David M Evans

List of Publications by Year
in descending order

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240 papers	48,246 citations	3149 92 h-index	2071 204 g-index
249 all docs	249 docs citations	249 times ranked	51776 citing authors

#	Article	IF	Citations
1	Mendelian randomization study of maternal coffee consumption and its influence on birthweight, stillbirth, miscarriage, gestational age and pre-term birth. International Journal of Epidemiology, 2023, 52, 165-177.	0.9	5
2	Using discrete event simulation to explore food wasted in the home. Journal of Simulation, 2022, 16, 415-435.	1.0	8
3	Tasting as a social practice: a methodological experiment in making taste public. Social and Cultural Geography, 2022, 23, 739-756.	1.6	9
4	The ontological politics of freshness: Qualities of food and sustainability governance. Environment and Planning A, 2022, 54, 461-476.	2.1	7
5	Investigating a Potential Causal Relationship Between Maternal Blood Pressure During Pregnancy and Future Offspring Cardiometabolic Health. Hypertension, 2022, 79, 170-177.	1.3	10
6	Food geographies â€˜inâ€™, â€˜ofâ€™ and â€˜forâ€™ the Anthropocene: Introducing the issue and main themes. Geographical Journal, 2022, 188, 310-317.	1.6	5
7	Evaluating indirect genetic effects of siblings using singletons. PLoS Genetics, 2022, 18, e1010247.	1.5	7
8	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.	1.5	36
9	Investigating the causal effect of maternal vitamin B12 and folate levels on offspring birthweight. International Journal of Epidemiology, 2021, 50, 179-189.	0.9	6
10	The Boulder Workshop Question Box. Behavior Genetics, 2021, 51, 181-190.	1.4	1
11	The Augmented Classical Twin Design: Incorporating Genomeâ€Wide Identity by Descent Sharing Into Twin Studies in Order to Model Violations of the Equal Environments Assumption. Behavior Genetics, 2021, 51, 223-236.	1.4	7
12	Genome-wide association study in almost 195,000 individuals identifies 50 previously unidentified genetic loci for eye color. Science Advances, 2021, 7, .	4.7	36
13	Shedding light on the genetics of fetal growth. Nature Genetics, 2021, 53, 1120-1121.	9.4	2
14	Higher maternal adiposity reduces offspring birthweight if associated with a metabolically favourable profile. Diabetologia, 2021, 64, 2790-2802.	2.9	9
15	Estimating direct and indirect genetic effects on offspring phenotypes using genome-wide summary results data. Nature Communications, 2021, 12, 5420.	5.8	9
16	Healthy soil, healthy food, healthy people: An outline of the H3 project. Nutrition Bulletin, 2021, 46, 497-505.	0.8	3
17	Environmental leapfrogging and everyday climate cultures: sustainable water consumption in the Global South. Climatic Change, 2020, 163, 83-97.	1.7	14
18	Introducing M-GCTA a Software Package to Estimate Maternal (or Paternal) Genetic Effects on Offspring Phenotypes. Behavior Genetics, 2020, 50, 51-66.	1.4	18

