci. Nature Genetics, 2013, 45, 730-738.	21.4	699
18	Collider scope: when selection bias can substantially influence observed associations. International Journal of Epidemiology, 2018, 47, 226-235.	1.9	631

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19	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. Nature Genetics, 2013, 45, 501-512.	21.4	578
20	Genome-wide association study of ankylosing spondylitis identifies non-MHC susceptibility loci. Nature Genetics, 2010, 42, 123-127.	21.4	573
21	An atlas of genetic influences on osteoporosis in humans and mice. Nature Genetics, 2019, 51, 258-266.	21.4	557
22	Multi-ancestry genome-wide association study of 21,000 cases and 95,000 controls identifies new risk loci for atopic dermatitis. Nature Genetics, 2015, 47, 1449-1456.	21.4	529
23	Genome-wide association study identifies five loci associated with lung function. Nature Genetics, 2010, 42, 36-44.	21.4	518
24	Systematic identification of genetic influences on methylation across the human life course. Genome Biology, 2016, 17, 61.	8.8	489
25	Wholeâ€genome sequencing identifies EN1 as a determinant of bone density and fracture. Nature, 2015, 526, 112-117.	27.8	483
26	Patterns of Cis Regulatory Variation in Diverse Human Populations. PLoS Genetics, 2012, 8, e1002639.	3.5	439
27	Novel Loci for Adiponectin Levels and Their Influence on Type 2 Diabetes and Metabolic Traits: A Multi-Ethnic Meta-Analysis of 45,891 Individuals. PLoS Genetics, 2012, 8, e1002607.	3.5	419
28	Genome-wide associations for birth weight and correlations with adult disease. Nature, 2016, 538, 248-252.	27.8	406
29	New gene functions in megakaryopoiesis and platelet formation. Nature, 2011, 480, 201-208.	27.8	401
30	Genome-wide meta-analyses of multiancestry cohorts identify multiple new susceptibility loci for refractive error and myopia. Nature Genetics, 2013, 45, 314-318.	21.4	398
31	Identification of 153 new loci associated with heel bone mineral density and functional involvement of GPC6 in osteoporosis. Nature Genetics, 2017, 49, 1468-1475.	21.4	391
32	Beyond the Throwaway Society: Ordinary Domestic Practice and a Sociological Approach to Household Food Waste. Sociology, 2012, 46, 41-56.	2.5	390
33	Association Between Telomere Length and Risk of Cancer and Non-Neoplastic Diseases. JAMA Oncology, 2017, 3, 636.	7.1	376
34	Genome-wide association and large-scale follow up identifies 16 new loci influencing lung function. Nature Genetics, 2011, 43, 1082-1090.	21.4	367
35	A genome-wide association meta-analysis identifies new childhood obesity loci. Nature Genetics, 2012, 44, 526-531.	21.4	352
36	Genome-wide meta-analysis identifies new susceptibility loci for migraine. Nature Genetics, 2013, 45, 912-917.	21.4	338

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37	Blaming the consumer â€“ once again: the social and material contexts of everyday food waste practices in some English households. Critical Public Health, 2011, 21, 429-440.	2.4	334
38	Genetic risk for autism spectrum disorders and neuropsychiatric variation in the general population. Nature Genetics, 2016, 48, 552-555.	21.4	326
39	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. American Journal of Human Genetics, 2018, 103, 691-706.	6.2	326
40	Seventy-five genetic loci influencing the human red blood cell. Nature, 2012, 492, 369-375.	27.8	320
41	Meta-analysis of genome-wide association studies identifies three new risk loci for atopic dermatitis. Nature Genetics, 2012, 44, 187-192.	21.4	311
42	Mendelian Randomization: New Applications in the Coming Age of Hypothesis-Free Causality. Annual Review of Genomics and Human Genetics, 2015, 16, 327-350.	6.2	298
