Massimo Mangino

List of Publications by Year in descending order

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270	77,620	1704 104	584 262
papers	citations	h-index	g-index

305	305	305	72862
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genome-wide association study of 14,000 cases of seven common diseases and 3,000 shared controls. Nature, 2007, 447, 661-678.	27.8	8,895
2	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823
3	Biological, clinical and population relevance of 95 loci for blood lipids. Nature, 2010, 466, 707-713.	27.8	3,249
4	Discovery and refinement of loci associated with lipid levels. Nature Genetics, 2013, 45, 1274-1283.	21.4	2,641
5	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nature Genetics, 2010, 42, 937-948.	21.4	2,634
6	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. Nature Genetics, 2010, 42, 105-116.	21.4	1,982
7	Genomewide Association Analysis of Coronary Artery Disease. New England Journal of Medicine, 2007, 357, 443-453.	27.0	1,865
8	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. Nature, 2011, 478, 103-109.	27.8	1,855
9	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	21.4	1,818
10	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	27.8	1,789
11	Six new loci associated with body mass index highlight a neuronal influence on body weight regulation. Nature Genetics, 2009, 41, 25-34.	21.4	1,572
12	Common genetic determinants of vitamin D insufficiency: a genome-wide association study. Lancet, The, 2010, 376, 180-188.	13.7	1,385
13	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	27.8	1,328
14	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	27.8	1,204
15	Common variants near MC4R are associated with fat mass, weight and risk of obesity. Nature Genetics, 2008, 40, 768-775.	21.4	1,179
16	Real-time tracking of self-reported symptoms to predict potential COVID-19. Nature Medicine, 2020, 26, 1037-1040.	30.7	1,173
17	The UK10K project identifies rare variants in health and disease. Nature, 2015, 526, 82-90.	27.8	1,014
18	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	27.8	952

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19	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	21.4	924
20	Human metabolic individuality in biomedical and pharmaceutical research. Nature, 2011, 477, 54-60.	27.8	916
21	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. Nature Genetics, 2010, 42, 949-960.	21.4	836
22	Identification of seven loci affecting mean telomere length and their association with disease. Nature Genetics, 2013, 45, 422-427.	21.4	808
23	Common variants associated with plasma triglycerides and risk for coronary artery disease. Nature Genetics, 2013, 45, 1345-1352.	21.4	754
24	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. Nature Genetics, 2012, 44, 991-1005.	21.4	746
25	Vaccine side-effects and SARS-CoV-2 infection after vaccination in users of the COVID Symptom Study app in the UK: a prospective observational study. Lancet Infectious Diseases, The, 2021, 21, 939-949.	9.1	744
26	Genome-wide association analysis identifies 20 loci that influence adult height. Nature Genetics, 2008, 40, 575-583.	21.4	742
27	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. Nature Genetics, 2013, 45, 145-154.	21.4	675
28	Sequence variants at CHRNB3â€“CHRNA6 and CYP2A6 affect smoking behavior. Nature Genetics, 2010, 42, 448-453.	21.4	649
29	Epigenome-Wide Scans Identify Differentially Methylated Regions for Age and Age-Related Phenotypes in a Healthy Ageing Population. PLoS Genetics, 2012, 8, e1002629.	3.5	620
30	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
31	Meta-Analysis of 28,141 Individuals Identifies Common Variants within Five New Loci That Influence Uric Acid Concentrations. PLoS Genetics, 2009, 5, e1000504.	3.5	572
32	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	27.8	548
33	Genome-wide association study identifies five loci associated with lung function. Nature Genetics, 2010, 42, 36-44.	21.4	518
34	The fecal metabolome as a functional readout of the gut microbiome. Nature Genetics, 2018, 50, 790-795.	21.4	482
35	A genome-wide meta-analysis identifies 22 loci associated with eight hematological parameters in the HaemGen consortium. Nature Genetics, 2009, 41, 1182-1190.	21.4	481
36	Genomic inflation factors under polygenic inheritance. European Journal of Human Genetics, 2011, 19, 807-812.	2.8	460