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19	Understanding plastic packaging: The co-evolution of materials and society. Global Environmental Change, 2020, 65, 102166.	3.6	36
20	Commentary: Proxy gene-by-environment Mendelian randomization for assessing causal effects of maternal exposures on offspring outcomes. International Journal of Epidemiology, 2020, 49, 1218-1220.	0.9	1
21	New consumption geographies, new geographies of consumption. Geographical Research, 2020, 58, 300-303.	0.9	5
22	RSPO3 impacts body fat distribution and regulates adipose cell biology in vitro. Nature Communications, 2020, 11, 2797.	5.8	34
23	After Practice? Material Semiotic Approaches to Consumption and Economy. Cultural Sociology, 2020, 14, 340-356.	0.7	27
24	Challenges and opportunities for re-framing resource use policy with practice theories: The change points approach. Global Environmental Change, 2020, 62, 102072.	3.6	50
25	The waterâ€“energyâ€“food nexus at home: New opportunities for policy interventions in household sustainability. Geographical Journal, 2019, 185, 406-418.	1.6	41
26	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.	0.9	56
27	Market coordination and the making of conventions: qualities, consumption and sustainability in the agro-food industry. Economy and Society, 2019, 48, 426-449.	1.3	22
28	Urban food sharing: Emerging geographies of production, consumption and exchange. Geoforum, 2019, 99, 154-159.	1.4	41
29	Antibody response to common human viruses is shaped by genetic factors. Journal of Allergy and Clinical Immunology, 2019, 143, 1640-1643.	1.5	2
30	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.	0.9	71
31	Review: Consumption-stage food waste reduction interventions â€“ What works and how to design better interventions. Food Policy, 2019, 83, 7-27.	2.8	253
32	Calculating Power to Detect Maternal and Offspring Genetic Effects in Genetic Association Studies. Behavior Genetics, 2019, 49, 327-339.	1.4	32
33	An atlas of genetic influences on osteoporosis in humans and mice. Nature Genetics, 2019, 51, 258-266.	9.4	557
34	The multiple ontologies of freshness in the <scp>UK</scp> and Portuguese agriâ€food sectors. Transactions of the Institute of British Geographers, 2019, 44, 79-93.	1.8	20
35	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.	3.1	47
36	What is consumption, where has it been going, and does it still matter?. Sociological Review, 2019, 67, 499-517.	0.9	112

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37	Elucidating the genetics of craniofacial shape. Nature Genetics, 2018, 50, 319-321.	9.4	4
38	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.	1.4	156
39	Partitioning Phenotypic Variance Due to Parent-of-Origin Effects Using Genomic Relatedness Matrices. Behavior Genetics, 2018, 48, 67-79.	1.4	7
40	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.	9.4	86
41	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.	1.4	36
42	Formalising recall by genotype as an efficient approach to detailed phenotyping and causal inference. Nature Communications, 2018, 9, 711.	5.8	54
43	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.	0.9	84
44	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.	1.4	34
45	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.	2.6	252
46	Collider scope: when selection bias can substantially influence observed associations. International Journal of Epidemiology, 2018, 47, 226-235.	0.9	631
47	Developmental Changes Within the Genetic Architecture of Social Communication Behavior: A Multivariate Study of Genetic Variance in Unrelated Individuals. Biological Psychiatry, 2018, 83, 598-606.	0.7	30
48	Identification of atopic dermatitis subgroups in children from 2 longitudinal birth cohorts. Journal of Allergy and Clinical Immunology, 2018, 141, 964-971.	1.5	136
49	Rethinking material cultures of sustainability: Commodity consumption, cultural biographies and following the thing. Transactions of the Institute of British Geographers, 2018, 43, 110-121.	1.8	50
50	Novel pleiotropic risk loci for melanoma and nevus density implicate multiple biological pathways. Nature Communications, 2018, 9, 4774.	5.8	87
51	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.	2.6	326
52	Assessing the Role of DNA Methylation-Derived Neutrophil-to-Lymphocyte Ratio in Rheumatoid Arthritis. Journal of Immunology Research, 2018, 2018, 1-10.	0.9	13
53	MHC-Dependent Mate Selection within 872 Spousal Pairs of European Ancestry from the Health and Retirement Study. Genes, 2018, 9, 53.	1.0	8
54	Assessment of the genetic and clinical determinants of fracture risk: genome wide association and mendelian randomisation study. BMJ: British Medical Journal, 2018, 362, k3225.	2.4	190

