David M Evans

List of Publications by Year
in descending order

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269 papers	48,203 citations	3334 91 h-index	2178 202 g-index
312 all docs	312 docs citations	312 times ranked	49551 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.	1.9	5
2	Investigating a Potential Causal Relationship Between Maternal Blood Pressure During Pregnancy and Future Offspring Cardiometabolic Health. Hypertension, 2022, 79, 170-177.	2.7	10
3	Limb development genes underlie variation in human fingerprint patterns. Cell, 2022, 185, 95-112.e18.	28.9	30
4	Exploring the causal effect of maternal pregnancy adiposity on offspring adiposity: Mendelian randomisation using polygenic risk scores. BMC Medicine, 2022, 20, 34.	5.5	14
5	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals. Nature Genetics, 2022, 54, 437-449.	21.4	215
6	DNA methylation in peripheral tissues and left-handedness. Scientific Reports, 2022, 12, 5606.	3.3	12
7	Fetal alleles predisposing to metabolically favorable adiposity are associated with higher birth weight. Human Molecular Genetics, 2022, 31, 1762-1775.	2.9	2
8	Within-sibship genome-wide association analyses decrease bias in estimates of direct genetic effects. Nature Genetics, 2022, 54, 581-592.	21.4	142
9	Evaluating indirect genetic effects of siblings using singletons. PLoS Genetics, 2022, 18, e1010247.	3.5	7
10	Integrating Family-Based and Mendelian Randomization Designs. Cold Spring Harbor Perspectives in Medicine, 2021, 11, a039503.	6.2	19
11	Genome-wide association study identifies 48 common genetic variants associated with handedness. Nature Human Behaviour, 2021, 5, 59-70.	12.0	79
12	Investigating the causal effect of maternal vitamin B12 and folate levels on offspring birthweight. International Journal of Epidemiology, 2021, 50, 179-189.	1.9	6
13	The Boulder Workshop Question Box. Behavior Genetics, 2021, 51, 181-190.	2.1	1
14	Direct and Indirect Effects of Maternal, Paternal, and Offspring Genotypes: Trio-GCTA. Behavior Genetics, 2021, 51, 154-161.	2.1	27
15	Modeling Parent-Specific Genetic Nurture in Families with Missing Parental Genotypes: Application to Birthweight and BMI. Behavior Genetics, 2021, 51, 289-300.	2.1	5
16	Genome-wide association study of circulating interleukin 6 levels identifies novel loci. Human Molecular Genetics, 2021, 30, 393-409.	2.9	32
17	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.	2.1	7
18	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

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19	Introduction to the Special Issue on Statistical Genetic Methods for Human Complex Traits. Behavior Genetics, 2021, 51, 165-169.	2.1	2
20	Osteocyte transcriptome mapping identifies a molecular landscape controlling skeletal homeostasis and susceptibility to skeletal disease. Nature Communications, 2021, 12, 2444.	12.8	58
21	Shedding light on the genetics of fetal growth. Nature Genetics, 2021, 53, 1120-1121.	21.4	2
22	Ten simple rules for conducting a mendelian randomization study. PLoS Computational Biology, 2021, 17, e1009238.	3.2	33
23	586Effects of maternal circulating amino acids on offspring birthweight: a Mendelian randomisation analysis. International Journal of Epidemiology, 2021, 50, .	1.9	1
24	Higher maternal adiposity reduces offspring birthweight if associated with a metabolically favourable profile. Diabetologia, 2021, 64, 2790-2802.	6.3	9
25	Estimating direct and indirect genetic effects on offspring phenotypes using genome-wide summary results data. Nature Communications, 2021, 12, 5420.	12.8	9
26	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.	1.4	21
27	Dnmt3a-mutated clonal hematopoiesis promotes osteoporosis. Journal of Experimental Medicine, 2021, 218, .	8.5	81
28	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.	1.9	18
29	Introducing M-GCTA a Software Package to Estimate Maternal (or Paternal) Genetic Effects on Offspring Phenotypes. Behavior Genetics, 2020, 50, 51-66.	2.1	18
30	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.	2.4	14
31	Septic Shock: A Genomewide Association Study and Polygenic Risk Score Analysis. Twin Research and Human Genetics, 2020, 23, 204-213.	0.6	9
32	Avoiding dynastic, assortative mating, and population stratification biases in Mendelian randomization through within-family analyses. Nature Communications, 2020, 11, 3519.	12.8	213
33	Mendelian randomization study of maternal influences on birthweight and future cardiometabolic risk in the HUNT cohort. Nature Communications, 2020, 11, 5404.	12.8	48
34	Exploring the genetic relationship between hearing impairment and Alzheimer's disease. Alzheimer's and Dementia: Diagnosis, Assessment and Disease Monitoring, 2020, 12, e12108.	2.4	13
35	Editorial. Twin Research and Human Genetics, 2020, 23, 67-67.	0.6	0
36	Itâ€™s in the Bloody Genes!. Twin Research and Human Genetics, 2020, 23, 96-97.	0.6	0

