David M Evans

List of Publications by Year in Descending Order

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	Limb development genes underlie variation in human fingerprint patterns.. *Cell*, **2022**, 185, 95-112.e18	56.2	2
276	Exploring the causal effect of maternal pregnancy adiposity on offspring adiposity: Mendelian randomisation using polygenic risk scores.. *BMC Medicine*, **2022**, 20, 34	11.4	0
275	Investigating a Potential Causal Relationship Between Maternal Blood Pressure During Pregnancy and Future Offspring Cardiometabolic Health. *Hypertension*, **2022**, 79, 170-177	8.5	1
274	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals.. *Nature Genetics*, **2022**,	36.3	7
273	DNA methylation in peripheral tissues and left-handedness.. *Scientific Reports*, **2022**, 12, 5606	4.9	0
272	Within-sibship genome-wide association analyses decrease bias in estimates of direct genetic effects.. *Nature Genetics*, **2022**, 54, 581-592	36.3	6
271	Dnmt3a-mutated clonal hematopoiesis promotes osteoporosis. *Journal of Experimental Medicine*, **2021**, 218,	16.6	9
270	A cautionary note on using Mendelian randomization to examine the Barker hypothesis and Developmental Origins of Health and Disease (DOHaD). *Journal of Developmental Origins of Health and Disease*, **2021**, 12, 688-693	2.4	7
269	Genome-wide association study in almost 195,000 individuals identifies 50 previously unidentified genetic loci for eye color. *Science Advances*, **2021**, 7,	14.3	11
268	Osteocyte transcriptome mapping identifies a molecular landscape controlling skeletal homeostasis and susceptibility to skeletal disease. *Nature Communications*, **2021**, 12, 2444	17.4	12
267	Shedding light on the genetics of fetal growth. *Nature Genetics*, **2021**, 53, 1120-1121	36.3	1
266	Integrating Family-Based and Mendelian Randomization Designs. *Cold Spring Harbor Perspectives in Medicine*, **2021**, 11,	5.4	9
265	Genome-wide association study identifies 48 common genetic variants associated with handedness. *Nature Human Behaviour*, **2021**, 5, 59-70	12.8	33
264	Investigating the causal effect of maternal vitamin B12 and folate levels on offspring birthweight. *International Journal of Epidemiology*, **2021**, 50, 179-189	7.8	1
263	The Boulder Workshop Question Box. *Behavior Genetics*, **2021**, 51, 181-190	3.2	0
262	Direct and Indirect Effects of Maternal, Paternal, and Offspring Genotypes: Trio-GCTA. *Behavior Genetics*, **2021**, 51, 154-161	3.2	4
261	Modeling Parent-Specific Genetic Nurture in Families with Missing Parental Genotypes: Application to Birthweight and BMI. *Behavior Genetics*, **2021**, 51, 289-300	3.2	1

260	Genome-wide association study of circulating interleukin 6 levels identifies novel loci. *Human Molecular Genetics*, **2021**, 30, 393-409	5.6	6
259	The Augmented Classical Twin Design: Incorporating Genome-Wide Identity by Descent Sharing Into Twin Studies in Order to Model Violations of the Equal Environments Assumption. *Behavior Genetics*, **2021**, 51, 223-236	3.2	2
258	Higher maternal adiposity reduces offspring birthweight if associated with a metabolically favourable profile. *Diabetologia*, **2021**, 64, 2790-2802	10.3	0
257	Estimating direct and indirect genetic effects on offspring phenotypes using genome-wide summary results data. *Nature Communications*, **2021**, 12, 5420	17.4	0
256	Editorial. *Twin Research and Human Genetics*, **2020**, 23, 67	2.2	
255	It's in the Bloody Genes!. *Twin Research and Human Genetics*, **2020**, 23, 96-97	2.2	
254	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	7.8	0
253	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
252	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
251	Maternal and paternal effects on offspring internalizing problems: Results from genetic and family-based analyses. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2020**, 183, 258-267	3.5	6
250	Estimating indirect parental genetic effects on offspring phenotypes using virtual parental genotypes derived from sibling and half sibling pairs. *PLoS Genetics*, **2020**, 16, e1009154	6	6
249	Variants associated with HHIP expression have sex-differential effects on lung function. *Wellcome Open Research*, **2020**, 5, 111	4.8	0
248	Introducing M-GCTA a Software Package to Estimate Maternal (or Paternal) Genetic Effects on Offspring Phenotypes. *Behavior Genetics*, **2020**, 50, 51-66	3.2	5
247	Metabolomics analysis in adults with high bone mass identifies a relationship between bone resorption and circulating citrate which replicates in the general population. *Clinical Endocrinology*, **2020**, 92, 29-37	3.4	9
246	Septic Shock: A Genomewide Association Study and Polygenic Risk Score Analysis. *Twin Research and Human Genetics*, **2020**, 23, 204-213	2.2	1
245	Avoiding dynastic, assortative mating, and population stratification biases in Mendelian randomization through within-family analyses. *Nature Communications*, **2020**, 11, 3519	17.4	83
244	Mendelian randomization study of maternal influences on birthweight and future cardiometabolic risk in the HUNT cohort. *Nature Communications*, **2020**, 11, 5404	17.4	14
243	Exploring the genetic relationship between hearing impairment and Alzheimer's disease. *Alzheimer's and Dementia: Diagnosis, Assessment and Disease Monitoring*, **2020**, 12, e12108	5.2	7

