Beben Benyamin

List of Publications by Year
in descending order

62	11,041	136950 32	106344 65
papers	citations	h-index	g-index

71	71	71	18543
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Common SNPs explain a large proportion of the heritability for human height. Nature Genetics, 2010, 42, 565-569.	21.4	3,888
2	Meta-analysis of the heritability of human traits based on fifty years of twin studies. Nature Genetics, 2015, 47, 702-709.	21.4	1,750
3	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508.	27.8	929
4	Comparative genetic architectures of schizophrenia in East Asian and European populations. Nature Genetics, 2019, 51, 1670-1678.	21.4	440
5	Seventy-five genetic loci influencing the human red blood cell. Nature, 2012, 492, 369-375.	27.8	320
6	Common genetic variants associated with cognitive performance identified using the proxy-phenotype method. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 13790-13794.	7.1	244
7	Childhood intelligence is heritable, highly polygenic and associated with FNBP1L. Molecular Psychiatry, 2014, 19, 253-258.	7.9	241
8	Common variants in TMPRSS6 are associated with iron status and erythrocyte volume. Nature Genetics, 2009, 41, 1173-1175.	21.4	226
9	Common and rare variant association analyses in amyotrophic lateral sclerosis identify 15 risk loci with distinct genetic architectures and neuron-specific biology. Nature Genetics, 2021, 53, 1636-1648.	21.4	223
10	Novel loci affecting iron homeostasis and their effects in individuals at risk for hemochromatosis. Nature Communications, 2014, 5, 4926.	12.8	192
11	The Role of Adiposity in Cardiometabolic Traits: A Mendelian Randomization Analysis. PLoS Medicine, 2013, 10, e1001474.	8.4	178
12	Variants in TF and HFE Explain â¹¼40% of Genetic Variation in Serum-Transferrin Levels. American Journal of Human Genetics, 2009, 84, 60-65.	6.2	155
13	A genome-wide association study of Cloninger's temperament scales: Implications for the evolutionary genetics of personality. Biological Psychology, 2010, 85, 306-317.	2.2	150
14	Large-scale GWAS identifies multiple loci for hand grip strength providing biological insights into muscular fitness. Nature Communications, 2017, 8, 16015.	12.8	149
15	Combined Genome Scans for Body Stature in 6,602 European Twins: Evidence for Common Caucasian Loci. PLoS Genetics, 2007, 3, e97.	3.5	145
16	Genome Partitioning of Genetic Variation for Height from 11,214 Sibling Pairs. American Journal of Human Genetics, 2007, 81, 1104-1110.	6.2	135
17	Adiposity as a cause of cardiovascular disease: a Mendelian randomization study. International Journal of Epidemiology, 2015, 44, 578-586.	1.9	123
18	Serum Iron Levels and the Risk of Parkinson Disease: A Mendelian Randomization Study. PLoS Medicine, 2013, 10, e1001462.	8.4	116

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19	Are there common genetic and environmental factors behind the endophenotypes associated with the metabolic syndrome?. Diabetologia, 2007, 50, 1880-1888.	6.3	104
20	Cross-ethnic meta-analysis identifies association of the GPX3-TNIP1 locus with amyotrophic lateral sclerosis. Nature Communications, 2017, 8, 611.	12.8	93
21	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
22	Unraveling the Genetic Etiology of Adult Antisocial Behavior: A Genome-Wide Association Study. PLoS ONE, 2012, 7, e45086.	2.5	80
23	Family-based genome-wide association studies. Pharmacogenomics, 2009, 10, 181-190.	1.3	69
24	EigenGWAS: finding loci under selection through genome-wide association studies of eigenvectors in structured populations. Heredity, 2016, 117, 51-61.	2.6	69
25	Age- and Sex-Specific Causal Effects of Adiposity on Cardiovascular Risk Factors. Diabetes, 2015, 64, 1841-1852.	0.6	63
26	C9orf72 hexanucleotide repeat expansions in Chinese sporadic amyotrophic lateral sclerosis. Neurobiology of Aging, 2015, 36, 2660.e1-2660.e8.	3.1	50
27	The genetic aetiology of cannabis use initiation: a meta-analysis of genome-wide association studies and a SNP-based heritability estimation. Addiction Biology, 2013, 18, 846-850.	2.6	49
28	Associations of genetically determined iron status across the phenome: A mendelian randomization study. PLoS Medicine, 2019, 16, e1002833.	8.4	48
29	Variance decomposition of apolipoproteins and lipids in Danish twins. Atherosclerosis, 2007, 191, 40-47.	0.8	47
30	GWAS of butyrylcholinesterase activity identifies four novel loci, independent effects within BCHE and secondary associations with metabolic risk factors. Human Molecular Genetics, 2011, 20, 4504-4514.	2.9	45
31	The Use of Linear Mixed Models to Estimate Variance Components from Data on Twin Pairs by Maximum Likelihood. Twin Research and Human Genetics, 2004, 7, 670-674.	1.0	38
32	Large, Consistent Estimates of the Heritability of Cognitive Ability in Two Entire Populations of 11-Year-Old Twins from Scottish Mental Surveys of 1932 and 1947. Behavior Genetics, 2005, 35, 525-534.	2.1	37
33	Monozygotic twins and triplets discordant for amyotrophic lateral sclerosis display differential methylation and gene expression. Scientific Reports, 2019, 9, 8254.	3.3	36
34	Maps of open chromatin highlight cell typeâ€“restricted patterns of regulatory sequence variation at hematological trait loci. Genome Research, 2013, 23, 1130-1141.	5.5	34
35	Cognitive Function in Adolescence: Testing for Interactions Between Breast-Feeding and FADS2 Polymorphisms. Journal of the American Academy of Child and Adolescent Psychiatry, 2011, 50, 55-62.e4.	0.5	32
36	Genome-wide association study identifies two loci strongly affecting transferrin glycosylation. Human Molecular Genetics, 2011, 20, 3710-3717.	2.9	31

