

Najaf Amin

List of Publications by Year in descending order

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Version: 2024-02-01

274
papers

59,573
citations

1704

104
h-index

1316

224
g-index

312
all docs

312
docs citations

312
times ranked

57457
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823
2	Meta-analysis of 74,046 individuals identifies 11 new susceptibility loci for Alzheimer's disease. Nature Genetics, 2013, 45, 1452-1458.	21.4	3,741
3	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
4	Genetic meta-analysis of diagnosed Alzheimer's disease identifies new risk loci and implicates A β , tau, immunity and lipid processing. Nature Genetics, 2019, 51, 414-430.	21.4	1,962
5	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. Nature, 2011, 478, 103-109.	27.8	1,855
6	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
7	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	27.8	1,789
8	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. Nature Genetics, 2010, 42, 579-589.	21.4	1,631
9	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	27.8	1,328
10	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	27.8	1,204
11	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.	21.4	1,100
12	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
13	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. Nature Genetics, 2016, 48, 624-633.	21.4	870
14	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
15	Identification of seven loci affecting mean telomere length and their association with disease. Nature Genetics, 2013, 45, 422-427.	21.4	808
16	Rare coding variants in PLCG2, ABI3, and TREM2 implicate microglial-mediated innate immunity in Alzheimer's disease. Nature Genetics, 2017, 49, 1373-1384.	21.4	783
17	A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. Nature Genetics, 2012, 44, 659-669.	21.4	762
18	GWAS of 126,559 Individuals Identifies Genetic Variants Associated with Educational Attainment. Science, 2013, 340, 1467-1471.	12.6	750

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19	New insights into the genetic etiology of Alzheimer's disease and related dementias. Nature Genetics, 2022, 54, 412-436.	21.4	700
20	Twenty bone-mineral-density loci identified by large-scale meta-analysis of genome-wide association studies. Nature Genetics, 2009, 41, 1199-1206.	21.4	660
21	Sequence variants at CHRNA6 and CYP2A6 affect smoking behavior. Nature Genetics, 2010, 42, 448-453.	21.4	649
22	Whole-genome sequence variation, population structure and demographic history of the Dutch population. Nature Genetics, 2014, 46, 818-825.	21.4	641
23	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
24	Genome-wide study for circulating metabolites identifies 62 loci and reveals novel systemic effects of LPA. Nature Communications, 2016, 7, 11122.	12.8	576
25	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	21.4	549
26	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	27.8	548
27	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. Nature Genetics, 2017, 49, 403-415.	21.4	492
28	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. Nature Communications, 2018, 9, 2098.	12.8	484
29	Whole-genome sequencing identifies EN1 as a determinant of bone density and fracture. Nature, 2015, 526, 112-117.	27.8	483
30	Genome-Wide Association Scan Meta-Analysis Identifies Three Loci Influencing Adiposity and Fat Distribution. PLoS Genetics, 2009, 5, e1000508.	3.5	453
31	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
32	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
33	Genome-wide association meta-analysis of 78,308 individuals identifies new loci and genes influencing human intelligence. Nature Genetics, 2017, 49, 1107-1112.	21.4	425
34	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.	3.5	419
35	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. Nature Genetics, 2011, 43, 1005-1011.	21.4	403
36	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