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55	Circulating Selenium and Prostate Cancer Risk: A Mendelian Randomization Analysis. Journal of the National Cancer Institute, 2018, 110, 1035-1038.	3.0	84
56	The MR-Base platform supports systematic causal inference across the human phenome. ELife, 2018, 7, .	2.8	3,639
57	Are serum concentrations of vitamin B-12 causally related to cardiometabolic risk factors and disease? A Mendelian randomization study. American Journal of Clinical Nutrition, 2018, 108, 398-404.	2.2	22
58	Genome-wide survey of parent-of-origin effects on DNA methylation identifies candidate imprinted loci in humans. Human Molecular Genetics, 2018, 27, 2927-2939.	1.4	22
59	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.	1.4	43
60	Genetic determinants of glucose levels in pregnancy: genetic risk scores analysis and GWAS in the Norwegian STORK cohort. European Journal of Endocrinology, 2018, 179, 363-372.	1.9	14
61	Association Between Telomere Length and Risk of Cancer and Non-Neoplastic Diseases. JAMA Oncology, 2017, 3, 636.	3.4	376
62	Pharmacogenetics of antidepressant response: A polygenic approach. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2017, 75, 128-134.	2.5	71
63	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.	9.4	257
64	Constructing and mobilizing â€˜the consumerâ€™: Responsibility, consumption and the politics of sustainability. Environment and Planning A, 2017, 49, 1396-1412.	2.1	172
65	Epigenome-wide Association of DNA Methylation in Whole Blood With Bone Mineral Density. Journal of Bone and Mineral Research, 2017, 32, 1644-1650.	3.1	49
66	Joint developmental trajectories of internalizing and externalizing disorders between childhood and adolescence. Development and Psychopathology, 2017, 29, 919-928.	1.4	66
67	Single Nucleotide Polymorphisms Associated with Reading Ability Show Connection to Socio-Economic Outcomes. Behavior Genetics, 2017, 47, 469-479.	1.4	13
68	Bivariate genome-wide association meta-analysis of pediatric musculoskeletal traits reveals pleiotropic effects at the SREBF1/TOM1L2 locus. Nature Communications, 2017, 8, 121.	5.8	82
69	Household Recycling and Consumption Work: Social and Moral Economies, by Kathryn Wheeler and Miriam Glucksmann. Journal of Cultural Economy, 2017, 10, 415-417.	0.8	1
70	HAPRAP: a haplotype-based iterative method for statistical fine mapping using GWAS summary statistics. Bioinformatics, 2017, 33, 79-86.	1.8	4
71	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.	1.8	822
72	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.	1.4	56

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73	Identification of 153 new loci associated with heel bone mineral density and functional involvement of GPC6 in osteoporosis. Nature Genetics, 2017, 49, 1468-1475.	9.4	391
74	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.	0.9	112
75	Dirtying Linen: Reâ€evaluating the sustainability of domestic laundry. Environmental Policy and Governance, 2016, 26, 101-115.	2.1	44
76	Exome-wide study of ankylosing spondylitis demonstrates additional shared genetic background with inflammatory bowel disease. Npj Genomic Medicine, 2016, 1, 16008.	1.7	32
77	Systematic identification of genetic influences on methylation across the human life course. Genome Biology, 2016, 17, 61.	3.8	489
78	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	13.7	1,204
79	Genome-wide associations for birth weight and correlations with adult disease. Nature, 2016, 538, 248-252.	13.7	406
80	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.	0.3	112
81	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.	1.1	153
82	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.	1.4	35
83	Meta-analysis of geneâ€“environment-wide association scans accounting for education level identifies additional loci for refractive error. Nature Communications, 2016, 7, 11008.	5.8	104
84	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.	1.6	80
85	Heritability and Genome-Wide Association Analyses of Sleep Duration in Children: The EAGLE Consortium. Sleep, 2016, 39, 1859-1869.	0.6	34
86	Genome-wide association study of copy number variation with lung function identifies a novel signal of association near BANP for forced vital capacity. BMC Genetics, 2016, 17, 116.	2.7	0
87	Genetic risk for autism spectrum disorders and neuropsychiatric variation in the general population. Nature Genetics, 2016, 48, 552-555.	9.4	326
88	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. Nature Communications, 2016, 7, 10495.	5.8	245
89	Genetic Evidence for Causal Relationships Between Maternal Obesity-Related Traits and Birth Weight. JAMA - Journal of the American Medical Association, 2016, 315, 1129.	3.8	220
90	Common Genetic Variants Influence Whorls inÂFingerprint Patterns. Journal of Investigative Dermatology, 2016, 136, 859-862.	0.3	19

