David M Evans

List of Publications by Citations

277 papers	34,438 citations	83 h-index	184 g-index
311 ext. papers	42,388 ext. citations	11.6 avg, IF	6.18 L-index

#	Paper	IF	Citations
277	A second generation human haplotype map of over 3.1 million SNPs. *Nature*, **2007**, 449, 851-61	50.4	3647
276	Six new loci associated with body mass index highlight a neuronal influence on body weight regulation. *Nature Genetics*, **2009**, 41, 25-34	36.3	1368
275	Genome-wide detection and characterization of positive selection in human populations. *Nature*, **2007**, 449, 913-8	50.4	1367
274	The MR-Base platform supports systematic causal inference across the human phenome. *ELife*, **2018**, 7,	8.9	1190
273	Association scan of 14,500 nonsynonymous SNPs in four diseases identifies autoimmunity variants. *Nature Genetics*, **2007**, 39, 1329-37	36.3	1130
272	Common variants near MC4R are associated with fat mass, weight and risk of obesity. *Nature Genetics*, **2008**, 40, 768-75	36.3	1048
271	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	36.3	866
270	Genome-wide association study identifies 74 loci associated with educational attainment. *Nature*, **2016**, 533, 539-42	50.4	850
269	The UK10K project identifies rare variants in health and disease. *Nature*, **2015**, 526, 82-90	50.4	776
268	A genome-wide association study identifies new psoriasis susceptibility loci and an interaction between HLA-C and ERAP1. *Nature Genetics*, **2010**, 42, 985-90	36.3	773
267	Genome-wide association analysis identifies 20 loci that influence adult height. *Nature Genetics*, **2008**, 40, 575-83	36.3	654
266	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, 761-7	36.3	646
265	Genome-wide association study of CNVs in 16,000 cases of eight common diseases and 3,000 shared controls. *Nature*, **2010**, 464, 713-20	50.4	639
264	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. *Nature Genetics*, **2012**, 44, 991-1005	36.3	621
263	GWAS of 126,559 individuals identifies genetic variants associated with educational attainment. *Science*, **2013**, 340, 1467-71	33.3	563
262	Identification of multiple risk variants for ankylosing spondylitis through high-density genotyping of immune-related loci. *Nature Genetics*, **2013**, 45, 730-8	36.3	551
261	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	7.2	541

260	Genome-wide association study of ankylosing spondylitis identifies non-MHC susceptibility loci. *Nature Genetics*, **2010**, 42, 123-7	36.3	484
259	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. *Nature Genetics*, **2013**, 45, 501-12	36.3	437
258	Genome-wide association study identifies five loci associated with lung function. *Nature Genetics*, **2010**, 42, 36-44	36.3	430
257	Collider scope: when selection bias can substantially influence observed associations. *International Journal of Epidemiology*, **2018**, 47, 226-235	7.8	354
256	Systematic identification of genetic influences on methylation across the human life course. *Genome Biology*, **2016**, 17, 61	18.3	331
255	New gene functions in megakaryopoiesis and platelet formation. *Nature*, **2011**, 480, 201-8	50.4	330
254	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	36.3	329
253	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	6	326
252	Genome-wide meta-analyses of multiancestry cohorts identify multiple new susceptibility loci for refractive error and myopia. *Nature Genetics*, **2013**, 45, 314-8	36.3	314
251	Genome-wide association and large-scale follow up identifies 16 new loci influencing lung function. *Nature Genetics*, **2011**, 43, 1082-90	36.3	313
250	Whole-genome sequencing identifies EN1 as a determinant of bone density and fracture. *Nature*, **2015**, 526, 112-7	50.4	308
249	A genome-wide association meta-analysis identifies new childhood obesity loci. *Nature Genetics*, **2012**, 44, 526-31	36.3	292
248	Genome-wide meta-analysis identifies new susceptibility loci for migraine. *Nature Genetics*, **2013**, 45, 912-917	36.3	276
247	An atlas of genetic influences on osteoporosis in humans and mice. *Nature Genetics*, **2019**, 51, 258-266	36.3	270
246	Genome-wide associations for birth weight and correlations with adult disease. *Nature*, **2016**, 538, 248-252	50.4	266
245	Seventy-five genetic loci influencing the human red blood cell. *Nature*, **2012**, 492, 369-75	50.4	257
244	Meta-analysis of genome-wide association studies identifies three new risk loci for atopic dermatitis. *Nature Genetics*, **2011**, 44, 187-92	36.3	244
243	Genetic risk for autism spectrum disorders and neuropsychiatric variation in the general population. *Nature Genetics*, **2016**, 48, 552-5	36.3	238