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37	Genome-Wide Association Scan Meta-Analysis Identifies Three Loci Influencing Adiposity and Fat Distribution. PLoS Genetics, 2009, 5, e1000508.	3.5	453
38	Physical Activity Attenuates the Influence of FTO Variants on Obesity Risk: A Meta-Analysis of 218,166 Adults and 19,268 Children. PLoS Medicine, 2011, 8, e1001116.	8.4	446
39	Thirty new loci for age at menarche identified by a meta-analysis of genome-wide association studies. Nature Genetics, 2010, 42, 1077-1085.	21.4	445
40	Lipidomics Profiling and Risk of Cardiovascular Disease in the Prospective Population-Based Bruneck Study. Circulation, 2014, 129, 1821-1831.	1.6	445
41	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. Science, 2016, 351, 1166-1171.	12.6	438
42	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. Nature Genetics, 2017, 49, 834-841.	21.4	426
43	Human postprandial responses to food and potential for precision nutrition. Nature Medicine, 2020, 26, 964-973.	30.7	418
44	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. Nature Genetics, 2011, 43, 1005-1011.	21.4	403
45	New gene functions in megakaryopoiesis and platelet formation. Nature, 2011, 480, 201-208.	27.8	401
46	Gender and telomere length: Systematic review and meta-analysis. Experimental Gerontology, 2014, 51, 15-27.	2.8	394
47	Common Variants at 10 Genomic Loci Influence Hemoglobin A1C Levels via Glycemic and Nonglycemic Pathways. Diabetes, 2010, 59, 3229-3239.	0.6	387
48	FTO genotype is associated with phenotypic variability of body mass index. Nature, 2012, 490, 267-272.	27.8	383
49	Meta-analysis of telomere length in 19â€‰713 subjects reveals high heritability, stronger maternal inheritance and a paternal age effect. European Journal of Human Genetics, 2013, 21, 1163-1168.	2.8	380
50	Association Between Telomere Length and Risk of Cancer and Non-Neoplastic Diseases. JAMA Oncology, 2017, 3, 636.	7.1	376
51	Identification of new susceptibility loci for osteoarthritis (arcOGEN): a genome-wide association study. Lancet, The, 2012, 380, 815-823.	13.7	373
52	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. PLoS Genetics, 2013, 9, e1003500.	3.5	371
53	Genome-wide association and large-scale follow up identifies 16 new loci influencing lung function. Nature Genetics, 2011, 43, 1082-1090.	21.4	367
54	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. Nature Genetics, 2015, 47, 1294-1303.	21.4	357

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55	Repeated Replication and a Prospective Meta-Analysis of the Association Between Chromosome 9p21.3 and Coronary Artery Disease. Circulation, 2008, 117, 1675-1684.	1.6	356
56	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	27.8	353
57	Whole-genome sequencing identifies common-to-rare variants associated with human blood metabolites. Nature Genetics, 2017, 49, 568-578.	21.4	341
58	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341
59	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. PLoS Genetics, 2015, 11, e1005378.	3.5	331
60	Trans-ethnic association study of blood pressure determinants in over 750,000 individuals. Nature Genetics, 2019, 51, 51-62.	21.4	328
61	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
62	Association of vitamin D status with arterial blood pressure and hypertension risk: a mendelian randomisation study. Lancet Diabetes and Endocrinology,the, 2014, 2, 719-729.	11.4	319
63	Meta-analysis of genome-wide association studies identifies three new risk loci for atopic dermatitis. Nature Genetics, 2012, 44, 187-192.	21.4	311
64	Meta-analyses identify 13 loci associated with age at menopause and highlight DNA repair and immune pathways. Nature Genetics, 2012, 44, 260-268.	21.4	303
65	Glycans Are a Novel Biomarker of Chronological and Biological Ages. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2014, 69, 779-789.	3.6	297
66	Common variants near TERC are associated with mean telomere length. Nature Genetics, 2010, 42, 197-199.	21.4	296
67	The Genetic Architecture of the Human Immune System: A Bioresource for Autoimmunity and Disease Pathogenesis. Cell, 2015, 161, 387-403.	28.9	292
68	Genetic variation near IRS1 associates with reduced adiposity and an impaired metabolic profile. Nature Genetics, 2011, 43, 753-760.	21.4	289
69	Genome-wide association and genetic functional studies identify autism susceptibility candidate 2 gene (AUTS2) in the regulation of alcohol consumption. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 7119-7124.	7.1	258
70	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. Nature Communications, 2016, 7, 10495.	12.8	245
71	Genome-wide association identifies OBFC1 as a locus involved in human leukocyte telomere biology. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 9293-9298.	7.1	244
72	Mapping of a Major Locus that Determines Telomere Length in Humans. American Journal of Human Genetics, 2005, 76, 147-151.	6.2	243