242	Variants associated with expression have sex-differential effects on lung function. *Wellcome Open Research*, **2020**, 5, 111	4.8	0
241	Exploring the role of genetic confounding in the association between maternal and offspring body mass index: evidence from three birth cohorts. *International Journal of Epidemiology*, **2020**, 49, 233-243	7.8	7
240	Development of a polygenic risk score to improve screening for fracture risk: A genetic risk prediction study **2020**, 17, e1003152		
239	Development of a polygenic risk score to improve screening for fracture risk: A genetic risk prediction study **2020**, 17, e1003152		
238	Development of a polygenic risk score to improve screening for fracture risk: A genetic risk prediction study **2020**, 17, e1003152		
237	Development of a polygenic risk score to improve screening for fracture risk: A genetic risk prediction study **2020**, 17, e1003152		
236	Development of a polygenic risk score to improve screening for fracture risk: A genetic risk prediction study **2020**, 17, e1003152		
235	Development of a polygenic risk score to improve screening for fracture risk: A genetic risk prediction study **2020**, 17, e1003152		
234	Antibody response to common human viruses is shaped by genetic factors. *Journal of Allergy and Clinical Immunology*, **2019**, 143, 1640-1643	11.5	1
233	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
232	A Metabolic Screen in Adolescents Reveals an Association Between Circulating Citrate and Cortical Bone Mineral Density. *Journal of Bone and Mineral Research*, **2019**, 34, 1306-1313	6.3	4
231	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
230	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
229	Within family Mendelian randomization studies. *Human Molecular Genetics*, **2019**, 28, R170-R179	5.6	47
228	Use of Mendelian Randomization to Examine Causal Inference in Osteoporosis. *Frontiers in Endocrinology*, **2019**, 10, 807	5.7	10
227	Calculating Power to Detect Maternal and Offspring Genetic Effects in Genetic Association Studies. *Behavior Genetics*, **2019**, 49, 327-339	3.2	15
226	An atlas of genetic influences on osteoporosis in humans and mice. *Nature Genetics*, **2019**, 51, 258-266	36.3	270
225	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

224	Elucidating the genetics of craniofacial shape. *Nature Genetics*, **2018**, 50, 319-321	36.3	4
223	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
222	Partitioning Phenotypic Variance Due to Parent-of-Origin Effects Using Genomic Relatedness Matrices. *Behavior Genetics*, **2018**, 48, 67-79	3.2	5
221	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
220	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
219	Formalising recall by genotype as an efficient approach to detailed phenotyping and causal inference. *Nature Communications*, **2018**, 9, 711	17.4	35
218	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
217	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
216	Collider scope: when selection bias can substantially influence observed associations. *International Journal of Epidemiology*, **2018**, 47, 226-235	7.8	354
215	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	7.9	15
214	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	7	15
213	Genome-wide survey of parent-of-origin effects on DNA methylation identifies candidate imprinted loci in humans. *Human Molecular Genetics*, **2018**, 27, 2927-2939	5.6	15
212	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
211	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	6.5	10
210	Author response: The MR-Base platform supports systematic causal inference across the human phenome **2018**,		17
209	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
208	Novel pleiotropic risk loci for melanoma and nevus density implicate multiple biological pathways. *Nature Communications*, **2018**, 9, 4774	17.4	47
207	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