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91	Meta-analysis of Genome-Wide Association Studies for Extraversion: Findings from the Genetics of Personality Consortium. Behavior Genetics, 2016, 46, 170-182.	1.4	178
92	Association of Forced Vital Capacity with the Developmental Gene NCOR2. PLoS ONE, 2016, 11, e0147388.	1.1	17
93	Are obesity risk genes associated with binge eating in adolescence?. Obesity, 2015, 23, 1729-1736.	1.5	44
94	Meta-analysis of Genome-wide Association Studies for Neuroticism, and the Polygenic Association With Major Depressive Disorder. JAMA Psychiatry, 2015, 72, 642.	6.0	289
95	Major histocompatibility complex associations of ankylosing spondylitis are complex and involve further epistasis with ERAP1. Nature Communications, 2015, 6, 7146.	5.8	220
96	A genome-wide association study of body mass index across early life and childhood. International Journal of Epidemiology, 2015, 44, 700-712.	0.9	114
97	Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation. Nature Communications, 2015, 6, 8658.	5.8	108
98	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.	0.8	33
99	ERAP2is associated with ankylosing spondylitis inHLA-B27-positive andHLA-B27-negative patients. Annals of the Rheumatic Diseases, 2015, 74, 1627-1629.	0.5	86
100	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.	0.3	75
101	Genome-wide association study for refractive astigmatism reveals genetic co-determination with spherical equivalent refractive error: the CREAM consortium. Human Genetics, 2015, 134, 131-146.	1.8	24
102	Heritability and genome-wide analyses of problematic peer relationships during childhood and adolescence. Human Genetics, 2015, 134, 539-551.	1.8	13
103	Data Resource Profile: Accessible Resource for Integrated Epigenomic Studies (ARIES). International Journal of Epidemiology, 2015, 44, 1181-1190.	0.9	238
104	Genome-wide association study of blood lead shows multiple associations near ALAD. Human Molecular Genetics, 2015, 24, 3871-3879.	1.4	28
105	Mendelian Randomization: New Applications in the Coming Age of Hypothesis-Free Causality. Annual Review of Genomics and Human Genetics, 2015, 16, 327-350.	2.5	298
106	Integrative pathway genomics of lung function and airflow obstruction. Human Molecular Genetics, 2015, 24, 6836-6848.	1.4	28
107	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.	9.4	529
108	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.	1.4	31