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73	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
74	Low copy number of the salivary amylase gene predisposes to obesity. Nature Genetics, 2014, 46, 492-497.	21.4	214
75	Genome-wide meta-analysis points to CTC1 and ZNF676 as genes regulating telomere homeostasis in humans. Human Molecular Genetics, 2012, 21, 5385-5394.	2.9	210
76	KLB is associated with alcohol drinking, and its gene product Î²-Klotho is necessary for FGF21 regulation of alcohol preference. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 14372-14377.	7.1	208
77	DNA methylation-based estimator of telomere length. Aging, 2019, 11, 5895-5923.	3.1	198
78	Deciphering osteoarthritis genetics across 826,690 individuals from 9 populations. Cell, 2021, 184, 4784-4818.e17.	28.9	188
79	Heritable components of the human fecal microbiome are associated with visceral fat. Genome Biology, 2016, 17, 189.	8.8	183
80	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	27.8	183
81	Gut microbial diversity is associated with lower arterial stiffness in women. European Heart Journal, 2018, 39, 2390-2397.	2.2	181
82	The Role of Adiposity in Cardiometabolic Traits: A Mendelian Randomization Analysis. PLoS Medicine, 2013, 10, e1001474.	8.4	178
83	Genome-wide association study identifies novel genetic variants contributing to variation in blood metabolite levels. Nature Communications, 2015, 6, 7208.	12.8	178
84	Genetic and environmental effects on body mass index from infancy to the onset of adulthood: an individual-based pooled analysis of 45 twin cohorts participating in the COllaborative project of Development of Anthropometrical measures in Twins (CODATwins) study. American Journal of Clinical Nutrition, 2016, 104, 371-379.	4.7	175
85	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	27.8	173
86	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. Nature Communications, 2017, 8, 14977.	12.8	169
87	Genome-wide physical activity interactions in adiposity â€• A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	3.5	158
88	Genome-wide association and functional studies identify the DOT1L gene to be involved in cartilage thickness and hip osteoarthritis. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 8218-8223.	7.1	154
89	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. Nature Communications, 2016, 7, 10494.	12.8	153
90	A Genome-Wide Association Meta-Analysis of Circulating Sex Hormoneâ€“Binding Globulin Reveals Multiple Loci Implicated in Sex Steroid Hormone Regulation. PLoS Genetics, 2012, 8, e1002805.	3.5	151

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91	Estimating telomere length from whole genome sequence data. Nucleic Acids Research, 2014, 42, e75-e75.	14.5	151
92	GWAS of epigenetic aging rates in blood reveals a critical role for TERT. Nature Communications, 2018, 9, 387.	12.8	151
93	Large-scale GWAS identifies multiple loci for hand grip strength providing biological insights into muscular fitness. Nature Communications, 2017, 8, 16015.	12.8	149
94	Genetic variation in the SMAD3 gene is associated with hip and knee osteoarthritis. Arthritis and Rheumatism, 2010, 62, 2347-2352.	6.7	145
95	Meta-Analysis of Genome-Wide Association Studies Identifies Six New Loci for Serum Calcium Concentrations. PLoS Genetics, 2013, 9, e1003796.	3.5	142
96	Within-sibship genome-wide association analyses decrease bias in estimates of direct genetic effects. Nature Genetics, 2022, 54, 581-592.	21.4	142
97	Lifelong Reduction of LDL-Cholesterol Related to a Common Variant in the LDL-Receptor Gene Decreases the Risk of Coronary Artery Diseaseâ€"A Mendelian Randomisation Study. PLoS ONE, 2008, 3, e2986.	2.5	137
98	Body mass index is negatively associated with telomere length: a collaborative cross-sectional meta-analysis of 87 observational studies. American Journal of Clinical Nutrition, 2018, 108, 453-475.	4.7	137
99	Genetics of skin color variation in Europeans: genome-wide association studies with functional follow-up. Human Genetics, 2015, 134, 823-835.	3.8	133
100	Genetic and environmental influences on height from infancy to early adulthood: An individual-based pooled analysis of 45 twin cohorts. Scientific Reports, 2016, 6, 28496.	3.3	133
101	Assignment of a locus for autosomal dominant idiopathic scoliosis (IS) to human chromosome 17p11. Human Genetics, 2002, 111, 401-404.	3.8	125
102	Adiposity as a cause of cardiovascular disease: a Mendelian randomization study. International Journal of Epidemiology, 2015, 44, 578-586.	1.9	123
103	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. Hypertension, 2017, 70, .	2.7	123
104	Genome-wide Association Analysis in Humans Links Nucleotide Metabolism to Leukocyte Telomere Length. American Journal of Human Genetics, 2020, 106, 389-404.	6.2	118
105	TwinsUK: The UK Adult Twin Registry Update. Twin Research and Human Genetics, 2019, 22, 523-529.	0.6	116
106	IRF4 Variants Have Age-Specific Effects on Nevus Count and Predispose to Melanoma. American Journal of Human Genetics, 2010, 87, 6-16.	6.2	114
107	Genome-wide association analysis of coffee drinking suggests association with CYP1A1/CYP1A2 and NRCAM. Molecular Psychiatry, 2012, 17, 1116-1129.	7.9	112
108	Novel loci associated with usual sleep duration: the CHARGE Consortium Genome-Wide Association Study. Molecular Psychiatry, 2015, 20, 1232-1239.	7.9	112