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37	Meta-analysis of telomere length in 19â€‰%713 subjects reveals high heritability, stronger maternal inheritance and a paternal age effect. <i>European Journal of Human Genetics</i> , 2013, 21, 1163-1168.	2.8	380
38	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. <i>PLoS Genetics</i> , 2013, 9, e1003500.	3.5	371
39	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. <i>Nature Genetics</i> , 2016, 48, 1171-1184.	21.4	362
40	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. <i>Nature Genetics</i> , 2015, 47, 1294-1303.	21.4	357
41	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. <i>Nature Genetics</i> , 2018, 50, 559-571.	21.4	356
42	Genetic contributions to variation in general cognitive function: a meta-analysis of genome-wide association studies in the CHARGE consortium (N=53â€‰%949). <i>Molecular Psychiatry</i> , 2015, 20, 183-192.	7.9	344
43	The trans-ancestral genomic architecture of glycemic traits. <i>Nature Genetics</i> , 2021, 53, 840-860.	21.4	341
44	Meta-analysis of genome-wide association studies for personality. <i>Molecular Psychiatry</i> , 2012, 17, 337-349.	7.9	340
45	Genome-wide meta-analysis identifies new susceptibility loci for migraine. <i>Nature Genetics</i> , 2013, 45, 912-917.	21.4	338
46	Genetic variation near IRS1 associates with reduced adiposity and an impaired metabolic profile. <i>Nature Genetics</i> , 2011, 43, 753-760.	21.4	289
47	Meta-analysis of Genome-wide Association Studies for Neuroticism, and the Polygenic Association With Major Depressive Disorder. <i>JAMA Psychiatry</i> , 2015, 72, 642.	11.0	289
48	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. <i>Nature Genetics</i> , 2016, 48, 1462-1472.	21.4	284
49	A novel Alzheimer disease locus located near the gene encoding tau protein. <i>Molecular Psychiatry</i> , 2016, 21, 108-117.	7.9	260
50	Genome-wide association and genetic functional studies identify <i>autism susceptibility candidate 2</i> gene (<i>AUTS2</i>) in the regulation of alcohol consumption. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 7119-7124.	7.1	258
51	Life-Course Genome-wide Association Study Meta-analysis of Total Body BMD and Assessment of Age-Specific Effects. <i>American Journal of Human Genetics</i> , 2018, 102, 88-102.	6.2	252
52	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. <i>Nature Genetics</i> , 2019, 51, 1459-1474.	21.4	251
53	Collaborative Meta-analysis: Associations of 150 Candidate Genes With Osteoporosis and Osteoporotic Fracture. <i>Annals of Internal Medicine</i> , 2009, 151, 528.	3.9	250
54	Genome-wide association scan for five major dimensions of personality. <i>Molecular Psychiatry</i> , 2010, 15, 647-656.	7.9	250

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55	Novel genetic loci associated with hippocampal volume. Nature Communications, 2017, 8, 13624.	12.8	250
56	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
57	Genome-wide association meta-analysis highlights light-induced signaling as a driver for refractive error. Nature Genetics, 2018, 50, 834-848.	21.4	239
58	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. Molecular Psychiatry, 2015, 20, 647-656.	7.9	235
59	A Genomic Background Based Method for Association Analysis in Related Individuals. PLoS ONE, 2007, 2, e1274.	2.5	233
60	NRXN3 Is a Novel Locus for Waist Circumference: A Genome-Wide Association Study from the CHARGE Consortium. PLoS Genetics, 2009, 5, e1000539.	3.5	230
61	Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. Nature Genetics, 2016, 48, 1162-1170.	21.4	223
62	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
63	A meta-analysis of genome-wide association studies identifies multiple longevity genes. Nature Communications, 2019, 10, 3669.	12.8	214
64	Novel genetic loci underlying human intracranial volume identified through genome-wide association. Nature Neuroscience, 2016, 19, 1569-1582.	14.8	213
65	Common variants at 12q14 and 12q24 are associated with hippocampal volume. Nature Genetics, 2012, 44, 545-551.	21.4	212
66	Genome-wide analysis of multi-ancestry cohorts identifies new loci influencing intraocular pressure and susceptibility to glaucoma. Nature Genetics, 2014, 46, 1126-1130.	21.4	212
67	KLB is associated with alcohol drinking, and its gene product 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
68	A genome-wide association study identifies a susceptibility locus for refractive errors and myopia at 15q14. Nature Genetics, 2010, 42, 897-901.	21.4	200
69	A Genome-Wide Association Search for Type 2 Diabetes Genes in African Americans. PLoS ONE, 2012, 7, e29202.	2.5	197
70	Novel loci affecting iron homeostasis and their effects in individuals at risk for hemochromatosis. Nature Communications, 2014, 5, 4926.	12.8	192
71	Genetic architecture of subcortical brain structures in 38,851 individuals. Nature Genetics, 2019, 51, 1624-1636.	21.4	192
72	Whole exome sequencing study identifies novel rare and common Alzheimer's-Associated variants involved in immune response and transcriptional regulation. Molecular Psychiatry, 2020, 25, 1859-1875.	7.9	191