206	Assessing the Role of DNA Methylation-Derived Neutrophil-to-Lymphocyte Ratio in Rheumatoid Arthritis. *Journal of Immunology Research*, **2018**, 2018, 2624981	4.5	8
205	MHC-Dependent Mate Selection within 872 Spousal Pairs of European Ancestry from the Health and Retirement Study. *Genes*, **2018**, 9,	4.2	6
204	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
203	Circulating Selenium and Prostate Cancer Risk: A Mendelian Randomization Analysis. *Journal of the National Cancer Institute*, **2018**, 110, 1035-1038	9.7	39
202	The MR-Base platform supports systematic causal inference across the human phenome. *ELife*, **2018**, 7,	8.9	1190
201	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
200	Pharmacogenetics of antidepressant response: A polygenic approach. *Progress in Neuro-Psychopharmacology and Biological Psychiatry*, **2017**, 75, 128-134	5.5	54
199	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
198	Role of a medical student: patient perspectives. *Clinical Teacher*, **2017**, 14, 284-288	1.1	6
197	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
196	Single Nucleotide Polymorphisms Associated with Reading Ability Show Connection to Socio-Economic Outcomes. *Behavior Genetics*, **2017**, 47, 469-479	3.2	8
195	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
194	Recent Developments in Mendelian Randomization Studies. *Current Epidemiology Reports*, **2017**, 4, 330-345	2.9	218
193	HAPRAP: a haplotype-based iterative method for statistical fine mapping using GWAS summary statistics. *Bioinformatics*, **2017**, 33, 79-86	7.2	4
192	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
191	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
190	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
189	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

188	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
187	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
186	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
185	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
184	Heritability and Genome-Wide Association Analyses of Sleep Duration in Children: The EAGLE Consortium. *Sleep*, **2016**, 39, 1859-1869	1.1	22
183	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	2.6	
182	Genetic risk for autism spectrum disorders and neuropsychiatric variation in the general population. *Nature Genetics*, **2016**, 48, 552-5	36.3	238
181	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. *Nature Communications*, **2016**, 7, 10495	17.4	180
180	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
179	Common Genetic Variants Influence Whorls in Fingerprint Patterns. *Journal of Investigative Dermatology*, **2016**, 136, 859-862	4.3	14
178	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
177	Association of Forced Vital Capacity with the Developmental Gene NCOR2. *PLoS ONE*, **2016**, 11, e0147388	3.7	15
176	The case for genome-wide association studies of bone acquisition in paediatric and adolescent populations. *BoneKEy Reports*, **2016**, 5, 796		5
175	Authors' response to Hartwig and Davies. *International Journal of Epidemiology*, **2016**, 45, 1678-1679	7.8	1
174	Exome-wide study of ankylosing spondylitis demonstrates additional shared genetic background with inflammatory bowel disease. *Npj Genomic Medicine*, **2016**, 1, 16008	6.2	21
173	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
172	Systematic identification of genetic influences on methylation across the human life course. *Genome Biology*, **2016**, 17, 61	18.3	331
171	Genome-wide association study identifies 74 loci associated with educational attainment. *Nature*, **2016**, 533, 539-42	50.4	850

170	Genome-wide associations for birth weight and correlations with adult disease. *Nature*, **2016**, 538, 248-252	50.4	266
169	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
168	A genome-wide approach to children's aggressive behavior: The EAGLE consortium. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2016**, 171, 562-72	3.5	111
167	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
166	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
165	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
164	Heritability and genome-wide analyses of problematic peer relationships during childhood and adolescence. *Human Genetics*, **2015**, 134, 539-51	6.3	7
163	Data Resource Profile: Accessible Resource for Integrated Epigenomic Studies (ARIES). *International Journal of Epidemiology*, **2015**, 44, 1181-90	7.8	162
162	Genome-wide association study of blood lead shows multiple associations near ALAD. *Human Molecular Genetics*, **2015**, 24, 3871-9	5.6	18
161	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
160	Integrative pathway genomics of lung function and airflow obstruction. *Human Molecular Genetics*, **2015**, 24, 6836-48	5.6	20
159	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
158	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
157	Whole-genome sequencing identifies EN1 as a determinant of bone density and fracture. *Nature*, **2015**, 526, 112-7	50.4	308
156	The UK10K project identifies rare variants in health and disease. *Nature*, **2015**, 526, 82-90	50.4	776
155	Genomic influences on alcohol problems in a population-based sample of young adults. *Addiction*, **2015**, 110, 461-70	4.6	16
154	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
153	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