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109	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
110	Smoking induces coordinated DNA methylation and gene expression changes in adipose tissue with consequences for metabolic health. Clinical Epigenetics, 2018, 10, 126.	4.1	110
111	Genome-wide association study of caffeine metabolites provides new insights to caffeine metabolism and dietary caffeine-consumption behavior. Human Molecular Genetics, 2016, 25, ddw334.	2.9	107
112	Innate and adaptive immune traits are differentially affected by genetic and environmental factors. Nature Communications, 2017, 8, 13850.	12.8	107
113	Differences in genetic and environmental variation in adult BMI by sex, age, time period, and region: an individual-based pooled analysis of 40 twin cohorts. American Journal of Clinical Nutrition, 2017, 106, 457-466.	4.7	107
114	Obligatory and facilitative allelic variation in the DNA methylome within common disease-associated loci. Nature Communications, 2018, 9, 8.	12.8	107
115	Multiple Loci Are Associated with White Blood Cell Phenotypes. PLoS Genetics, 2011, 7, e1002113.	3.5	106
116	Circulating Proteomic Signatures of Chronological Age. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2015, 70, 809-816.	3.6	106
117	A Genomewide Linkage Study of 1,933 Families Affected by Premature Coronary Artery Disease: The British Heart Foundation (BHF) Family Heart Study. American Journal of Human Genetics, 2005, 77, 1011-1020.	6.2	105
118	Glycosylation of Immunoglobulin G: Role of Genetic and Epigenetic Influences. PLoS ONE, 2013, 8, e82558.	2.5	105
119	Inference of the Genetic Architecture Underlying BMI and Height with the Use of 20,240 Sibling Pairs. American Journal of Human Genetics, 2013, 93, 865-875.	6.2	104
120	A genome-wide association study of early menopause and the combined impact of identified variants. Human Molecular Genetics, 2013, 22, 1465-1472.	2.9	104
121	Telomere length in circulating leukocytes is associated with lung function and disease. European Respiratory Journal, 2014, 43, 983-992.	6.7	103
122	Identification of a novel NOG gene mutation (P35S) in an Italian family with symphalangism. Human Mutation, 2002, 19, 308-308.	2.5	102
123	Multivariate discovery and replication of five novel loci associated with Immunoglobulin G N-glycosylation. Nature Communications, 2017, 8, 447.	12.8	102
124	Identification and Functional Characterization of G6PC2 Coding Variants Influencing Glycemic Traits Define an Effector Transcript at the G6PC2-ABCB11 Locus. PLoS Genetics, 2015, 11, e1004876.	3.5	95
125	Six Novel Susceptibility Loci for Early-Onset Androgenetic Alopecia and Their Unexpected Association with Common Diseases. PLoS Genetics, 2012, 8, e1002746.	3.5	92
126	Characterizing Blood Metabolomics Profiles Associated with Self-Reported Food Intakes in Female Twins. PLoS ONE, 2016, 11, e0158568.	2.5	92