43	New loci associated with birth weight identify genetic links between intrauterine growth and adult height and metabolism. Nature Genetics, 2013, 45, 76-82.	21.4	293
44	Meta-analysis of Genome-wide Association Studies for Neuroticism, and the Polygenic Association With Major Depressive Disorder. JAMA Psychiatry, 2015, 72, 642.	11.0	289
45	Identification of heart rateâ€“associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	21.4	282
46	Harnessing the information contained within genome-wide association studies to improve individual prediction of complex disease risk. Human Molecular Genetics, 2009, 18, 3525-3531.	2.9	281
47	Genome-wide association analyses for lung function and chronic obstructive pulmonary disease identify new loci and potential druggable targets. Nature Genetics, 2017, 49, 416-425.	21.4	257
48	Review: Consumption-stage food waste reduction interventions â€“ What works and how to design better interventions. Food Policy, 2019, 83, 7-27.	6.0	253
49	Life-Course Genome-wide Association Study Meta-analysis of Total Body BMD and Assessment of Age-Specific Effects. American Journal of Human Genetics, 2018, 102, 88-102.	6.2	252
50	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. Nature Communications, 2016, 7, 10495.	12.8	245
51	WNT16 Influences Bone Mineral Density, Cortical Bone Thickness, Bone Strength, and Osteoporotic Fracture Risk. PLoS Genetics, 2012, 8, e1002745.	3.5	240
52	Data Resource Profile: Accessible Resource for Integrated Epigenomic Studies (ARIES). International Journal of Epidemiology, 2015, 44, 1181-1190.	1.9	238
53	Genome-Wide Association Study Using Extreme Truncate Selection Identifies Novel Genes Affecting Bone Mineral Density and Fracture Risk. PLoS Genetics, 2011, 7, e1001372.	3.5	233
54	A genome-wide association meta-analysis of self-reported allergy identifies shared and allergy-specific susceptibility loci. Nature Genetics, 2013, 45, 907-911.	21.4	232

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55	Variants in ADCY5 and near CCNL1 are associated with fetal growth and birth weight. Nature Genetics, 2010, 42, 430-435.	21.4	223
56	Major histocompatibility complex associations of ankylosing spondylitis are complex and involve further epistasis with ERAP1. Nature Communications, 2015, 6, 7146.	12.8	220
57	Genetic Evidence for Causal Relationships Between Maternal Obesity-Related Traits and Birth Weight. JAMA - Journal of the American Medical Association, 2016, 315, 1129.	7.4	220
58	Genome-wide Association Study of Three-Dimensional Facial Morphology Identifies a Variant in PAX3 Associated with Nasion Position. American Journal of Human Genetics, 2012, 90, 478-485.	6.2	202
59	Two-Stage Two-Locus Models in Genome-Wide Association. PLoS Genetics, 2006, 2, e157.	3.5	201
60	Genome-wide association analysis identifies 11 risk variants associated with the asthma with hay fever phenotype. Journal of Allergy and Clinical Immunology, 2014, 133, 1564-1571.	2.9	195
61	Assessment of the genetic and clinical determinants of fracture risk: genome wide association and mendelian randomisation study. BMJ: British Medical Journal, 2018, 362, k3225.	2.3	190
62	Genome-wide association and longitudinal analyses reveal genetic loci linking pubertal height growth, pubertal timing and childhood adiposity. Human Molecular Genetics, 2013, 22, 2735-2747.	2.9	188
63	Meta-analysis of Genome-Wide Association Studies for Extraversion: Findings from the Genetics of Personality Consortium. Behavior Genetics, 2016, 46, 170-182.	2.1	178
64	Constructing and mobilizing â€˜the consumerâ€™: Responsibility, consumption and the politics of sustainability. Environment and Planning A, 2017, 49, 1396-1412.	3.6	172
65	Thrifty, green or frugal: Reflections on sustainable consumption in a changing economic climate. Geoforum, 2011, 42, 550-557.	2.5	167
