Najaf Amin

List of Publications by Year
in descending order

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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	Fat metabolism is associated with telomere length in six population-based studies. Human Molecular Genetics, 2022, 31, 1159-1170.	2.9	7
2	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
3	New insights into the genetic etiology of Alzheimerâ€™s disease and related dementias. Nature Genetics, 2022, 54, 412-436.	21.4	700
4	Microbiomics, Metabolomics, Predicted Metagenomics, and Hepatic Steatosis in a Populationâ€Based Study of 1,355 Adults. Hepatology, 2021, 73, 968-982.	7.3	43
5	Association of Circulating Metabolites in Plasma or Serum and Risk of Stroke. Neurology, 2021, 96, .	1.1	24
6	Multi-ancestry genome-wide association study accounting for gene-psychosocial factor interactions identifies novel loci for blood pressure traits. Human Genetics and Genomics Advances, 2021, 2, 100013.	1.7	2
7	Circulating metabolites are associated with brain atrophy and white matter hyperintensities. Alzheimer's and Dementia, 2021, 17, 205-214.	0.8	17
8	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. Nature Communications, 2021, 12, 24.	12.8	87
9	Multi-ancestry genome-wide geneâ€“sleep interactions identify novel loci for blood pressure. Molecular Psychiatry, 2021, 26, 6293-6304.	7.9	13
10	Plasma amyloid Î² levels are driven by genetic variants near APOE, BACE1, APP, PSEN2: A genomeâ€wide association study in over 12,000 nonâ€demented participants. Alzheimer's and Dementia, 2021, 17, 1663-1674.	0.8	20
11	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341
12	Genetic association study of childhood aggression across raters, instruments, and age. Translational Psychiatry, 2021, 11, 413.	4.8	31
13	Genome-wide association study of frontotemporal dementia identifies a C9ORF72 haplotype with a median of 12-G4C2 repeats that predisposes to pathological repeat expansions. Translational Psychiatry, 2021, 11, 451.	4.8	6
14	Whole exome sequencing study identifies novel rare and common Alzheimerâ€™s-Associated variants involved in immune response and transcriptional regulation. Molecular Psychiatry, 2020, 25, 1859-1875.	7.9	191
15	Novel Rare Genetic Variants Associated with Airflow Obstruction in the General Population. American Journal of Respiratory and Critical Care Medicine, 2020, 201, 485-488.	5.6	2
16	Metabolomics Profile in Depression: A Pooled Analysis of 230 Metabolic Markers in 5283 Cases With Depression and 10,145 Controls. Biological Psychiatry, 2020, 87, 409-418.	1.3	129
17	Association of lysophosphatidic acids with cerebrospinal fluid biomarkers and progression to Alzheimerâ€™s disease. Alzheimer's Research and Therapy, 2020, 12, 124.	6.2	12
18	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

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19	A cross-omics integrative study of metabolic signatures of chronic obstructive pulmonary disease. BMC Pulmonary Medicine, 2020, 20, 193.	2.0	15
20	Genetic Studies of Leptin Concentrations Implicate Leptin in the Regulation of Early Adiposity. Diabetes, 2020, 69, 2806-2818.	0.6	26
21	Exome sequencing identifies three novel ADâ€associated genes. Alzheimer's and Dementia, 2020, 16, e041592.	0.8	6
22	The role of the gut microbiome in cognitive function and Alzheimerâ€™s disease. Alzheimer's and Dementia, 2020, 16, e043197.	0.8	1
23	SORL1 â€variant carriers in ADESâ€ADSP: A higher level of variant pathogenicity associates with earlier age at onset of Alzheimer's disease. Alzheimer's and Dementia, 2020, 16, e044492.	0.8	1
24	Clostridium shows a higher abundance in less neurovascular and neurodegenerative changes: A microbiomeâ€wide association study. Alzheimer's and Dementia, 2020, 16, e044743.	0.8	4
25	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. Molecular Psychiatry, 2020, 26, 2111-2125.	7.9	17
26	CDH6 and HAGH protein levels in plasma associate with Alzheimerâ€™s disease in APOE Îµ4 carriers. Scientific Reports, 2020, 10, 8233.	3.3	17
27	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. PLoS ONE, 2020, 15, e0230815.	2.5	10
28	Common Genetic Variation Indicates Separate Causes for Periventricular and Deep White Matter Hyperintensities. Stroke, 2020, 51, 2111-2121.	2.0	71
29	Prion protein codon 129 polymorphism in mild cognitive impairment and dementia: the Rotterdam Study. Brain Communications, 2020, 2, fcaa030.	3.3	3
30	Measurement and genetic architecture of lifetime depression in the Netherlands as assessed by LIDAS (Lifetime Depression Assessment Self-report). Psychological Medicine, 2020, , 1-10.	4.5	4
31	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
32	Integration of epidemiologic, pharmacologic, genetic and gut microbiome data in a drugâ€“metabolite atlas. Nature Medicine, 2020, 26, 110-117.	30.7	54
33	Exome Sequencing Analysis Identifies Rare Variants in ATM and RPL8 That Are Associated With Shorter Telomere Length. Frontiers in Genetics, 2020, 11, 337.	2.3	4
34	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815.		0
35	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815.		0
36	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815.		0