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127	Metabolomic Identification of a Novel Pathway of Blood Pressure Regulation Involving Hexadecanedioate. Hypertension, 2015, 66, 422-429.	2.7	90
128	Glycosylation of immunoglobulin G is regulated by a large network of genes pleiotropic with inflammatory diseases. Science Advances, 2020, 6, eaax0301.	10.3	90
129	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. Genome Biology, 2021, 22, 194.	8.8	90
130	Eight Common Genetic Variants Associated with Serum DHEAS Levels Suggest a Key Role in Ageing Mechanisms. PLoS Genetics, 2011, 7, e1002025.	3.5	87
131	Glycosylation Profile of Immunoglobulin G Is Cross-Sectionally Associated With Cardiovascular Disease Risk Score and Subclinical Atherosclerosis in Two Independent Cohorts. Circulation Research, 2018, 122, 1555-1564.	4.5	87
132	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. Molecular Psychiatry, 2020, 25, 2392-2409.	7.9	83
133	Probable delirium is a presenting symptom of COVID-19 in frail, older adults: a cohort study of 322 hospitalised and 535 community-based older adults. Age and Ageing, 2021, 50, 40-48.	1.6	82
134	Telomeres and the natural lifespan limit in humans. Aging, 2017, 9, 1130-1142.	3.1	82
135	The Consortium of Metabolomics Studies (COMETS): Metabolomics in 47 Prospective Cohort Studies. American Journal of Epidemiology, 2019, 188, 991-1012.	3.4	81
136	The novel genetic variant predisposing to coronary artery disease in the region of the PSRC1 and CELSR2 genes on chromosome 1 associates with serum cholesterol. Journal of Molecular Medicine, 2008, 86, 1233-1241.	3.9	80
137	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.	6.2	80
138	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
139	Alcohol-induced metabolomic differences in humans. Translational Psychiatry, 2013, 3, e276-e276.	4.8	79
140	Genome-wide association study identifies 48 common genetic variants associated with handedness. Nature Human Behaviour, 2021, 5, 59-70.	12.0	79
141	A genome-wide association study identifies a novel locus on chromosome 18q12.2 influencing white cell telomere length. Journal of Medical Genetics, 2009, 46, 451-454.	3.2	76
142	Glycosylation Profile of IgG in Moderate Kidney Dysfunction. Journal of the American Society of Nephrology: JASN, 2016, 27, 933-941.	6.1	75
143	New alcohol-related genes suggest shared genetic mechanisms with neuropsychiatric disorders. Nature Human Behaviour, 2019, 3, 950-961.	12.0	75
144	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. Nature Communications, 2016, 7, 13357.	12.8	74

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145	A meta-analysis of 120 246 individuals identifies 18 new loci for fibrinogen concentration. Human Molecular Genetics, 2016, 25, 358-370.	2.9	73
146	Exome Chip Meta-analysis Fine Maps Causal Variants and Elucidates the Genetic Architecture of Rare Coding Variants in Smoking and AlcoholÂUse. Biological Psychiatry, 2019, 85, 946-955.	1.3	69
147	Genetic Influences on Metabolite Levels: A Comparison across Metabolomic Platforms. PLoS ONE, 2016, 11, e0153672.	2.5	69
148	DCAF4, a novel gene associated with leucocyte telomere length. Journal of Medical Genetics, 2015, 52, 157-162.	3.2	66
149	Serum metabolites reflecting gut microbiome alpha diversity predict type 2 diabetes. Gut Microbes, 2020, 11, 1632-1642.	9.8	65
150	CNV-association meta-analysis in 191,161 European adults reveals new loci associated with anthropometric traits. Nature Communications, 2017, 8, 744.	12.8	64
151	Modulation of Genetic Associations with Serum Urate Levels by Body-Mass-Index in Humans. PLoS ONE, 2015, 10, e0119752.	2.5	64
152	Age- and Sex-Specific Causal Effects of Adiposity on Cardiovascular Risk Factors. Diabetes, 2015, 64, 1841-1852.	0.6	63
153	A rare variant in APOC3 is associated with plasma triglyceride and VLDL levels in Europeans. Nature Communications, 2014, 5, 4871.	12.8	62
154	Meta-analysis of Gene-Level Associations for Rare Variants Based on Single-Variant Statistics. American Journal of Human Genetics, 2013, 93, 236-248.	6.2	60
155	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	12.8	59
156	A regulatory SNP of the BICD1 gene contributes to telomere length variation in humans. Human Molecular Genetics, 2008, 17, 2518-2523.	2.9	58
157	Metabolomic study of carotidâ€“femoral pulse-wave velocity in women. Journal of Hypertension, 2015, 33, 791-796.	0.5	57
158	Self-Reported Symptoms of COVID-19, Including Symptoms Most Predictive of SARS-CoV-2 Infection, Are Heritable. Twin Research and Human Genetics, 2020, 23, 316-321.	0.6	57
159	A Comprehensive Evaluation of Potential Lung Function Associated Genes in the SpiroMeta General Population Sample. PLoS ONE, 2011, 6, e19382.	2.5	56
160	The CODATwins Project: The Cohort Description of Collaborative Project of Development of Anthropometrical Measures in Twins to Study Macro-Environmental Variation in Genetic and Environmental Effects on Anthropometric Traits. Twin Research and Human Genetics, 2015, 18, 348-360.	0.6	55
161	A polymorphism associated with entrepreneurship: evidence from dopamine receptor candidate genes. Small Business Economics, 2011, 36, 151-155.	6.7	53
162	Association of Adiposity Genetic Variants With Menarche Timing in 92,105 Women of European Descent. American Journal of Epidemiology, 2013, 178, 451-460.	3.4	51