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109	Wholeâ€genome sequencing identifies EN1 as a determinant of bone density and fracture. Nature, 2015, 526, 112-117.	13.7	483
110	The UK10K project identifies rare variants in health and disease. Nature, 2015, 526, 82-90.	13.7	1,014
111	Genomic influences on alcohol problems in a population-based sample of young adults. Addiction, 2015, 110, 461-470.	1.7	18
112	A novel common variant in DCST2 is associated with length in early life and height in adulthood. Human Molecular Genetics, 2015, 24, 1155-1168.	1.4	109
113	Genetic Dissection of Acute Anterior Uveitis Reveals Similarities and Differences in Associations Observed With Ankylosing Spondylitis. Arthritis and Rheumatology, 2015, 67, 140-151.	2.9	114
114	Incorporating Known Genetic Variants Does Not Improve the Accuracy of PSA Testing to Identify High Risk Prostate Cancer on Biopsy. PLoS ONE, 2015, 10, e0136735.	1.1	6
115	Researching (with) Major Food Retailers. Gastronomica, 2015, 15, 33-39.	0.1	4
116	Polygenic Scores Predict Alcohol Problems in an Independent Sample and Show Moderation by the Environment. Genes, 2014, 5, 330-346.	1.0	71
117	Cis and Trans Effects of Human Genomic Variants on Gene Expression. PLoS Genetics, 2014, 10, e1004461.	1.5	117
118	A Population-Based Study of Genetic Variation and Psychotic Experiences in Adolescents. Schizophrenia Bulletin, 2014, 40, 1254-1262.	2.3	74
119	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.	1.5	134
120	Genome Wide Association Identifies Common Variants at the SERPINA6/SERPINA1 Locus Influencing Plasma Cortisol and Corticosteroid Binding Globulin. PLoS Genetics, 2014, 10, e1004474.	1.5	105
121	Effects of BMI, Fat Mass, and Lean Mass on Asthma in Childhood: A Mendelian Randomization Study. PLoS Medicine, 2014, 11, e1001669.	3.9	93
122	Applying polygenic risk scores to postpartum depression. Archives of Women's Mental Health, 2014, 17, 519-528.	1.2	62
123	Genome-wide association study of height-adjusted BMI in childhood identifies functional variant inADCY3. Obesity, 2014, 22, 2252-2259.	1.5	86
124	Genetic Variation in Prostate-Specific Antigenâ€"Detected Prostate Cancer and the Effect of Control Selection on Genetic Association Studies. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 1356-1365.	1.1	26
125	Common variation near ROBO2 is associated with expressive vocabulary in infancy. Nature Communications, 2014, 5, 4831.	5.8	82
126	The Association between Primary Tooth Emergence and Anthropometric Measures in Young Adults: Findings from a Large Prospective Cohort Study. PLoS ONE, 2014, 9, e96355.	1.1	9

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127	Does Bone Resorption Stimulate Periosteal Expansion? A Cross-Sectional Analysis of Î²-C-telopeptides of Type I Collagen (CTX), Genetic Markers of the RANKL Pathway, and Periosteal Circumference as Measured by pQCT. Journal of Bone and Mineral Research, 2014, 29, 1015-1024.	3.1	24
128	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.	1.5	33
129	Genome-wide association study for radiographic vertebral fractures: A potential role for the 16q24 BMD locus. Bone, 2014, 59, 20-27.	1.4	32
130	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.	1.5	195
131	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.	1.4	67
132	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.	1.4	103
133	Variability in the common genetic architecture of social-communication spectrum phenotypes during childhood and adolescence. Molecular Autism, 2014, 5, 18.	2.6	53
134	Genetic Variation Associated with Differential Educational Attainment in Adults Has Anticipated Associations with School Performance in Children. PLoS ONE, 2014, 9, e100248.	1.1	31
135	Food Waste. , 2014, , .		91
136	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.	1.4	188
137	Common variation contributes to the genetic architecture of social communication traits. Molecular Autism, 2013, 4, 34.	2.6	34
138	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.	2.6	139
139	Examination of the relationship between variation at 17q21 and childhood wheeze phenotypes. Journal of Allergy and Clinical Immunology, 2013, 131, 685-694.	1.5	66
140	Genome-wide association study identifies loci affecting blood copper, selenium and zinc. Human Molecular Genetics, 2013, 22, 3998-4006.	1.4	140
141	Genome-wide meta-analyses of multiancestry cohorts identify multiple new susceptibility loci for refractive error and myopia. Nature Genetics, 2013, 45, 314-318.	9.4	398
142	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.	3.1	87
143	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. Nature Genetics, 2013, 45, 501-512.	9.4	578
144	Identification of heart rateâ€“associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	9.4	282