152	Are obesity risk genes associated with binge eating in adolescence?. *Obesity*, **2015**, 23, 1729-36	8	36
151	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
150	Major histocompatibility complex associations of ankylosing spondylitis are complex and involve further epistasis with ERAP1. *Nature Communications*, **2015**, 6, 7146	17.4	164
149	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
148	Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation. *Nature Communications*, **2015**, 6, 8658	17.4	79
147	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
146	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	3.7	5
145	Assumption-free estimation of the genetic contribution to refractive error across childhood. *Molecular Vision*, **2015**, 21, 621-32	2.3	28
144	FAM129B, a Novel Protein, Suppresses the TNF□Apoptotic pathway and Promotes the NF-kB Survival Pathway in Cancer Cells by Interacting with KEAP1. *FASEB Journal*, **2015**, 29, 569.1	0.9	
143	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
142	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
141	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
140	Variability in the common genetic architecture of social-communication spectrum phenotypes during childhood and adolescence. *Molecular Autism*, **2014**, 5, 18	6.5	48
139	Polygenic scores predict alcohol problems in an independent sample and show moderation by the environment. *Genes*, **2014**, 5, 330-46	4.2	58
138	Cis and trans effects of human genomic variants on gene expression. *PLoS Genetics*, **2014**, 10, e1004461	6	92
137	A population-based study of genetic variation and psychotic experiences in adolescents. *Schizophrenia Bulletin*, **2014**, 40, 1254-62	1.3	59
136	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
135	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

134	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
133	Effects of BMI, fat mass, and lean mass on asthma in childhood: a Mendelian randomization study. *PLoS Medicine*, **2014**, 11, e1001669	11.6	70
132	Genome-wide association study of height-adjusted BMI in childhood identifies functional variant in ADCY3. *Obesity*, **2014**, 22, 2252-9	8	53
131	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
130	Common variation near ROBO2 is associated with expressive vocabulary in infancy. *Nature Communications*, **2014**, 5, 4831	17.4	54
129	The association between primary tooth emergence and anthropometric measures in young adults: findings from a large prospective cohort study. *PLoS ONE*, **2014**, 9, e96355	3.7	5
128	Does bone resorption stimulate periosteal expansion? A cross-sectional analysis of ßC-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
127	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
126	Genome-wide association study for radiographic vertebral fractures: A potential role for the 16q24 BMD locus. *Bone*, **2014**, 59, 20-27	4.7	29
125	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
124	Genome-wide association study for radiographic vertebral fractures: a potential role for the 16q24 BMD locus. *Bone*, **2014**, 59, 20-7	4.7	16
123	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
122	Common variation contributes to the genetic architecture of social communication traits. *Molecular Autism*, **2013**, 4, 34	6.5	29
121	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
120	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
119	Genome-wide association study identifies loci affecting blood copper, selenium and zinc. *Human Molecular Genetics*, **2013**, 22, 3998-4006	5.6	76
118	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
117	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

116	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
115	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
114	GWAS of 126,559 individuals identifies genetic variants associated with educational attainment. *Science*, **2013**, 340, 1467-71	33.3	563
113	Genome-wide meta-analysis identifies new susceptibility loci for migraine. *Nature Genetics*, **2013**, 45, 912-917	36.3	276
112	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
111	Genetic determinants of trabecular and cortical volumetric bone mineral densities and bone microstructure. *PLoS Genetics*, **2013**, 9, e1003247	6	87
110	Mining the human phenome using allelic scores that index biological intermediates. *PLoS Genetics*, **2013**, 9, e1003919	6	58
109	Common variants in left/right asymmetry genes and pathways are associated with relative hand skill. *PLoS Genetics*, **2013**, 9, e1003751	6	112
108	Coordinated genetic scaling of the human eye: shared determination of axial eye length and corneal curvature **2013**, 54, 1715-21		20
107	Genetic influences on trajectories of systolic blood pressure across childhood and adolescence. *Circulation: Cardiovascular Genetics*, **2013**, 6, 608-14		24
106	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
105	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
104	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
103	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
102	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
101	Seventy-five genetic loci influencing the human red blood cell. *Nature*, **2012**, 492, 369-75	50.4	257
100	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
99	A genome-wide association meta-analysis identifies new childhood obesity loci. *Nature Genetics*, **2012**, 44, 526-31	36.3	292

98	Molecular and population analysis of natural selection on the human haptoglobin duplication. *Annals of Human Genetics*, **2012**, 76, 352-62	2.2	15
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