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163	<scp>GWAS</scp> analysis of handgrip and lower body strength in older adults in the <scp>CHARGE</scp> consortium. Aging Cell, 2016, 15, 792-800.	6.7	51
164	A Low-Frequency Inactivating AKT2 Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. Diabetes, 2017, 66, 2019-2032.	0.6	47
165	Genome-Wide Association Study Identifies Variants in Casein Kinase II (CSNK2A2) to be Associated With Leukocyte Telomere Length in a Punjabi Sikh Diabetic Cohort. Circulation: Cardiovascular Genetics, 2014, 7, 287-295.	5.1	46
166	Genetic and environmental influences on adult human height across birth cohorts from 1886 to 1994. ELife, 2016, 5, .	6.0	42
167	Genome-Wide Meta-Analysis of Cotinine Levels in Cigarette Smokers Identifies Locus at 4q13.2. Scientific Reports, 2016, 6, 20092.	3.3	42
168	Omega-6 oxylipins generated by soluble epoxide hydrolase are associated with knee osteoarthritis. Journal of Lipid Research, 2018, 59, 1763-1770.	4.2	41
169	Defining the genetic control of human blood plasma N-glycome using genome-wide association study. Human Molecular Genetics, 2019, 28, 2062-2077.	2.9	40
170	Variation in the SERPINA6/SERPINA1 locus alters morning plasma cortisol, hepatic corticosteroid binding globulin expression, gene expression in peripheral tissues, and risk of cardiovascular disease. Journal of Human Genetics, 2021, 66, 625-636.	2.3	40
171	Identification of novel RP2 mutations in a subset of X-linked retinitis pigmentosa families and prediction of new domains. Human Mutation, 2001, 18, 109-119.	2.5	39
172	A Common Variant in the Telomerase RNA Component Is Associated with Short Telomere Length. PLoS ONE, 2010, 5, e13048.	2.5	39
173	Paternal age and telomere length in twins: the germ stem cell selection paradigm. Aging Cell, 2015, 14, 701-703.	6.7	38
174	Heritability analyses show visit-to-visit blood pressure variability reflects different pathological phenotypes in younger and older adults. Journal of Hypertension, 2013, 31, 2356-2361.	0.5	36
175	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
176	Better governance, better access: practising responsible data sharing in the METADAC governance infrastructure. Human Genomics, 2018, 12, 24.	2.9	36
177	Leukocyte telomere length and marital status among middle-aged adults. Age and Ageing, 2011, 40, 73-78.	1.6	35
178	Cross-trait analyses with migraine reveal widespread pleiotropy and suggest a vascular component to migraine headache. International Journal of Epidemiology, 2020, 49, 1022-1031.	1.9	34
179	Genome-wide meta-analysis of common variant differences between men and women. Human Molecular Genetics, 2012, 21, 4805-4815.	2.9	33
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