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37	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.	1.9	1
38	The Effect of Plasma Lipids and Lipidâ€Lowering Interventions on Bone Mineral Density: A Mendelian Randomization Study. Journal of Bone and Mineral Research, 2020, 35, 1224-1235.	2.8	45
39	Development of a polygenic risk score to improve screening for fracture risk: A genetic risk prediction study. PLoS Medicine, 2020, 17, e1003152.	8.4	45
40	Maternal and paternal effects on offspring internalizing problems: Results from genetic and familyâ€based analyses. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2020, 183, 258-267.	1.7	17
41	Variants associated with HHIP expression have sex-differential effects on lung function. Wellcome Open Research, 2020, 5, 111.	1.8	3
42	Estimating indirect parental genetic effects on offspring phenotypes using virtual parental genotypes derived from sibling and half sibling pairs. PLoS Genetics, 2020, 16, e1009154.	3.5	22
43	Variants associated with HHIP expression have sex-differential effects on lung function. Wellcome Open Research, 2020, 5, 111.	1.8	4
44	Title is missing!. , 2020, 17, e1003152.		0
45	Title is missing!. , 2020, 17, e1003152.		0
46	Title is missing!. , 2020, 17, e1003152.		0
47	Title is missing!. , 2020, 17, e1003152.		0
48	Title is missing!. , 2020, 17, e1003152.		0
49	Title is missing!. , 2020, 17, e1003152.		0
50	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
51	Within family Mendelian randomization studies. Human Molecular Genetics, 2019, 28, R170-R179.	2.9	105
52	Use of Mendelian Randomization to Examine Causal Inference in Osteoporosis. Frontiers in Endocrinology, 2019, 10, 807.	3.5	23
53	Antibody response to common human viruses is shaped by genetic factors. Journal of Allergy and Clinical Immunology, 2019, 143, 1640-1643.	2.9	2
54	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. Nature Genetics, 2019, 51, 804-814.	21.4	402

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55	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.	2.8	5
56	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
57	Calculating Power to Detect Maternal and Offspring Genetic Effects in Genetic Association Studies. Behavior Genetics, 2019, 49, 327-339.	2.1	32
58	An atlas of genetic influences on osteoporosis in humans and mice. Nature Genetics, 2019, 51, 258-266.	21.4	557
59	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
60	Elucidating the genetics of craniofacial shape. Nature Genetics, 2018, 50, 319-321.	21.4	4
61	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
62	Partitioning Phenotypic Variance Due to Parent-of-Origin Effects Using Genomic Relatedness Matrices. Behavior Genetics, 2018, 48, 67-79.	2.1	7
63	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
64	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
65	Formalising recall by genotype as an efficient approach to detailed phenotyping and causal inference. Nature Communications, 2018, 9, 711.	12.8	54
66	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
67	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
68	Collider scope: when selection bias can substantially influence observed associations. International Journal of Epidemiology, 2018, 47, 226-235.	1.9	631
69	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.	1.3	30
70	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
71	Novel pleiotropic risk loci for melanoma and nevus density implicate multiple biological pathways. Nature Communications, 2018, 9, 4774.	12.8	87
72	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