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73	Stratifying Type 2 Diabetes Cases by BMI Identifies Genetic Risk Variants in LAMA1 and Enrichment for Risk Variants in Lean Compared to Obese Cases. PLoS Genetics, 2012, 8, e1002741.	3.5	190
74	A metabolic profile of all-cause mortality risk identified in an observational study of 44,168 individuals. Nature Communications, 2019, 10, 3346.	12.8	188
75	A Genome-Wide Association Study of Optic Disc Parameters. PLoS Genetics, 2010, 6, e1000978.	3.5	187
76	The Role of Adiposity in Cardiometabolic Traits: A Mendelian Randomization Analysis. PLoS Medicine, 2013, 10, e1001474.	8.4	178
77	Genome-wide association study identifies novel genetic variants contributing to variation in blood metabolite levels. Nature Communications, 2015, 6, 7208.	12.8	178
78	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
79	The effect of APOE and other common genetic variants on the onset of Alzheimer's disease and dementia: a community-based cohort study. Lancet Neurology, The, 2018, 17, 434-444.	10.2	177
80	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. Nature Communications, 2015, 6, 5897.	12.8	173
81	Directional dominance on stature and cognition in diverse human populations. Nature, 2015, 523, 459-462.	27.8	173
82	Convergent genetic and expression data implicate immunity in Alzheimer's disease. Alzheimer's and Dementia, 2015, 11, 658-671.	0.8	173
83	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
84	Association of genetic variation with systolic and diastolic blood pressure among African Americans: the Candidate Gene Association Resource study. Human Molecular Genetics, 2011, 20, 2273-2284.	2.9	168
85	Relationship between gut microbiota and circulating metabolites in population-based cohorts. Nature Communications, 2019, 10, 5813.	12.8	168
86	Common Genetic Determinants of Intraocular Pressure and Primary Open-Angle Glaucoma. PLoS Genetics, 2012, 8, e1002611.	3.5	164
87	Genome-wide physical activity interactions in adiposity • A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	3.5	158
88	Gene-Wide Analysis Detects Two New Susceptibility Genes for Alzheimer's Disease. PLoS ONE, 2014, 9, e94661.	2.5	155
89	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. Nature Communications, 2016, 7, 10494.	12.8	153
90	Common genetic variants associated with open-angle glaucoma. Human Molecular Genetics, 2011, 20, 2464-2471.	2.9	152