66	Genome-wide association study of offspring birth weight in 86â€‰577 women identifies five novel loci and highlights maternal genetic effects that are independent of fetal genetics. Human Molecular Genetics, 2018, 27, 742-756.	2.9	156
67	A genomeâ€wide approach to children's aggressive behavior: The EAGLE consortium. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2016, 171, 562-572.	1.7	153
68	A Genome-Wide Association Study Reveals Variants in ARL15 that Influence Adiponectin Levels. PLoS Genetics, 2009, 5, e1000768.	3.5	148
69	Clear detection of ADIPOQ locus as the major gene for plasma adiponectin: Results of genome-wide association analyses including 4659 European individuals. Atherosclerosis, 2010, 208, 412-420.	0.8	146
70	Meta-Analysis of Genome-Wide Scans for Total Body BMD in Children and Adults Reveals Allelic Heterogeneity and Age-Specific Effects at the WNT16 Locus. PLoS Genetics, 2012, 8, e1002718.	3.5	142
71	Genome-wide association study identifies loci affecting blood copper, selenium and zinc. Human Molecular Genetics, 2013, 22, 3998-4006.	2.9	140
72	Nine Loci for Ocular Axial Length Identified through Genome-wide Association Studies, Including Shared Loci with Refractive Error. American Journal of Human Genetics, 2013, 93, 264-277.	6.2	139

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73	Identification of atopic dermatitis subgroups in children from 2 longitudinal birth cohorts. Journal of Allergy and Clinical Immunology, 2018, 141, 964-971.	2.9	136
74	Guidelines for Genotyping in Genomewide Linkage Studies: Single-Nucleotideâ€“Polymorphism Maps Versus Microsatellite Maps. American Journal of Human Genetics, 2004, 75, 687-692.	6.2	135
75	Phenotypic Dissection of Bone Mineral Density Reveals Skeletal Site Specificity and Facilitates the Identification of Novel Loci in the Genetic Regulation of Bone Mass Attainment. PLoS Genetics, 2014, 10, e1004423.	3.5	134
76	A Comparison of Linkage Disequilibrium Patterns and Estimated Population Recombination Rates across Multiple Populations. American Journal of Human Genetics, 2005, 76, 681-687.	6.2	133
77	Common variants at 12q15 and 12q24 are associated with infant head circumference. Nature Genetics, 2012, 44, 532-538.	21.4	130
78	Common Variants in Left/Right Asymmetry Genes and Pathways Are Associated with Relative Hand Skill. PLoS Genetics, 2013, 9, e1003751.	3.5	129
79	Investigating the genetic association between ERAP1 and ankylosing spondylitis. Human Molecular Genetics, 2009, 18, 4204-4212.	2.9	123
80	Biometrical genetics. Biological Psychology, 2002, 61, 33-51.	2.2	119
81	Common variants in the region around Osterix are associated with bone mineral density and growth in childhood. Human Molecular Genetics, 2009, 18, 1510-1517.	2.9	117
82	Cis and Trans Effects of Human Genomic Variants on Gene Expression. PLoS Genetics, 2014, 10, e1004461.	3.5	117
83	Binning, Gifting and Recovery: The Conduits of Disposal in Household Food Consumption. Environment and Planning D: Society and Space, 2012, 30, 1123-1137.	3.4	115
84	A genome-wide association study of body mass index across early life and childhood. International Journal of Epidemiology, 2015, 44, 700-712.	1.9	114
85	Genetic Dissection of Acute Anterior Uveitis Reveals Similarities and Differences in Associations Observed With Ankylosing Spondylitis. Arthritis and Rheumatology, 2015, 67, 140-151.	5.6	114
86	A Genome-Wide Association Meta-Analysis of Attention-Deficit/Hyperactivity Disorder Symptoms in Population-Based Pediatric Cohorts. Journal of the American Academy of Child and Adolescent Psychiatry, 2016, 55, 896-905.e6.	0.5	112
87	What is consumption, where has it been going, and does it still matter?. Sociological Review, 2019, 67, 499-517.	1.6	112