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73	Assessing the Role of DNA Methylation-Derived Neutrophil-to-Lymphocyte Ratio in Rheumatoid Arthritis. Journal of Immunology Research, 2018, 2018, 1-10.	2.2	13
74	MHC-Dependent Mate Selection within 872 Spousal Pairs of European Ancestry from the Health and Retirement Study. Genes, 2018, 9, 53.	2.4	8
75	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
76	Circulating Selenium and Prostate Cancer Risk: A Mendelian Randomization Analysis. Journal of the National Cancer Institute, 2018, 110, 1035-1038.	6.3	84
77	The MR-Base platform supports systematic causal inference across the human phenome. ELife, 2018, 7, .	6.0	3,639
78	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.	4.7	22
79	Genome-wide survey of parent-of-origin effects on DNA methylation identifies candidate imprinted loci in humans. Human Molecular Genetics, 2018, 27, 2927-2939.	2.9	22
80	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
81	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.	3.7	14
82	Association Between Telomere Length and Risk of Cancer and Non-Neoplastic Diseases. JAMA Oncology, 2017, 3, 636.	7.1	376
83	Pharmacogenetics of antidepressant response: A polygenic approach. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2017, 75, 128-134.	4.8	71
84	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
85	Role of a medical student: patient perspectives. Clinical Teacher, 2017, 14, 284-288.	0.8	6
86	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
87	Single Nucleotide Polymorphisms Associated with Reading Ability Show Connection to Socio-Economic Outcomes. Behavior Genetics, 2017, 47, 469-479.	2.1	13
88	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
89	Recent Developments in Mendelian Randomization Studies. Current Epidemiology Reports, 2017, 4, 330-345.	2.4	553
90	HAPRAP: a haplotype-based iterative method for statistical fine mapping using GWAS summary statistics. Bioinformatics, 2017, 33, 79-86.	4.1	4

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91	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
92	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
93	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
94	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
95	Authorsâ€™ response to Hartwig and Davies. International Journal of Epidemiology, 2016, 45, 1678-1679.	1.9	1
96	Exome-wide study of ankylosing spondylitis demonstrates additional shared genetic background with inflammatory bowel disease. Npj Genomic Medicine, 2016, 1, 16008.	3.8	32
97	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.	1.9	56
98	Systematic identification of genetic influences on methylation across the human life course. Genome Biology, 2016, 17, 61.	8.8	489
99	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	27.8	1,204
100	Genome-wide associations for birth weight and correlations with adult disease. Nature, 2016, 538, 248-252.	27.8	406
101	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
102	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
103	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
104	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
105	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
106	Genetic variants linked to education predict longevity. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13366-13371.	7.1	110
107	Heritability and Genome-Wide Association Analyses of Sleep Duration in Children: The EAGLE Consortium. Sleep, 2016, 39, 1859-1869.	1.1	34
108	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

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109	Genetic risk for autism spectrum disorders and neuropsychiatric variation in the general population. Nature Genetics, 2016, 48, 552-555.	21.4	326
110	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. Nature Communications, 2016, 7, 10495.	12.8	245
111	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
112	Common Genetic Variants Influence Whorls inÂFingerprint Patterns. Journal of Investigative Dermatology, 2016, 136, 859-862.	0.7	19
113	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
114	The case for genome-wide association studies of bone acquisition in paediatric and adolescent populations. BoneKEy Reports, 2016, 5, 796.	2.7	5
115	Association of Forced Vital Capacity with the Developmental Gene NCOR2. PLoS ONE, 2016, 11, e0147388.	2.5	17
116	Are obesity risk genes associated with binge eating in adolescence?. Obesity, 2015, 23, 1729-1736.	3.0	44
117	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
118	Major histocompatibility complex associations of ankylosing spondylitis are complex and involve further epistasis with ERAP1. Nature Communications, 2015, 6, 7146.	12.8	220
119	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
120	Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation. Nature Communications, 2015, 6, 8658.	12.8	108
121	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
122	ERAP2is associated with ankylosing spondylitis inHLA-B27-positive andHLA-B27-negative patients. Annals of the Rheumatic Diseases, 2015, 74, 1627-1629.	0.9	86
123	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
124	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.	3.8	24
125	Heritability and genome-wide analyses of problematic peer relationships during childhood and adolescence. Human Genetics, 2015, 134, 539-551.	3.8	13
126	Data Resource Profile: Accessible Resource for Integrated Epigenomic Studies (ARIES). International Journal of Epidemiology, 2015, 44, 1181-1190.	1.9	238