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91	A Genome-Wide Association Study of Depressive Symptoms. <i>Biological Psychiatry</i> , 2013, 73, 667-678.	1.3	149
92	Large-scale GWAS identifies multiple loci for hand grip strength providing biological insights into muscular fitness. <i>Nature Communications</i> , 2017, 8, 16015.	12.8	149
93	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. <i>Nature Communications</i> , 2017, 8, 80.	12.8	147
94	Clear detection of ADIPOQ locus as the major gene for plasma adiponectin: Results of genome-wide association analyses including 4659 European individuals. <i>Atherosclerosis</i> , 2010, 208, 412-420.	0.8	146
95	Circulating metabolites and general cognitive ability and dementia: Evidence from 11 cohort studies. <i>Alzheimer's and Dementia</i> , 2018, 14, 707-722.	0.8	143
96	Nine Loci for Ocular Axial Length Identified through Genome-wide Association Studies, Including Shared Loci with Refractive Error. <i>American Journal of Human Genetics</i> , 2013, 93, 264-277.	6.2	139
97	Genetic risk profiles for depression and anxiety in adult and elderly cohorts. <i>Molecular Psychiatry</i> , 2011, 16, 773-783.	7.9	135
98	GWAS for executive function and processing speed suggests involvement of the CADM2 gene. <i>Molecular Psychiatry</i> , 2016, 21, 189-197.	7.9	134
99	A KATP channel gene effect on sleep duration: from genome-wide association studies to function in <i>Drosophila</i> . <i>Molecular Psychiatry</i> , 2013, 18, 122-132.	7.9	132
100	Metabolomics Profile in Depression: A Pooled Analysis of 230 Metabolic Markers in 5283 Cases With Depression and 10,145 Controls. <i>Biological Psychiatry</i> , 2020, 87, 409-418.	1.3	129
101	Genome-wide Association Study of Smoking Initiation and Current Smoking. <i>American Journal of Human Genetics</i> , 2009, 84, 367-379.	6.2	125
102	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. <i>Hypertension</i> , 2017, 70, .	2.7	123
103	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. <i>American Journal of Human Genetics</i> , 2018, 102, 375-400.	6.2	123
104	New insights into the genetics of primary open-angle glaucoma based on meta-analyses of intraocular pressure and optic disc characteristics.. <i>Human Molecular Genetics</i> , 2017, 26, ddw399.	2.9	120
105	<i>SIRT1</i> Genetic Variation Is Related to BMI and Risk of Obesity. <i>Diabetes</i> , 2009, 58, 2828-2834.	0.6	118
106	Genome-wide meta-analysis associates HLA-DQA1/DRB1 and LPA and lifestyle factors with human longevity. <i>Nature Communications</i> , 2017, 8, 910.	12.8	118
107	Genome-wide Association Analysis in Humans Links Nucleotide Metabolism to Leukocyte Telomere Length. <i>American Journal of Human Genetics</i> , 2020, 106, 389-404.	6.2	118
108	Genome-wide analysis of BMI in adolescents and young adults reveals additional insight into the effects of genetic loci over the life course. <i>Human Molecular Genetics</i> , 2013, 22, 3597-3607.	2.9	116

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109	Characteristics of de novo structural changes in the human genome. <i>Genome Research</i> , 2015, 25, 792-801.	5.5	115
110	Leveraging Cross-Species Transcription Factor Binding Site Patterns: From Diabetes Risk Loci to Disease Mechanisms. <i>Cell</i> , 2014, 156, 343-358.	28.9	113
111	Genome-wide association analysis of coffee drinking suggests association with CYP1A1/CYP1A2 and NRCAM. <i>Molecular Psychiatry</i> , 2012, 17, 1116-1129.	7.9	112
112	Genome-wide association study meta-analysis of chronic widespread pain: evidence for involvement of the 5p15.2 region. <i>Annals of the Rheumatic Diseases</i> , 2013, 72, 427-436.	0.9	112
113	Multi-ancestry genome-wide gene-smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. <i>Nature Genetics</i> , 2019, 51, 636-648.	21.4	112
114	Genetic variants linked to education predict longevity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 13366-13371.	7.1	110
115	Gene-Age Interactions in Blood Pressure Regulation: A Large-Scale Investigation with the CHARGE, Global BPgen, and ICBP Consortia. <i>American Journal of Human Genetics</i> , 2014, 95, 24-38.	6.2	109
116	Meta-analysis of gene-environment-wide association scans accounting for education level identifies additional loci for refractive error. <i>Nature Communications</i> , 2016, 7, 11008.	12.8	104
117	Harmonization of Neuroticism and Extraversion phenotypes across inventories and cohorts in the Genetics of Personality Consortium: an application of Item Response Theory. <i>Behavior Genetics</i> , 2014, 44, 295-313.	2.1	103
118	Telomere length in circulating leukocytes is associated with lung function and disease. <i>European Respiratory Journal</i> , 2014, 43, 983-992.	6.7	103
119	Characterization of pathogenic SORL1 genetic variants for association with Alzheimer's disease: a clinical interpretation strategy. <i>European Journal of Human Genetics</i> , 2017, 25, 973-981.	2.8	102
120	Association Between Chromosome 9p21 Variants and the Ankle-Brachial Index Identified by a Meta-Analysis of 21 Genome-Wide Association Studies. <i>Circulation: Cardiovascular Genetics</i> , 2012, 5, 100-112.	5.1	98
121	Discovery and functional prioritization of Parkinson's disease candidate genes from large-scale whole exome sequencing. <i>Genome Biology</i> , 2017, 18, 22.	8.8	96
122	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. <i>PLoS ONE</i> , 2018, 13, e0198166.	2.5	94
123	The genetic association between personality and major depression or bipolar disorder. A polygenic score analysis using genome-wide association data. <i>Translational Psychiatry</i> , 2011, 1, e50-e50.	4.8	90
124	Meta-analysis of genome-wide association studies identifies novel loci that influence cupping and the glaucomatous process. <i>Nature Communications</i> , 2014, 5, 4883.	12.8	89
125	Causal Effect of Plasminogen Activator Inhibitor Type 1 on Coronary Heart Disease. <i>Journal of the American Heart Association</i> , 2017, 6, .	3.7	89
126	Meta-analysis of genome-wide association for migraine in six population-based European cohorts. <i>European Journal of Human Genetics</i> , 2011, 19, 901-907.	2.8	87