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37	Association of rs1344706 in the ZNF804A gene with schizophrenia in a case/control sample from Indonesia. Schizophrenia Research, 2013, 147, 46-52.	2.0	30
38	Loci affecting gamma-glutamyl transferase in adults and adolescents show age Ã— SNP interaction and cardiometabolic disease associations. Human Molecular Genetics, 2012, 21, 446-455.	2.9	26
39	Genome-wide Association Meta-analysis of Childhood and Adolescent Internalizing Symptoms. Journal of the American Academy of Child and Adolescent Psychiatry, 2022, 61, 934-945.	0.5	26
40	Significant out-of-sample classification from methylation profile scoring for amyotrophic lateral sclerosis. Npj Genomic Medicine, 2020, 5, 10.	3.8	25
41	Common Genetic Components of Obesity Traits and Serum Leptin. Obesity, 2008, 16, 2723-2729.	3.0	24
42	Iron and hepcidin as risk factors in atherosclerosis: what do the genes say?. BMC Genetics, 2015, 16, 79.	2.7	23
43	Serum iron level and kidney function: a Mendelian randomization study. Nephrology Dialysis Transplantation, 2016, 32, gfw215.	0.7	23
44	Whole-exome sequencing in amyotrophic lateral sclerosis suggests NEK1 is a risk gene in Chinese. Genome Medicine, 2017, 9, 97.	8.2	23
45	Multicenter dizygotic twin cohort study confirms two linkage susceptibility loci for body mass index at 3q29 and 7q36 and identifies three further potential novel loci. International Journal of Obesity, 2009, 33, 1235-1242.	3.4	21
46	Beyond the Single SNP: Emerging Developments in Mendelian Randomization in the â€œOmicsâ€•Era. Current Epidemiology Reports, 2014, 1, 228-236.	2.4	18
47	Polygenic risk score analysis for amyotrophic lateral sclerosis leveraging cognitive performance, educational attainment and schizophrenia. European Journal of Human Genetics, 2022, 30, 532-539.	2.8	16
48	Whole exome sequencing and <scp>DNA</scp> methylation analysis in a clinical amyotrophic lateral sclerosis cohort. Molecular Genetics & Genomic Medicine, 2017, 5, 418-428.	1.2	14
49	Urinary neopterin: A novel biomarker of disease progression in amyotrophic lateral sclerosis. European Journal of Neurology, 2022, 29, 990-999.	3.3	14
50	Within-family outliers: segregating alleles or environmental effects? A linkage analysis of height from 5815 sibling pairs. European Journal of Human Genetics, 2008, 16, 516-524.	2.8	13
51	Identification of novel loci affecting circulating chromogranins and related peptides. Human Molecular Genetics, 2016, 26, ddw380.	2.9	13
52	Precision and Bias of a Normal Finite Mixture Distribution Model to Analyze Twin Data When Zygosity is Unknown: Simulations and Application to IQ Phenotypes on a Large Sample of Twin Pairs. Behavior Genetics, 2006, 36, 935-946.	2.1	10
53	No Genetic Overlap Between Circulating Iron Levels and Alzheimerâ€™s Disease. Journal of Alzheimer's Disease, 2017, 59, 85-99.	2.6	10
54	Investigating the relationship between iron and depression. Journal of Psychiatric Research, 2017, 94, 148-155.	3.1	10

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55	Hepcidin-regulating iron metabolism genes and pancreatic ductal adenocarcinoma: a pathway analysis of genome-wide association studies. American Journal of Clinical Nutrition, 2021, 114, 1408-1417.	4.7	9
56	Genetic Variation Within a Metabolic Motif in the Chromogranin A Promoter: Pleiotropic Influence on Cardiometabolic Risk Traits in Twins. American Journal of Hypertension, 2012, 25, 29-40.	2.0	6
57	Sharing a Placenta is Associated With a Greater Similarity in DNA Methylation in Monochorionic Versus Dichorionic Twin Pars in Blood at Age 14. Twin Research and Human Genetics, 2015, 18, 680-685.	0.6	6
58	The Use of Linear Mixed Models to Estimate Variance Components from Data on Twin Pairs by Maximum Likelihood. Twin Research and Human Genetics, 2004, 7, 670-674.	1.0	5
59	Lifestyle Modifies the Diabetes-Related Metabolic Risk, Conditional on Individual Genetic Differences. Frontiers in Genetics, 2022, 13, 759309.	2.3	4
60	Association of CamK2A genetic variants with transition time from occasional to regular heroin use in a sample of heroin-dependent individuals. Psychiatric Genetics, 2019, 29, 18-25.	1.1	3
61	Transferrin Saturation and Mortality. Clinical Chemistry, 2011, 57, 921-923.	3.2	1
62	Bodyweight QTL on mouse chromosomes 4 and 11 by selective genotyping: regression v. maximum likelihood. Australian Journal of Experimental Agriculture, 2007, 47, 677.	1.0	1