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127	Genome-wide association study of blood lead shows multiple associations near ALAD. Human Molecular Genetics, 2015, 24, 3871-3879.	2.9	28
128	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
129	Integrative pathway genomics of lung function and airflow obstruction. Human Molecular Genetics, 2015, 24, 6836-6848.	2.9	28
130	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
131	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
132	Wholeâ€genome sequencing identifies EN1 as a determinant of bone density and fracture. Nature, 2015, 526, 112-117.	27.8	483
133	The UK10K project identifies rare variants in health and disease. Nature, 2015, 526, 82-90.	27.8	1,014
134	Genomic influences on alcohol problems in a population-based sample of young adults. Addiction, 2015, 110, 461-470.	3.3	18
135	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
136	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
137	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.	2.5	6
138	FAM129B, a Novel Protein, Suppresses the TNFÎ± Apoptotic pathway and Promotes the NFâ€kB Survival Pathway in Cancer Cells by Interacting with KEAP1. FASEB Journal, 2015, 29, 569.1.	0.5	0
139	Assumption-free estimation of the genetic contribution to refractive error across childhood. Molecular Vision, 2015, 21, 621-32.	1.1	36
140	Polygenic Scores Predict Alcohol Problems in an Independent Sample and Show Moderation by the Environment. Genes, 2014, 5, 330-346.	2.4	71
141	Cis and Trans Effects of Human Genomic Variants on Gene Expression. PLoS Genetics, 2014, 10, e1004461.	3.5	117
142	A Population-Based Study of Genetic Variation and Psychotic Experiences in Adolescents. Schizophrenia Bulletin, 2014, 40, 1254-1262.	4.3	74
143	Novel Approach Identifies SNPs in SLC2A10 and KCNK9 with Evidence for Parent-of-Origin Effect on Body Mass Index. PLoS Genetics, 2014, 10, e1004508.	3.5	80
144	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

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145	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
146	Effects of BMI, Fat Mass, and Lean Mass on Asthma in Childhood: A Mendelian Randomization Study. PLoS Medicine, 2014, 11, e1001669.	8.4	93
147	Genome-wide association study of height-adjusted BMI in childhood identifies functional variant inADCY3. Obesity, 2014, 22, 2252-2259.	3.0	86
148	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.	2.5	26
149	Common variation near ROBO2 is associated with expressive vocabulary in infancy. Nature Communications, 2014, 5, 4831.	12.8	82
150	The Association between Primary Tooth Emergence and Anthropometric Measures in Young Adults: Findings from a Large Prospective Cohort Study. PLoS ONE, 2014, 9, e96355.	2.5	9
151	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.	2.8	24
152	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
153	Genome-wide association study for radiographic vertebral fractures: A potential role for the 16q24 BMD locus. Bone, 2014, 59, 20-27.	2.9	32
154	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
155	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
156	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
157	Variability in the common genetic architecture of social-communication spectrum phenotypes during childhood and adolescence. Molecular Autism, 2014, 5, 18.	4.9	53
158	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
159	Genome-wide association study for radiographic vertebral fractures: a potential role for the 16q24 BMD locus. Bone, 2014, 59, 20-7.	2.9	17
160	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
161	Common variation contributes to the genetic architecture of social communication traits. Molecular Autism, 2013, 4, 34.	4.9	34
162	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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163	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
164	Genome-wide association study identifies loci affecting blood copper, selenium and zinc. Human Molecular Genetics, 2013, 22, 3998-4006.	2.9	140
165	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
166	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
167	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
168	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
169	GWAS of 126,559 Individuals Identifies Genetic Variants Associated with Educational Attainment. Science, 2013, 340, 1467-1471.	12.6	750
170	Genome-wide meta-analysis identifies new susceptibility loci for migraine. Nature Genetics, 2013, 45, 912-917.	21.4	338
171	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
172	Genetic Determinants of Trabecular and Cortical Volumetric Bone Mineral Densities and Bone Microstructure. PLoS Genetics, 2013, 9, e1003247.	3.5	100
173	Mining the Human Phenome Using Allelic Scores That Index Biological Intermediates. PLoS Genetics, 2013, 9, e1003919.	3.5	84
174	Common Variants in Left/Right Asymmetry Genes and Pathways Are Associated with Relative Hand Skill. PLoS Genetics, 2013, 9, e1003751.	3.5	129
175	Coordinated Genetic Scaling of the Human Eye: Shared Determination of Axial Eye Length and Corneal Curvature. , 2013, 54, 1715.		27
176	Genetic Influences on Trajectories of Systolic Blood Pressure Across Childhood and Adolescence. Circulation: Cardiovascular Genetics, 2013, 6, 608-614.	5.1	32
177	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.	2.5	22
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