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127	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. Nature Communications, 2021, 12, 24.	12.8	87
128	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	3.4	85
129	Transmission of human mtDNA heteroplasmy in the Genome of the Netherlands families: support for a variable-size bottleneck. Genome Research, 2016, 26, 417-426.	5.5	84
130	An Analysis of Two Genome-wide Association Meta-analyses Identifies a New Locus for Broad Depression Phenotype. Biological Psychiatry, 2017, 82, 322-329.	1.3	84
131	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	12.8	84
132	Evidence of Inbreeding Depression on Human Height. PLoS Genetics, 2012, 8, e1002655.	3.5	79
133	ARHGEF12 influences the risk of glaucoma by increasing intraocular pressure. Human Molecular Genetics, 2015, 24, 2689-2699.	2.9	79
134	DNA Methylation Signatures of Depressive Symptoms in Middle-aged and Elderly Persons. JAMA Psychiatry, 2018, 75, 949.	11.0	78
135	Effects of Long-Term Averaging of Quantitative Blood Pressure Traits on the Detection of Genetic Associations. American Journal of Human Genetics, 2014, 95, 49-65.	6.2	73
136	Meta-analysis of Genome-Wide Association Studies Identifies Novel Loci Associated With Optic Disc Morphology. Genetic Epidemiology, 2015, 39, 207-216.	1.3	72
137	Long-term Air Pollution Exposure, Genome-wide DNA Methylation and Lung Function in the LifeLines Cohort Study. Environmental Health Perspectives, 2018, 126, 027004.	6.0	71
138	Common Genetic Variation Indicates Separate Causes for Periventricular and Deep White Matter Hyperintensities. Stroke, 2020, 51, 2111-2121.	2.0	71
139	Insight in Genome-Wide Association of Metabolite Quantitative Traits by Exome Sequence Analyses. PLoS Genetics, 2015, 11, e1004835.	3.5	70
140	Meta-analysis of epigenome-wide association studies of cognitive abilities. Molecular Psychiatry, 2018, 23, 2133-2144.	7.9	68
141	Large scale international replication and meta-analysis study confirms association of the 15q14 locus with myopia. The CREAM consortium. Human Genetics, 2012, 131, 1467-1480.	3.8	67
142	Genome-wide Studies of Verbal Declarative Memory in Nondemented Older People: The Cohorts for Heart and Aging Research in Genomic Epidemiology Consortium. Biological Psychiatry, 2015, 77, 749-763.	1.3	67
143	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. Nature Genetics, 2016, 48, 1303-1312.	21.4	66
144	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	12.8	64

