David M Evans

List of Publications by Year
in descending order

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269 papers	48,203 citations	3333 91 h-index	2238 201 g-index
312 all docs	312 docs citations	312 times ranked	49551 citing authors

#	Article	IF	Citations
1	A second generation human haplotype map of over 3.1 million SNPs. Nature, 2007, 449, 851-861.	13.7	4,137
2	The MR-Base platform supports systematic causal inference across the human phenome. ELife, 2018, 7, .	2.8	3,639
3	Genome-wide detection and characterization of positive selection in human populations. Nature, 2007, 449, 913-918.	13.7	1,788
4	Six new loci associated with body mass index highlight a neuronal influence on body weight regulation. Nature Genetics, 2009, 41, 25-34.	9.4	1,572
5	Association scan of 14,500 nonsynonymous SNPs in four diseases identifies autoimmunity variants. Nature Genetics, 2007, 39, 1329-1337.	9.4	1,298
6	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	13.7	1,204
7	Common variants near MC4R are associated with fat mass, weight and risk of obesity. Nature Genetics, 2008, 40, 768-775.	9.4	1,179
8	Genome-wide meta-analysis identifies 56 bone mineral density loci and reveals 14 loci associated with risk of fracture. Nature Genetics, 2012, 44, 491-501.	9.4	1,100
9	The UK10K project identifies rare variants in health and disease. Nature, 2015, 526, 82-90.	13.7	1,014
10	A genome-wide association study identifies new psoriasis susceptibility loci and an interaction between HLA-C and ERAP1. Nature Genetics, 2010, 42, 985-990.	9.4	918
11	LD Hub: a centralized database and web interface to perform LD score regression that maximizes the potential of summary level GWAS data for SNP heritability and genetic correlation analysis. Bioinformatics, 2017, 33, 272-279.	1.8	822
12	Interaction between ERAP1 and HLA-B27 in ankylosing spondylitis implicates peptide handling in the mechanism for HLA-B27 in disease susceptibility. Nature Genetics, 2011, 43, 761-767.	9.4	778
13	GWAS of 126,559 Individuals Identifies Genetic Variants Associated with Educational Attainment. Science, 2013, 340, 1467-1471.	6.0	750
14	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. Nature Genetics, 2012, 44, 991-1005.	9.4	746
15	Genome-wide association analysis identifies 20 loci that influence adult height. Nature Genetics, 2008, 40, 575-583.	9.4	742
16	Genome-wide association study of CNVs in 16,000 cases of eight common diseases and 3,000 shared controls. Nature, 2010, 464, 713-720.	13.7	737
17	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
18	Collider scope: when selection bias can substantially influence observed associations. International Journal of Epidemiology, 2018, 47, 226-235.	0.9	631

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19	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. Nature Genetics, 2013, 45, 501-512.	9.4	578
20	Genome-wide association study of ankylosing spondylitis identifies non-MHC susceptibility loci. Nature Genetics, 2010, 42, 123-127.	9.4	573
21	An atlas of genetic influences on osteoporosis in humans and mice. Nature Genetics, 2019, 51, 258-266.	9.4	557
22	Recent Developments in Mendelian Randomization Studies. Current Epidemiology Reports, 2017, 4, 330-345.	1.1	553
23	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
24	Genome-wide association study identifies five loci associated with lung function. Nature Genetics, 2010, 42, 36-44.	9.4	518
25	Systematic identification of genetic influences on methylation across the human life course. Genome Biology, 2016, 17, 61.	3.8	489
26	Wholeâ€genome sequencing identifies EN1 as a determinant of bone density and fracture. Nature, 2015, 526, 112-117.	13.7	483
27	Novel Loci for Adiponectin Levels and Their Influence on Type 2 Diabetes and Metabolic Traits: A Multi-Ethnic Meta-Analysis of 45,891 Individuals. PLoS Genetics, 2012, 8, e1002607.	1.5	419
28	Genome-wide associations for birth weight and correlations with adult disease. Nature, 2016, 538, 248-252.	13.7	406
29	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. Nature Genetics, 2019, 51, 804-814.	9.4	402
30	New gene functions in megakaryopoiesis and platelet formation. Nature, 2011, 480, 201-208.	13.7	401
31	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
32	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
33	Association Between Telomere Length and Risk of Cancer and Non-Neoplastic Diseases. JAMA Oncology, 2017, 3, 636.	3.4	376
34	Genome-wide association and large-scale follow up identifies 16 new loci influencing lung function. Nature Genetics, 2011, 43, 1082-1090.	9.4	367
35	A genome-wide association meta-analysis identifies new childhood obesity loci. Nature Genetics, 2012, 44, 526-531.	9.4	352
36	Genome-wide meta-analysis identifies new susceptibility loci for migraine. Nature Genetics, 2013, 45, 912-917.	9.4	338