242	Harnessing the information contained within genome-wide association studies to improve individual prediction of complex disease risk. *Human Molecular Genetics*, **2009**, 18, 3525-31	5.6	237
241	Association Between Telomere Length and Risk of Cancer and Non-Neoplastic Diseases: A Mendelian Randomization Study. *JAMA Oncology*, **2017**, 3, 636-651	13.4	236
240	Identification of 153 new loci associated with heel bone mineral density and functional involvement of GPC6 in osteoporosis. *Nature Genetics*, **2017**, 49, 1468-1475	36.3	235
239	New loci associated with birth weight identify genetic links between intrauterine growth and adult height and metabolism. *Nature Genetics*, **2013**, 45, 76-82	36.3	232
238	Meta-analysis of Genome-wide Association Studies for Neuroticism, and the Polygenic Association With Major Depressive Disorder. *JAMA Psychiatry*, **2015**, 72, 642-50	14.5	222
237	Recent Developments in Mendelian Randomization Studies. *Current Epidemiology Reports*, **2017**, 4, 330-345	2.9	218
236	Genome-wide association study using extreme truncate selection identifies novel genes affecting bone mineral density and fracture risk. *PLoS Genetics*, **2011**, 7, e1001372	6	199
235	WNT16 influences bone mineral density, cortical bone thickness, bone strength, and osteoporotic fracture risk. *PLoS Genetics*, **2012**, 8, e1002745	6	192
234	A genome-wide association meta-analysis of self-reported allergy identifies shared and allergy-specific susceptibility loci. *Nature Genetics*, **2013**, 45, 907-11	36.3	191
233	Variants in ADCY5 and near CCNL1 are associated with fetal growth and birth weight. *Nature Genetics*, **2010**, 42, 430-5	36.3	184
232	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. *Nature Genetics*, **2019**, 51, 804-814	36.3	181
231	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. *Nature Communications*, **2016**, 7, 10495	17.4	180
230	Two-stage two-locus models in genome-wide association. *PLoS Genetics*, **2006**, 2, e157	6	173
229	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	36.3	170
228	Major histocompatibility complex associations of ankylosing spondylitis are complex and involve further epistasis with ERAP1. *Nature Communications*, **2015**, 6, 7146	17.4	164
227	Data Resource Profile: Accessible Resource for Integrated Epigenomic Studies (ARIES). *International Journal of Epidemiology*, **2015**, 44, 1181-90	7.8	162
226	Mendelian Randomization: New Applications in the Coming Age of Hypothesis-Free Causality. *Annual Review of Genomics and Human Genetics*, **2015**, 16, 327-50	9.7	162
225	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	11	151