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145	Identification of multiple risk variants for ankylosing spondylitis through high-density genotyping of immune-related loci. Nature Genetics, 2013, 45, 730-738.	9.4	699
146	GWAS of 126,559 Individuals Identifies Genetic Variants Associated with Educational Attainment. Science, 2013, 340, 1467-1471.	6.0	750
147	Genome-wide meta-analysis identifies new susceptibility loci for migraine. Nature Genetics, 2013, 45, 912-917.	9.4	338
148	A genome-wide association meta-analysis of self-reported allergy identifies shared and allergy-specific susceptibility loci. Nature Genetics, 2013, 45, 907-911.	9.4	232
149	Genetic Determinants of Trabecular and Cortical Volumetric Bone Mineral Densities and Bone Microstructure. PLoS Genetics, 2013, 9, e1003247.	1.5	100
150	Mining the Human Phenome Using Allelic Scores That Index Biological Intermediates. PLoS Genetics, 2013, 9, e1003919.	1.5	84
151	Common Variants in Left/Right Asymmetry Genes and Pathways Are Associated with Relative Hand Skill. PLoS Genetics, 2013, 9, e1003751.	1.5	129
152	Coordinated Genetic Scaling of the Human Eye: Shared Determination of Axial Eye Length and Corneal Curvature. , 2013, 54, 1715.		27
153	Genetic Influences on Trajectories of Systolic Blood Pressure Across Childhood and Adolescence. Circulation: Cardiovascular Genetics, 2013, 6, 608-614.	5.1	32
154	Using Genetic Proxies for Lifecourse Sun Exposure to Assess the Causal Relationship of Sun Exposure with Circulating Vitamin D and Prostate Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2013, 22, 597-606.	1.1	22
155	Genome-wide association study of primary tooth eruption identifies pleiotropic loci associated with height and craniofacial distances. Human Molecular Genetics, 2013, 22, 3807-3817.	1.4	84
156	New loci associated with birth weight identify genetic links between intrauterine growth and adult height and metabolism. Nature Genetics, 2013, 45, 76-82.	9.4	293
157	Association Study of 25 Type 2 Diabetes Related Loci with Measures of Obesity in Indian Sib Pairs. PLoS ONE, 2013, 8, e53944.	1.1	19
158	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.	1.5	419
159	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.	1.5	142
160	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.	3.9	110
161	Patterns of Cis Regulatory Variation in Diverse Human Populations. PLoS Genetics, 2012, 8, e1002639.	1.5	439
162	WNT16 Influences Bone Mineral Density, Cortical Bone Thickness, Bone Strength, and Osteoporotic Fracture Risk. PLoS Genetics, 2012, 8, e1002745.	1.5	240

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163	Power Calculations in Genetic Studies. Cold Spring Harbor Protocols, 2012, 2012, pdb.top069559-pdb.top069559.	0.2	16
164	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. Nature Genetics, 2012, 44, 991-1005.	9.4	746
165	Common variants at 12q15 and 12q24 are associated with infant head circumference. Nature Genetics, 2012, 44, 532-538.	9.4	130
166	Postnatal Growth and DNA Methylation Are Associated With Differential Gene Expression of the TACSTD2 Gene and Childhood Fat Mass. Diabetes, 2012, 61, 391-400.	0.3	55
167	Binning, Gifting and Recovery: The Conduits of Disposal in Household Food Consumption. Environment and Planning D: Society and Space, 2012, 30, 1123-1137.	2.3	115
168	A Brief Pre-History of Food Waste and the Social Sciences. Sociological Review, 2012, 60, 5-26.	0.9	77
169	Unravelling the Threads: Discourses of Sustainability and Consumption in an Online Forum. Environmental Communication, 2012, 6, 101-118.	1.2	33
170	Seventy-five genetic loci influencing the human red blood cell. Nature, 2012, 492, 369-375.	13.7	320
171	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.	9.4	1,100
172	A genome-wide association meta-analysis identifies new childhood obesity loci. Nature Genetics, 2012, 44, 526-531.	9.4	352
173	Beyond the Throwaway Society: Ordinary Domestic Practice and a Sociological Approach to Household Food Waste. Sociology, 2012, 46, 41-56.	1.7	390
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175	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.	1.5	50
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