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37	Genetic risk for autism spectrum disorders and neuropsychiatric variation in the general population. Nature Genetics, 2016, 48, 552-555.	9.4	326
38	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
39	Seventy-five genetic loci influencing the human red blood cell. Nature, 2012, 492, 369-375.	13.7	320
40	Meta-analysis of genome-wide association studies identifies three new risk loci for atopic dermatitis. Nature Genetics, 2012, 44, 187-192.	9.4	311
41	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
42	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
43	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
44	Harnessing the information contained within genome-wide association studies to improve individual prediction of complex disease risk. Human Molecular Genetics, 2009, 18, 3525-3531.	1.4	281
45	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
46	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
47	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. Nature Communications, 2016, 7, 10495.	5.8	245
48	WNT16 Influences Bone Mineral Density, Cortical Bone Thickness, Bone Strength, and Osteoporotic Fracture Risk. PLoS Genetics, 2012, 8, e1002745.	1.5	240
49	Data Resource Profile: Accessible Resource for Integrated Epigenomic Studies (ARIES). International Journal of Epidemiology, 2015, 44, 1181-1190.	0.9	238
50	Genome-Wide Association Study Using Extreme Truncate Selection Identifies Novel Genes Affecting Bone Mineral Density and Fracture Risk. PLoS Genetics, 2011, 7, e1001372.	1.5	233
51	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
52	Variants in ADCY5 and near CCNL1 are associated with fetal growth and birth weight. Nature Genetics, 2010, 42, 430-435.	9.4	223
53	Major histocompatibility complex associations of ankylosing spondylitis are complex and involve further epistasis with ERAP1. Nature Communications, 2015, 6, 7146.	5.8	220
54	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

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55	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals. Nature Genetics, 2022, 54, 437-449.	9.4	215
56	Avoiding dynastic, assortative mating, and population stratification biases in Mendelian randomization through within-family analyses. Nature Communications, 2020, 11, 3519.	5.8	213
57	Genome-wide Association Study of Three-Dimensional Facial Morphology Identifies a Variant in PAX3 Associated with Nasion Position. American Journal of Human Genetics, 2012, 90, 478-485.	2.6	202
58	Two-Stage Two-Locus Models in Genome-Wide Association. PLoS Genetics, 2006, 2, e157.	1.5	201
59	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
60	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
61	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
62	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
63	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
64	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
65	A Genome-Wide Association Study Reveals Variants in ARL15 that Influence Adiponectin Levels. PLoS Genetics, 2009, 5, e1000768.	1.5	148
66	Clear detection of ADIPOQ locus as the major gene for plasma adiponectin: Results of genome-wide association analyses including 4659 European individuals. Atherosclerosis, 2010, 208, 412-420.	0.4	146
67	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
68	Within-sibship genome-wide association analyses decrease bias in estimates of direct genetic effects. Nature Genetics, 2022, 54, 581-592.	9.4	142
69	Genome-wide association study identifies loci affecting blood copper, selenium and zinc. Human Molecular Genetics, 2013, 22, 3998-4006.	1.4	140
70	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
71	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
72	Guidelines for Genotyping in Genomewide Linkage Studies: Single-Nucleotideâ€“Polymorphism Maps Versus Microsatellite Maps. American Journal of Human Genetics, 2004, 75, 687-692.	2.6	135

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73	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
74	Genetic and environmental causes of variation in basal levels of blood cells. Twin Research and Human Genetics, 1999, 2, 250-257.	1.3	133
75	A Comparison of Linkage Disequilibrium Patterns and Estimated Population Recombination Rates across Multiple Populations. American Journal of Human Genetics, 2005, 76, 681-687.	2.6	133
76	Common variants at 12q15 and 12q24 are associated with infant head circumference. Nature Genetics, 2012, 44, 532-538.	9.4	130
77	Common Variants in Left/Right Asymmetry Genes and Pathways Are Associated with Relative Hand Skill. PLoS Genetics, 2013, 9, e1003751.	1.5	129
78	Investigating the genetic association between ERAP1 and ankylosing spondylitis. Human Molecular Genetics, 2009, 18, 4204-4212.	1.4	123
79	Biometrical genetics. Biological Psychology, 2002, 61, 33-51.	1.1	119
80	Common variants in the region around Osterix are associated with bone mineral density and growth in childhood. Human Molecular Genetics, 2009, 18, 1510-1517.	1.4	117
81	Cis and Trans Effects of Human Genomic Variants on Gene Expression. PLoS Genetics, 2014, 10, e1004461.	1.5	117
82	Genetic and environmental causes of variation in basal levels of blood cells. Twin Research and Human Genetics, 1999, 2, 250-257.	1.3	115
83	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
84	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
85	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
86	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
87	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
88	Genetic variants linked to education predict longevity. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13366-13371.	3.3	110
89	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
90	Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation. Nature Communications, 2015, 6, 8658.	5.8	108