88	Using Mendelian randomization to determine causal effects of maternal pregnancy (intrauterine) exposures on offspring outcomes: Sources of bias and methods for assessing them. Wellcome Open Research, 2017, 2, 11.	1.8	112
89	Genetic Predictors of Response to Serotonergic and Noradrenergic Antidepressants in Major Depressive Disorder: A Genome-Wide Analysis of Individual-Level Data and a Meta-Analysis. PLoS Medicine, 2012, 9, e1001326.	8.4	110
90	A novel common variant in DCST2 is associated with length in early life and height in adulthood. Human Molecular Genetics, 2015, 24, 1155-1168.	2.9	109

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91	Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation. Nature Communications, 2015, 6, 8658.	12.8	108
92	Functional Gene Group Analysis Reveals a Role of Synaptic Heterotrimeric G Proteins in Cognitive Ability. American Journal of Human Genetics, 2010, 86, 113-125.	6.2	106
93	Genome-Wide Population-Based Association Study of Extremely Overweight Young Adults â€“ The GOYA Study. PLoS ONE, 2011, 6, e24303.	2.5	105
94	Genome Wide Association Identifies Common Variants at the SERPINA6/SERPINA1 Locus Influencing Plasma Cortisol and Corticosteroid Binding Globulin. PLoS Genetics, 2014, 10, e1004474.	3.5	105
95	Meta-analysis of geneâ€“environment-wide association scans accounting for education level identifies additional loci for refractive error. Nature Communications, 2016, 7, 11008.	12.8	104
96	Association of Genetic Loci With Glucose Levels in Childhood and Adolescence. Diabetes, 2011, 60, 1805-1812.	0.6	103
97	Harmonization of Neuroticism and Extraversion phenotypes across inventories and cohorts in the Genetics of Personality Consortium: an application of Item Response Theory. Behavior Genetics, 2014, 44, 295-313.	2.1	103
98	Genetic Determinants of Trabecular and Cortical Volumetric Bone Mineral Densities and Bone Microstructure. PLoS Genetics, 2013, 9, e1003247.	3.5	100
99	Effects of BMI, Fat Mass, and Lean Mass on Asthma in Childhood: A Mendelian Randomization Study. PLoS Medicine, 2014, 11, e1001669.	8.4	93
100	A Genome Scan for Eye Color in 502 Twin Families: Most Variation is due to a QTL on Chromosome 15q. Twin Research and Human Genetics, 2004, 7, 197-210.	1.0	91
101	Food Waste. , 2014, , .		91
102	Meta-analysis of genome-wide studies identifies WNT16 and ESR1 SNPs associated with bone mineral density in premenopausal women. Journal of Bone and Mineral Research, 2013, 28, 547-558.	2.8	87
103	Novel pleiotropic risk loci for melanoma and nevus density implicate multiple biological pathways. Nature Communications, 2018, 9, 4774.	12.8	87
104	Genome-wide association study of height-adjusted BMI in childhood identifies functional variant inADCY3. Obesity, 2014, 22, 2252-2259.	3.0	86
105	ERAP2is associated with ankylosing spondylitis inHLA-B27-positive andHLA-B27-negative patients. Annals of the Rheumatic Diseases, 2015, 74, 1627-1629.	0.9	86
106	Genome-wide association meta-analysis of individuals of European ancestry identifies new loci explaining a substantial fraction of hair color variation and heritability. Nature Genetics, 2018, 50, 652-656.	21.4	86
107	Mining the Human Phenome Using Allelic Scores That Index Biological Intermediates. PLoS Genetics, 2013, 9, e1003919.	3.5	84
108	Genome-wide association study of primary tooth eruption identifies pleiotropic loci associated with height and craniofacial distances. Human Molecular Genetics, 2013, 22, 3807-3817.	2.9	84

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109	Using structural equation modelling to jointly estimate maternal and fetal effects on birthweight in the UK Biobank. International Journal of Epidemiology, 2018, 47, 1229-1241.	1.9	84