224	Genetic Evidence for Causal Relationships Between Maternal Obesity-Related Traits and Birth Weight. *JAMA - Journal of the American Medical Association*, **2016**, 315, 1129-40	27.4	149
223	Genome-wide association analysis identifies 11 risk variants associated with the asthma with hay fever phenotype. *Journal of Allergy and Clinical Immunology*, **2014**, 133, 1564-71	11.5	143
222	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, 478-85	11	142
221	Genome-wide association and longitudinal analyses reveal genetic loci linking pubertal height growth, pubertal timing and childhood adiposity. *Human Molecular Genetics*, **2013**, 22, 2735-47	5.6	138
220	A genome-wide association study reveals variants in ARL15 that influence adiponectin levels. *PLoS Genetics*, **2009**, 5, e1000768	6	129
219	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, 412-20	3.1	128
218	Guidelines for genotyping in genomewide linkage studies: single-nucleotide-polymorphism maps versus microsatellite maps. *American Journal of Human Genetics*, **2004**, 75, 687-92	11	127
217	Genetic and environmental causes of variation in basal levels of blood cells. *Twin Research and Human Genetics*, **1999**, 2, 250-257		124
216	Meta-analysis of Genome-Wide Association Studies for Extraversion: Findings from the Genetics of Personality Consortium. *Behavior Genetics*, **2016**, 46, 170-82	3.2	122
215	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	11	119
214	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	6	118
213	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, 264-77	11	116
212	Assessment of the genetic and clinical determinants of fracture risk: genome wide association and mendelian randomisation study. *BMJ, The*, **2018**, 362, k3225	5.9	114
211	Common variants in left/right asymmetry genes and pathways are associated with relative hand skill. *PLoS Genetics*, **2013**, 9, e1003751	6	112
210	A genome-wide approach to children aggressive behavior: The EAGLE consortium. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2016**, 171, 562-72	3.5	111
209	Investigating the genetic association between ERAP1 and ankylosing spondylitis. *Human Molecular Genetics*, **2009**, 18, 4204-12	5.6	110
208	Biometrical genetics. *Biological Psychology*, **2002**, 61, 33-51	3.2	110
207	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	6	107

206	Common variants in the region around Osterix are associated with bone mineral density and growth in childhood. *Human Molecular Genetics*, **2009**, 18, 1510-7	5.6	107
205	A comparison of linkage disequilibrium patterns and estimated population recombination rates across multiple populations. *American Journal of Human Genetics*, **2005**, 76, 681-7	11	103
204	Genome-wide association study of offspring birth weight in 86 577 women identifies five novel loci and highlights maternal genetic effects that are independent of fetal genetics. *Human Molecular Genetics*, **2018**, 27, 742-756	5.6	98
203	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	11.6	94
202	Common variants at 12q15 and 12q24 are associated with infant head circumference. *Nature Genetics*, **2012**, 44, 532-538	36.3	94
201	A genome-wide association study of body mass index across early life and childhood. *International Journal of Epidemiology*, **2015**, 44, 700-12	7.8	92
200	Cis and trans effects of human genomic variants on gene expression. *PLoS Genetics*, **2014**, 10, e1004461	6	92
199	Genetic variants linked to education predict longevity. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, 13366-13371	11.5	90
198	Genome-wide population-based association study of extremely overweight young adults--the GOYA study. *PLoS ONE*, **2011**, 6, e24303	3.7	90
197	Genetic and environmental causes of variation in basal levels of blood cells. *Twin Research and Human Genetics*, **1999**, 2, 250-7		90
196	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		88
195	Genetic determinants of trabecular and cortical volumetric bone mineral densities and bone microstructure. *PLoS Genetics*, **2013**, 9, e1003247	6	87
194	Association of genetic Loci with glucose levels in childhood and adolescence: a meta-analysis of over 6,000 children. *Diabetes*, **2011**, 60, 1805-12	0.9	83
193	Avoiding dynastic, assortative mating, and population stratification biases in Mendelian randomization through within-family analyses. *Nature Communications*, **2020**, 11, 3519	17.4	83
192	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	3.2	80
191	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	7.2	80
190	Meta-analysis of gene-environment-wide association scans accounting for education level identifies additional loci for refractive error. *Nature Communications*, **2016**, 7, 11008	17.4	79
189	Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation. *Nature Communications*, **2015**, 6, 8658	17.4	79