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91	Genome-Wide Population-Based Association Study of Extremely Overweight Young Adults â€“ The GOYA Study. PLoS ONE, 2011, 6, e24303.	1.1	105
92	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
93	Within family Mendelian randomization studies. Human Molecular Genetics, 2019, 28, R170-R179.	1.4	105
94	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
95	Association of Genetic Loci With Glucose Levels in Childhood and Adolescence. Diabetes, 2011, 60, 1805-1812.	0.3	103
96	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
97	Genetic Determinants of Trabecular and Cortical Volumetric Bone Mineral Densities and Bone Microstructure. PLoS Genetics, 2013, 9, e1003247.	1.5	100
98	Effects of BMI, Fat Mass, and Lean Mass on Asthma in Childhood: A Mendelian Randomization Study. PLoS Medicine, 2014, 11, e1001669.	3.9	93
99	A Genome Scan for Eye Color in 502 Twin Families: Most Variation is due to a QTL on Chromosome 15q. Twin Research and Human Genetics, 2004, 7, 197-210.	1.3	91
100	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
101	Novel pleiotropic risk loci for melanoma and nevus density implicate multiple biological pathways. Nature Communications, 2018, 9, 4774.	5.8	87
102	Genome-wide association study of height-adjusted BMI in childhood identifies functional variant inADCY3. Obesity, 2014, 22, 2252-2259.	1.5	86
103	ERAP2is associated with ankylosing spondylitis inHLA-B27-positive andHLA-B27-negative patients. Annals of the Rheumatic Diseases, 2015, 74, 1627-1629.	0.5	86
104	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
105	Mining the Human Phenome Using Allelic Scores That Index Biological Intermediates. PLoS Genetics, 2013, 9, e1003919.	1.5	84
106	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
107	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
108	Circulating Selenium and Prostate Cancer Risk: A Mendelian Randomization Analysis. Journal of the National Cancer Institute, 2018, 110, 1035-1038.	3.0	84

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109	Common variation near ROBO2 is associated with expressive vocabulary in infancy. Nature Communications, 2014, 5, 4831.	5.8	82
110	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
111	Dnmt3a-mutated clonal hematopoiesis promotes osteoporosis. Journal of Experimental Medicine, 2021, 218, .	4.2	81
112	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.	2.6	80
113	Novel Approach Identifies SNPs in SLC2A10 and KCNK9 with Evidence for Parent-of-Origin Effect on Body Mass Index. PLoS Genetics, 2014, 10, e1004508.	1.5	80
114	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
115	A Variant in LIN28B Is Associated with 2D:4D Finger-Length Ratio, a Putative Retrospective Biomarker of Prenatal Testosterone Exposure. American Journal of Human Genetics, 2010, 86, 519-525.	2.6	79
116	Genome-wide association study identifies 48 common genetic variants associated with handedness. Nature Human Behaviour, 2021, 5, 59-70.	6.2	79
117	The validity of twin studies. GeneScreen, 2000, 1, 77-79.	0.7	78
118	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
119	A Population-Based Study of Genetic Variation and Psychotic Experiences in Adolescents. Schizophrenia Bulletin, 2014, 40, 1254-1262.	2.3	74
120	Sequence Variants in Three Loci Influence Monocyte Counts and Erythrocyte Volume. American Journal of Human Genetics, 2009, 85, 745-749.	2.6	73
121	Polygenic Scores Predict Alcohol Problems in an Independent Sample and Show Moderation by the Environment. Genes, 2014, 5, 330-346.	1.0	71
122	Pharmacogenetics of antidepressant response: A polygenic approach. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2017, 75, 128-134.	2.5	71
123	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
124	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.	1.5	69
125	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
126	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