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145	Exome sequencing and functional analyses suggest that SIX6 is a gene involved in an altered proliferation–differentiation balance early in life and optic nerve degeneration at old age. Human Molecular Genetics, 2014, 23, 1320-1332.	2.9	63
146	Evidence for three genetic loci involved in both anorexia nervosa risk and variation of body mass index. Molecular Psychiatry, 2017, 22, 192-201.	7.9	63
147	Predicting Stroke Through Genetic Risk Functions. Stroke, 2014, 45, 403-412.	2.0	62
148	Multi-ancestry sleep-by-SNP interaction analysis in 126,926 individuals reveals lipid loci stratified by sleep duration. Nature Communications, 2019, 10, 5121.	12.8	62
149	Phenome-wide investigation of health outcomes associated with genetic predisposition to loneliness. Human Molecular Genetics, 2019, 28, 3853-3865.	2.9	62
150	An integrative cross-omics analysis of DNA methylation sites of glucose and insulin homeostasis. Nature Communications, 2019, 10, 2581.	12.8	62
151	Genetic analysis for a shared biological basis between migraine and coronary artery disease. Neurology: Genetics, 2015, 1, e10.	1.9	61
152	Occupational exposure to pesticides is associated with differential DNA methylation. Occupational and Environmental Medicine, 2018, 75, 427-435.	2.8	61
153	Genetic correlations and genome-wide associations of cortical structure in general population samples of 22,824 adults. Nature Communications, 2020, 11, 4796.	12.8	61
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	Meta-analysis of genome-wide association studies in five cohorts reveals common variants in RBFOX1, a regulator of tissue-specific splicing, associated with refractive error. Human Molecular Genetics, 2013, 22, 2754-2764.	2.9	60
156	The protocadherin 17 gene affects cognition, personality, amygdala structure and function, synapse development and risk of major mood disorders. Molecular Psychiatry, 2018, 23, 400-412.	7.9	60
157	The association between lower educational attainment and depression owing to shared genetic effects? Results in ~25%000 subjects. Molecular Psychiatry, 2015, 20, 735-743.	7.9	59
158	European lactase persistence genotype shows evidence of association with increase in body mass index. Human Molecular Genetics, 2010, 19, 1129-1136.	2.9	58
159	Shared genetic contribution to ischemic stroke and Alzheimer's disease. Annals of Neurology, 2016, 79, 739-747.	5.3	56
160	Genome-wide analyses of borderline personality features. Molecular Psychiatry, 2014, 19, 923-929.	7.9	55
161	Multiethnic Exome-Wide Association Study of Subclinical Atherosclerosis. Circulation: Cardiovascular Genetics, 2016, 9, 511-520.	5.1	54
162	Integration of epidemiologic, pharmacologic, genetic and gut microbiome data in a drug–metabolite atlas. Nature Medicine, 2020, 26, 110-117.	30.7	54

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163	Candidate CSPG4 mutations and induced pluripotent stem cell modeling implicate oligodendrocyte progenitor cell dysfunction in familial schizophrenia. <i>Molecular Psychiatry</i> , 2019, 24, 757-771.	7.9	51
164	PLD3 variants in population studies. <i>Nature</i> , 2015, 520, E2-E3.	27.8	49
165	Exome-sequencing in a large population-based study reveals a rare Asn396Ser variant in the LIPG gene associated with depressive symptoms. <i>Molecular Psychiatry</i> , 2017, 22, 537-543.	7.9	49
166	New Blood Pressure-Associated Loci Identified in Meta-Analyses of 475,000 Individuals. <i>Circulation: Cardiovascular Genetics</i> , 2017, 10, .	5.1	48
167	Assessment of gene-by-sex interaction effect on bone mineral density. <i>Journal of Bone and Mineral Research</i> , 2012, 27, 2051-2064.	2.8	47
168	From blood to lung tissue: effect of cigarette smoke on DNA methylation and lung function. <i>Respiratory Research</i> , 2018, 19, 212.	3.6	47
169	Rare Functional Variant in TM2D3 is Associated with Late-Onset Alzheimer's Disease. <i>PLoS Genetics</i> , 2016, 12, e1006327.	3.5	47
170	Genome-wide association study on the FEV1/FVC ratio in never-smokers identifies HHIP and FAM13A. <i>Journal of Allergy and Clinical Immunology</i> , 2017, 139, 533-540.	2.9	45
171	Rare Exome Sequence Variants in <i>CLCN6</i> Reduce Blood Pressure Levels and Hypertension Risk. <i>Circulation: Cardiovascular Genetics</i> , 2016, 9, 64-70.	5.1	44
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