188	Genetic dissection of acute anterior uveitis reveals similarities and differences in associations observed with ankylosing spondylitis. *Arthritis and Rheumatology*, **2015**, 67, 140-51	9.5	78
187	Identification of atopic dermatitis subgroups in children from 2 longitudinal birth cohorts. *Journal of Allergy and Clinical Immunology*, **2018**, 141, 964-971	11.5	78
186	A novel common variant in DCST2 is associated with length in early life and height in adulthood. *Human Molecular Genetics*, **2015**, 24, 1155-68	5.6	77
185	MR-Base: a platform for systematic causal inference across the phenome using billions of genetic associations		77
184	Genome-wide association study identifies loci affecting blood copper, selenium and zinc. *Human Molecular Genetics*, **2013**, 22, 3998-4006	5.6	76
183	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, 547-58	6.3	74
182	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, 519-25	11	74
181	Genome wide association identifies common variants at the SERPINA6/SERPINA1 locus influencing plasma cortisol and corticosteroid binding globulin. *PLoS Genetics*, **2014**, 10, e1004474	6	71
180	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	11	71
179	Effects of BMI, fat mass, and lean mass on asthma in childhood: a Mendelian randomization study. *PLoS Medicine*, **2014**, 11, e1001669	11.6	70
178	Sequence variants in three loci influence monocyte counts and erythrocyte volume. *American Journal of Human Genetics*, **2009**, 85, 745-9	11	67
177	The validity of twin studies. *GeneScreen*, **2000**, 1, 77-79		67
176	ERAP2 is associated with ankylosing spondylitis in HLA-B27-positive and HLA-B27-negative patients. *Annals of the Rheumatic Diseases*, **2015**, 74, 1627-9	2.4	63
175	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	4.8	63
174	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, 2874-81	4	60
173	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	36.3	59
172	A population-based study of genetic variation and psychotic experiences in adolescents. *Schizophrenia Bulletin*, **2014**, 40, 1254-62	1.3	59
171	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	6	59

170	Polygenic scores predict alcohol problems in an independent sample and show moderation by the environment. *Genes*, **2014**, 5, 330-46	4.2	58
169	Mining the human phenome using allelic scores that index biological intermediates. *PLoS Genetics*, **2013**, 9, e1003919	6	58
168	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	4.9	57
167	Genome-wide association study of primary tooth eruption identifies pleiotropic loci associated with height and craniofacial distances. *Human Molecular Genetics*, **2013**, 22, 3807-17	5.6	57
166	Pharmacogenetics of antidepressant response: A polygenic approach. *Progress in Neuro-Psychopharmacology and Biological Psychiatry*, **2017**, 75, 128-134	5.5	54
165	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, 322-7	7.2	54
164	Common variation near ROBO2 is associated with expressive vocabulary in infancy. *Nature Communications*, **2014**, 5, 4831	17.4	54
163	Genome-wide association study of height-adjusted BMI in childhood identifies functional variant in ADCY3. *Obesity*, **2014**, 22, 2252-9	8	53
162	Bivariate genome-wide association meta-analysis of pediatric musculoskeletal traits reveals pleiotropic effects at the SREBF1/TOM1L2 locus. *Nature Communications*, **2017**, 8, 121	17.4	52
161	Examination of the relationship between variation at 17q21 and childhood wheeze phenotypes. *Journal of Allergy and Clinical Immunology*, **2013**, 131, 685-94	11.5	51
160	Genome-wide association study reveals multiple loci associated with primary tooth development during infancy. *PLoS Genetics*, **2010**, 6, e1000856	6	50
159	Variability in the common genetic architecture of social-communication spectrum phenotypes during childhood and adolescence. *Molecular Autism*, **2014**, 5, 18	6.5	48
158	The power of multivariate quantitative-trait loci linkage analysis is influenced by the correlation between variables. *American Journal of Human Genetics*, **2002**, 70, 1599-602	11	48
157	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	7.8	47
156	Within family Mendelian randomization studies. *Human Molecular Genetics*, **2019**, 28, R170-R179	5.6	47
155	Novel pleiotropic risk loci for melanoma and nevus density implicate multiple biological pathways. *Nature Communications*, **2018**, 9, 4774	17.4	47
154	Novel approach identifies SNPs in SLC2A10 and KCNK9 with evidence for parent-of-origin effect on body mass index. *PLoS Genetics*, **2014**, 10, e1004508	6	45
153	Meta-analysis of 20 genome-wide linkage studies evidenced new regions linked to asthma and atopy. *European Journal of Human Genetics*, **2010**, 18, 700-6	5.3	44