110	Circulating Selenium and Prostate Cancer Risk: A Mendelian Randomization Analysis. Journal of the National Cancer Institute, 2018, 110, 1035-1038.	6.3	84
111	Consuming conventions: sustainable consumption, ecological citizenship and the worlds of worth. Journal of Rural Studies, 2011, 27, 109-115.	4.7	83
112	Common variation near ROBO2 is associated with expressive vocabulary in infancy. Nature Communications, 2014, 5, 4831.	12.8	82
113	Bivariate genome-wide association meta-analysis of pediatric musculoskeletal traits reveals pleiotropic effects at the SREBF1/TOM1L2 locus. Nature Communications, 2017, 8, 121.	12.8	82
114	Beyond rhetoric: the possibilities of and for â€˜sustainable lifestylesâ€™. Environmental Politics, 2009, 18, 486-502.	5.4	81
115	Quantitative Trait Loci for CD4:CD8 Lymphocyte Ratio Are Associated with Risk of Type 1 Diabetes and HIV-1 Immune Control. American Journal of Human Genetics, 2010, 86, 88-92.	6.2	80
116	Childhood gene-environment interactions and age-dependent effects of genetic variants associated with refractive error and myopia: The CREAM Consortium. Scientific Reports, 2016, 6, 25853.	3.3	80
117	A Variant in LIN28B Is Associated with 2D:4D Finger-Length Ratio, a Putative Retrospective Biomarker of Prenatal Testosterone Exposure. American Journal of Human Genetics, 2010, 86, 519-525.	6.2	79
118	A Brief Pre-History of Food Waste and the Social Sciences. Sociological Review, 2012, 60, 5-26.	1.6	77
119	Shared Genetic Influences Between Attention-Deficit/Hyperactivity Disorder (ADHD) Traits in Children and Clinical ADHD. Journal of the American Academy of Child and Adolescent Psychiatry, 2015, 54, 322-327.	0.5	75
120	A Population-Based Study of Genetic Variation and Psychotic Experiences in Adolescents. Schizophrenia Bulletin, 2014, 40, 1254-1262.	4.3	74
121	Sequence Variants in Three Loci Influence Monocyte Counts and Erythrocyte Volume. American Journal of Human Genetics, 2009, 85, 745-749.	6.2	73
122	Polygenic Scores Predict Alcohol Problems in an Independent Sample and Show Moderation by the Environment. Genes, 2014, 5, 330-346.	2.4	71
123	Pharmacogenetics of antidepressant response: A polygenic approach. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2017, 75, 128-134.	4.8	71
124	Elucidating the role of maternal environmental exposures on offspring health and disease using two-sample Mendelian randomization. International Journal of Epidemiology, 2019, 48, 861-875.	1.9	71
125	Genome-Wide Association Meta-Analysis of Cortical Bone Mineral Density Unravels Allelic Heterogeneity at the RANKL Locus and Potential Pleiotropic Effects on Bone. PLoS Genetics, 2010, 6, e1001217.	3.5	69
126	Resolving the Effects of Maternal and Offspring Genotype on Dyadic Outcomes in Genome Wide Complex Trait Analysis (â€œM-GCTAâ€). Behavior Genetics, 2014, 44, 445-455.	2.1	67

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127	Do the Genetic or Environmental Determinants of Anxiety and Depression Change with Age? A Longitudinal Study of Australian Twins. Twin Research and Human Genetics, 2004, 7, 39-53.	1.0	66
128	Examination of the relationship between variation at 17q21 and childhood wheeze phenotypes. Journal of Allergy and Clinical Immunology, 2013, 131, 685-694.	2.9	66
129	Joint developmental trajectories of internalizing and externalizing disorders between childhood and adolescence. Development and Psychopathology, 2017, 29, 919-928.	2.3	66
130	Genetic Variants in the Vitamin D Receptor Are Associated with Advanced Prostate Cancer at Diagnosis: Findings from the Prostate Testing for Cancer and Treatment Study and a Systematic Review. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 2874-2881.	2.5	64