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127	Genetic Variants in the Vitamin D Receptor Are Associated with Advanced Prostate Cancer at Diagnosis: Findings from the Prostate Testing for Cancer and Treatment Study and a Systematic Review. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 2874-2881.	1.1	64
128	Genome-Wide Association Study Reveals Multiple Loci Associated with Primary Tooth Development during Infancy. PLoS Genetics, 2010, 6, e1000856.	1.5	64
129	A Genome Scan for Eye Color in 502 Twin Families: Most Variation is due to a QTL on Chromosome 15q. Twin Research and Human Genetics, 2004, 7, 197-210.	1.3	62
130	Osteocyte transcriptome mapping identifies a molecular landscape controlling skeletal homeostasis and susceptibility to skeletal disease. Nature Communications, 2021, 12, 2444.	5.8	58
131	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.	0.9	56
132	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
133	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
134	A Comprehensive Evaluation of Potential Lung Function Associated Genes in the SpiroMeta General Population Sample. PLoS ONE, 2011, 6, e19382.	1.1	56
135	Meta-analysis of 20 genome-wide linkage studies evidenced new regions linked to asthma and atopy. European Journal of Human Genetics, 2010, 18, 700-706.	1.4	54
136	Formalising recall by genotype as an efficient approach to detailed phenotyping and causal inference. Nature Communications, 2018, 9, 711.	5.8	54
137	Variability in the common genetic architecture of social-communication spectrum phenotypes during childhood and adolescence. Molecular Autism, 2014, 5, 18.	2.6	53
138	The Power of Multivariate Quantitative-Trait Loci Linkage Analysis Is Influenced by the Correlation between Variables. American Journal of Human Genetics, 2002, 70, 1599-1602.	2.6	50
139	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
140	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
141	Mendelian randomization study of maternal influences on birthweight and future cardiometabolic risk in the HUNT cohort. Nature Communications, 2020, 11, 5404.	5.8	48
142	Adult height variants affect birth length and growth rate in children. Human Molecular Genetics, 2011, 20, 4069-4075.	1.4	47
143	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
144	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.	3.1	45

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145	Development of a polygenic risk score to improve screening for fracture risk: A genetic risk prediction study. PLoS Medicine, 2020, 17, e1003152.	3.9	45
146	Are obesity risk genes associated with binge eating in adolescence?. Obesity, 2015, 23, 1729-1736.	1.5	44
147	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
148	Genome-Wide Association Study Identifies Four Loci Associated with Eruption of Permanent Teeth. PLoS Genetics, 2011, 7, e1002275.	1.5	42
149	Prospects and pitfalls in whole genome association studies. Philosophical Transactions of the Royal Society B: Biological Sciences, 2005, 360, 1589-1595.	1.8	38
150	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
151	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
152	Assumption-free estimation of the genetic contribution to refractive error across childhood. Molecular Vision, 2015, 21, 621-32.	1.1	36
153	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
154	Common variation contributes to the genetic architecture of social communication traits. Molecular Autism, 2013, 4, 34.	2.6	34
155	Heritability and Genome-Wide Association Analyses of Sleep Duration in Children: The EAGLE Consortium. Sleep, 2016, 39, 1859-1869.	0.6	34
156	A genome-wide association study for corneal curvature identifies the platelet-derived growth factor receptor Î± gene as a quantitative trait locus for eye size in white Europeans. Molecular Vision, 2013, 19, 243-53.	1.1	34
157	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
158	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
159	Ten simple rules for conducting a mendelian randomization study. PLoS Computational Biology, 2021, 17, e1009238.	1.5	33
160	Major quantitative trait locus for eosinophil count is located on chromosome 2q. Journal of Allergy and Clinical Immunology, 2004, 114, 826-830.	1.5	32
161	Genetic Influences on Trajectories of Systolic Blood Pressure Across Childhood and Adolescence. Circulation: Cardiovascular Genetics, 2013, 6, 608-614.	5.1	32
162	Genome-wide association study for radiographic vertebral fractures: A potential role for the 16q24 BMD locus. Bone, 2014, 59, 20-27.	1.4	32

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163	Exome-wide study of ankylosing spondylitis demonstrates additional shared genetic background with inflammatory bowel disease. Npj Genomic Medicine, 2016, 1, 16008.	1.7	32
164	Calculating Power to Detect Maternal and Offspring Genetic Effects in Genetic Association Studies. Behavior Genetics, 2019, 49, 327-339.	1.4	32
165	Genome-wide association study of circulating interleukin 6 levels identifies novel loci. Human Molecular Genetics, 2021, 30, 393-409.	1.4	32
166	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
167	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
168	Molecular and Population Analysis of Natural Selection on the Human Haptoglobin Duplication. Annals of Human Genetics, 2012, 76, 352-362.	0.3	30
169	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
170	Limb development genes underlie variation in human fingerprint patterns. Cell, 2022, 185, 95-112.e18.	13.5	30
171	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, 223-231.e3.	1.5	28
172	Genome-wide association study of blood lead shows multiple associations near ALAD. Human Molecular Genetics, 2015, 24, 3871-3879.	1.4	28
173	Integrative pathway genomics of lung function and airflow obstruction. Human Molecular Genetics, 2015, 24, 6836-6848.	1.4	28
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175	Genome-wide association: a promising start to a long race. Trends in Genetics, 2006, 22, 350-354.	2.9	27
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