152	Resolving the effects of maternal and offspring genotype on dyadic outcomes in genome wide complex trait analysis ("M-GCTA"). *Behavior Genetics*, **2014**, 44, 445-55	3.2	43
151	Adult height variants affect birth length and growth rate in children. *Human Molecular Genetics*, **2011**, 20, 4069-75	5.6	43
150	Genome-wide prediction of childhood asthma and related phenotypes in a longitudinal birth cohort. *Journal of Allergy and Clinical Immunology*, **2012**, 130, 503-9.e7	11.5	41
149	A comprehensive evaluation of potential lung function associated genes in the SpiroMeta general population sample. *PLoS ONE*, **2011**, 6, e19382	3.7	41
148	Circulating Selenium and Prostate Cancer Risk: A Mendelian Randomization Analysis. *Journal of the National Cancer Institute*, **2018**, 110, 1035-1038	9.7	39
147	Using Mendelian randomization to investigate a possible causal relationship between adiposity and increased bone mineral density at different skeletal sites in children. *International Journal of Epidemiology*, **2016**, 45, 1560-1572	7.8	38
146	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	7.8	36
145	Are obesity risk genes associated with binge eating in adolescence?. *Obesity*, **2015**, 23, 1729-36	8	36
144	Formalising recall by genotype as an efficient approach to detailed phenotyping and causal inference. *Nature Communications*, **2018**, 9, 711	17.4	35
143	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	5.6	34
142	Prospects and pitfalls in whole genome association studies. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **2005**, 360, 1589-95	5.8	34
141	Epigenome-wide Association of DNA Methylation in Whole Blood With Bone Mineral Density. *Journal of Bone and Mineral Research*, **2017**, 32, 1644-1650	6.3	33
140	Genome-wide association study identifies 48 common genetic variants associated with handedness. *Nature Human Behaviour*, **2021**, 5, 59-70	12.8	33
139	Within-family studies for Mendelian randomization: avoiding dynastic, assortative mating, and population stratification biases		32
138	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	6.3	32
137	A genome-wide association study for corneal curvature identifies the platelet-derived growth factor receptor gene as a quantitative trait locus for eye size in white Europeans. *Molecular Vision* , **2013**, 19, 243-53	2.3	30
136	Common variation contributes to the genetic architecture of social communication traits. *Molecular Autism*, **2013**, 4, 34	6.5	29
135	Genome-wide association study for radiographic vertebral fractures: A potential role for the 16q24 BMD locus. *Bone*, **2014**, 59, 20-27	4.7	29