131	Genome-Wide Association Study Reveals Multiple Loci Associated with Primary Tooth Development during Infancy. PLoS Genetics, 2010, 6, e1000856.	3.5	64
132	Applying polygenic risk scores to postpartum depression. Archives of Women's Mental Health, 2014, 17, 519-528.	2.6	62
133	Evaluation of shared genetic aetiology between osteoarthritis and bone mineral density identifies SMAD3 as a novel osteoarthritis risk locus. Human Molecular Genetics, 2017, 26, 3850-3858.	2.9	56
134	Using a two-sample Mendelian randomization design to investigate a possible causal effect of maternal lipid concentrations on offspring birth weight. International Journal of Epidemiology, 2019, 48, 1457-1467.	1.9	56
135	A Comprehensive Evaluation of Potential Lung Function Associated Genes in the SpiroMeta General Population Sample. PLoS ONE, 2011, 6, e19382.	2.5	56
136	Postnatal Growth and DNA Methylation Are Associated With Differential Gene Expression of the TACSTD2 Gene and Childhood Fat Mass. Diabetes, 2012, 61, 391-400.	0.6	55
137	Meta-analysis of 20 genome-wide linkage studies evidenced new regions linked to asthma and atopy. European Journal of Human Genetics, 2010, 18, 700-706.	2.8	54
138	Formalising recall by genotype as an efficient approach to detailed phenotyping and causal inference. Nature Communications, 2018, 9, 711.	12.8	54
139	Variability in the common genetic architecture of social-communication spectrum phenotypes during childhood and adolescence. Molecular Autism, 2014, 5, 18.	4.9	53
140	The Power of Multivariate Quantitative-Trait Loci Linkage Analysis Is Influenced by the Correlation between Variables. American Journal of Human Genetics, 2002, 70, 1599-1602.	6.2	50
141	Genome-wide prediction of childhood asthma and related phenotypes in a longitudinal birth cohort. Journal of Allergy and Clinical Immunology, 2012, 130, 503-509.e7.	2.9	50
142	Rethinking material cultures of sustainability: Commodity consumption, cultural biographies and following the thing. Transactions of the Institute of British Geographers, 2018, 43, 110-121.	2.9	50
143	Challenges and opportunities for re-framing resource use policy with practice theories: The change points approach. Global Environmental Change, 2020, 62, 102072.	7.8	50
144	Epigenome-wide Association of DNA Methylation in Whole Blood With Bone Mineral Density. Journal of Bone and Mineral Research, 2017, 32, 1644-1650.	2.8	49

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145	Adult height variants affect birth length and growth rate in children. Human Molecular Genetics, 2011, 20, 4069-4075.	2.9	47
146	Identification of Novel Loci Associated With Hip Shape: A Meta-Analysis of Genomewide Association Studies. Journal of Bone and Mineral Research, 2019, 34, 241-251.	2.8	47
147	Are obesity risk genes associated with binge eating in adolescence?. Obesity, 2015, 23, 1729-1736.	3.0	44
148	Dirtying Linen: Reâ€evaluating the sustainability of domestic laundry. Environmental Policy and Governance, 2016, 26, 101-115.	3.7	44
149	Genome-wide association study of extreme high bone mass: Contribution of common genetic variation to extreme BMD phenotypes and potential novel BMD-associated genes. Bone, 2018, 114, 62-71.	2.9	43
150	Genome-Wide Association Study Identifies Four Loci Associated with Eruption of Permanent Teeth. PLoS Genetics, 2011, 7, e1002275.	3.5	42
151	The waterâ€“energyâ€“food nexus at home: New opportunities for policy interventions in household sustainability. Geographical Journal, 2019, 185, 406-418.	3.1	41
152	Urban food sharing: Emerging geographies of production, consumption and exchange. Geoforum, 2019, 99, 154-159.	2.5	41
153	Prospects and pitfalls in whole genome association studies. Philosophical Transactions of the Royal Society B: Biological Sciences, 2005, 360, 1589-1595.	4.0	38
154	Genome-wide association study identifies nine novel loci for 2D:4D finger ratio, a putative retrospective biomarker of testosterone exposure in utero. Human Molecular Genetics, 2018, 27, 2025-2038.	2.9	36
155	Understanding plastic packaging: The co-evolution of materials and society. Global Environmental Change, 2020, 65, 102166.	7.8	36
156	Whoâ€™s responsible for food waste? Consumers, retailers and the food waste discourse coalition in the United Kingdom. Journal of Consumer Culture, 2021, 21, 236-256.	2.5	36
157	Genome-wide association study in almost 195,000 individuals identifies 50 previously unidentified genetic loci for eye color. Science Advances, 2021, 7, .	10.3	36
158	A genome-wide association meta-analysis of diarrhoeal disease in young children identifiesFUT2locus and provides plausible biological pathways. Human Molecular Genetics, 2016, 25, 4127-4142.	2.9	35
159	Common variation contributes to the genetic architecture of social communication traits. Molecular Autism, 2013, 4, 34.	4.9	34
160	Heritability and Genome-Wide Association Analyses of Sleep Duration in Children: The EAGLE Consortium. Sleep, 2016, 39, 1859-1869.	1.1	34
161	Profit, reputation and â€˜doing the right thingâ€™: Convention theory and the problem of food waste in the UK retail sector. Geoforum, 2018, 89, 43-51.	2.5	34
162	RSPO3 impacts body fat distribution and regulates adipose cell biology in vitro. Nature Communications, 2020, 11, 2797.	12.8	34

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163	Effects of Memory Load and Distraction on Performance and Event-Related Slow Potentials in a Visuospatial Working Memory Task. Journal of Cognitive Neuroscience, 1997, 9, 743-757.	2.3	33
164	Unravelling the Threads: Discourses of Sustainability and Consumption in an Online Forum. Environmental Communication, 2012, 6, 101-118.	2.5	33
165	Fraction of exhaled nitric oxide values in childhood are associated with 17q11.2-q12 and 17q12-q21 variants. Journal of Allergy and Clinical Immunology, 2014, 134, 46-55.	2.9	33
166	Associations of vitamin D pathway genes with circulating 25-hydroxyvitamin-D, 1,25-dihydroxyvitamin-D, and prostate cancer: a nested caseâ€“control study. Cancer Causes and Control, 2015, 26, 205-218.	1.8	33
167	Major quantitative trait locus for eosinophil count is located on chromosome 2q. Journal of Allergy and Clinical Immunology, 2004, 114, 826-830.	2.9	32
168	Genetic Influences on Trajectories of Systolic Blood Pressure Across Childhood and Adolescence. Circulation: Cardiovascular Genetics, 2013, 6, 608-614.	5.1	32
169	Genome-wide association study for radiographic vertebral fractures: A potential role for the 16q24 BMD locus. Bone, 2014, 59, 20-27.	2.9	32
170	Exome-wide study of ankylosing spondylitis demonstrates additional shared genetic background with inflammatory bowel disease. Npj Genomic Medicine, 2016, 1, 16008.	3.8	32
171	Calculating Power to Detect Maternal and Offspring Genetic Effects in Genetic Association Studies. Behavior Genetics, 2019, 49, 327-339.	2.1	32
172	Genetic variants in adult bone mineral density and fracture risk genes are associated with the rate of bone mineral density acquisition in adolescence. Human Molecular Genetics, 2015, 24, 4158-4166.	2.9	31
173	Genetic Variation Associated with Differential Educational Attainment in Adults Has Anticipated Associations with School Performance in Children. PLoS ONE, 2014, 9, e100248.	2.5	31
174	Molecular and Population Analysis of Natural Selection on the Human Haptoglobin Duplication. Annals of Human Genetics, 2012, 76, 352-362.	0.8	30
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