134	Associations of vitamin D pathway genes with circulating 25-hydroxyvitamin-D, 1,25-dihydroxyvitamin-D, and prostate cancer: a nested case-control study. *Cancer Causes and Control*, **2015**, 26, 205-218	2.8	28
133	Assumption-free estimation of the genetic contribution to refractive error across childhood. *Molecular Vision*, **2015**, 21, 621-32	2.3	28
132	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	5.6	27
131	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	11.5	27
130	A genome-wide association study to identify genetic determinants of atopy in subjects from the United Kingdom. *Journal of Allergy and Clinical Immunology*, **2011**, 127, 223-31, 231.e1-3	11.5	26
129	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	4.7	25
128	A genome-wide scan for Eysenckian personality dimensions in adolescent twin sibships: psychoticism, extraversion, neuroticism, and lie. *Journal of Personality*, **2008**, 76, 1415-46	4.4	25
127	Genome-wide association: a promising start to a long race. *Trends in Genetics*, **2006**, 22, 350-4	8.5	25
126	Genotype prediction using a dense map of SNPs. *Genetic Epidemiology*, **2004**, 27, 375-84	2.6	25
125	Major quantitative trait locus for eosinophil count is located on chromosome 2q. *Journal of Allergy and Clinical Immunology*, **2004**, 114, 826-30	11.5	25
124	A genome-wide association meta-analysis of diarrhoeal disease in young children identifies FUT2 locus and provides plausible biological pathways. *Human Molecular Genetics*, **2016**, 25, 4127-4142	5.6	24
123	Genetic variation in prostate-specific antigen-detected prostate cancer and the effect of control selection on genetic association studies. *Cancer Epidemiology Biomarkers and Prevention*, **2014**, 23, 1356-1365	4	24
122	Genetic influences on trajectories of systolic blood pressure across childhood and adolescence. *Circulation: Cardiovascular Genetics*, **2013**, 6, 608-14		24
121	Does bone resorption stimulate periosteal expansion? A cross-sectional analysis of EC-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, 1015-24	6.3	23
120	To what extent do scans of non-synonymous SNPs complement denser genome-wide association studies?. *European Journal of Human Genetics*, **2008**, 16, 718-23	5.3	23
119	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, 4158-66	5.6	22
118	Heritability and Genome-Wide Association Analyses of Sleep Duration in Children: The EAGLE Consortium. *Sleep*, **2016**, 39, 1859-1869	1.1	22
117	Genetically indistinguishable SNPs and their influence on inferring the location of disease-associated variants. *Genome Research*, **2005**, 15, 1503-10	9.7	22

116	Exome-wide study of ankylosing spondylitis demonstrates additional shared genetic background with inflammatory bowel disease. *Npj Genomic Medicine*, **2016**, 1, 16008	6.2	21
115	Genome-wide association study for refractive astigmatism reveals genetic co-determination with spherical equivalent refractive error: the CREAM consortium. *Human Genetics*, **2015**, 134, 131-46	6.3	20
114	Integrative pathway genomics of lung function and airflow obstruction. *Human Molecular Genetics*, **2015**, 24, 6836-48	5.6	20
113	Coordinated genetic scaling of the human eye: shared determination of axial eye length and corneal curvature **2013**, 54, 1715-21		20
112	The Effect of Plasma Lipids and Lipid-Lowering Interventions on Bone Mineral Density: A Mendelian Randomization Study. *Journal of Bone and Mineral Research*, **2020**, 35, 1224-1235	6.3	19
111	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	4	19
110	Genetic variation associated with differential educational attainment in adults has anticipated associations with school performance in children. *PLoS ONE*, **2014**, 9, e100248	3.7	19
109	Genome-wide association study of blood lead shows multiple associations near ALAD. *Human Molecular Genetics*, **2015**, 24, 3871-9	5.6	18
108	Genome-wide association study identifies four loci associated with eruption of permanent teeth. *PLoS Genetics*, **2011**, 7, e1002275	6	18
107	Collider Scope: When selection bias can substantially influence observed associations		18
106	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	7.8	17
105	Is there a higher genetic load of susceptibility loci in familial ankylosing spondylitis?. *Arthritis Care and Research*, **2012**, 64, 780-4	4.7	17
104	Association study of 25 type 2 diabetes related Loci with measures of obesity in Indian sib pairs. *PLoS ONE*, **2013**, 8, e53944	3.7	17
103	Multivariate QTL linkage analysis suggests a QTL for platelet count on chromosome 19q. *European Journal of Human Genetics*, **2004**, 12, 835-42	5.3	17
102	Author response: The MR-Base platform supports systematic causal inference across the human phenome **2018**,		17
101	Genomic influences on alcohol problems in a population-based sample of young adults. *Addiction*, **2015**, 110, 461-70	4.6	16
100	Development of a polygenic risk score to improve screening for fracture risk: A genetic risk prediction study. *PLoS Medicine*, **2020**, 17, e1003152	11.6	16
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