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37	Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. , 2020, 15, e0230815.		0
38	Linkage analysis and whole exome sequencing identify a novel candidate gene in a Dutch multiple sclerosis family. Multiple Sclerosis Journal, 2019, 25, 909-917.	3.0	19
39	Quality control and integration of genotypes from two calling pipelines for whole genome sequence data in the Alzheimer's disease sequencing project. Genomics, 2019, 111, 808-818.	2.9	26
40	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
41	A genome-wide association study identifies genetic loci associated with specific lobar brain volumes. Communications Biology, 2019, 2, 285.	4.4	27
42	A meta-analysis of genome-wide association studies identifies multiple longevity genes. Nature Communications, 2019, 10, 3669.	12.8	214
43	Metabolomics reveals a link between homocysteine and lipid metabolism and leukocyte telomere length: the ENGAGE consortium. Scientific Reports, 2019, 9, 11623.	3.3	13
44	Disentangling the genetics of lean mass. American Journal of Clinical Nutrition, 2019, 109, 276-287.	4.7	38
45	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	12.8	84
46	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
47	Phenome-wide investigation of health outcomes associated with genetic predisposition to loneliness. Human Molecular Genetics, 2019, 28, 3853-3865.	2.9	62
48	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	21.4	251
49	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	3.4	85
50	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	12.8	64
51	Occupational exposure to gases/fumes and mineral dust affect DNA methylation levels of genes regulating expression. Human Molecular Genetics, 2019, 28, 2477-2485.	2.9	9
52	Exome-Derived Adiponectin-Associated Variants Implicate Obesity and Lipid Biology. American Journal of Human Genetics, 2019, 105, 15-28.	6.2	21
53	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	21.4	549
54	An integrative cross-omics analysis of DNA methylation sites of glucose and insulin homeostasis. Nature Communications, 2019, 10, 2581.	12.8	62

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55	Limited overlap in significant hits between genome-wide association studies on two airflow obstruction definitions in the same population. BMC Pulmonary Medicine, 2019, 19, 58.	2.0	4
56	A multi-ancestry genome-wide study incorporating geneâ€“smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. Human Molecular Genetics, 2019, 28, 2615-2633.	2.9	31
57	Multi-ancestry genome-wide geneâ€“smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. Nature Genetics, 2019, 51, 636-648.	21.4	112
58	Large-scale plasma metabolome analysis reveals alterations in HDL metabolism in migraine. Neurology, 2019, 92, e1899-e1911.	1.1	42
59	Genetic meta-analysis of diagnosed Alzheimerâ€™s disease identifies new risk loci and implicates AÎ², tau, immunity and lipid processing. Nature Genetics, 2019, 51, 414-430.	21.4	1,962
60	Relationship between gut microbiota and circulating metabolites in population-based cohorts. Nature Communications, 2019, 10, 5813.	12.8	168
61	DNA methylation is associated with lung function in never smokers. Respiratory Research, 2019, 20, 268.	3.6	14
62	Multi-trait genome-wide association study identifies new loci associated with optic disc parameters. Communications Biology, 2019, 2, 435.	4.4	22
63	Genetic architecture of subcortical brain structures in 38,851 individuals. Nature Genetics, 2019, 51, 1624-1636.	21.4	192
64	Candidate CSPG4 mutations and induced pluripotent stem cell modeling implicate oligodendrocyte progenitor cell dysfunction in familial schizophrenia. Molecular Psychiatry, 2019, 24, 757-771.	7.9	51
65	Disentangling the biological pathways involved in early features of Alzheimer's disease in the Rotterdam Study. , 2018, 14, 848-857.		36
66	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. Nature Genetics, 2018, 50, 559-571.	21.4	356
67	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. American Journal of Human Genetics, 2018, 102, 375-400.	6.2	123
68	COPD GWAS variant at 19q13.2 in relation with DNA methylation and gene expression. Human Molecular Genetics, 2018, 27, 396-405.	2.9	24
69	Understanding the role of the chromosome 15q25.1 in COPD through epigenetics and transcriptomics. European Journal of Human Genetics, 2018, 26, 709-722.	2.8	21
70	Circulating metabolites and general cognitive ability and dementia: Evidence from 11 cohort studies. Alzheimer's and Dementia, 2018, 14, 707-722.	0.8	143
71	Meta-analysis of epigenome-wide association studies of cognitive abilities. Molecular Psychiatry, 2018, 23, 2133-2144.	7.9	68
72	Life-Course Genome-wide Association Study Meta-analysis of Total Body BMD and Assessment of Age-Specific Effects. American Journal of Human Genetics, 2018, 102, 88-102.	6.2	252

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73	Whole-Exome Sequencing in Age-Related Macular Degeneration Identifies Rare Variants in COL8A1, a Component of Bruchâ€™s Membrane. Ophthalmology, 2018, 125, 1433-1443.	5.2	35
74	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
75	Metabolic profiling of intra- and extracranial carotid artery atherosclerosis. Atherosclerosis, 2018, 272, 60-65.	0.8	24
76	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
77	A rare missense variant in RCL1 segregates with depression in extended families. Molecular Psychiatry, 2018, 23, 1120-1126.	7.9	34
78	F3â€02â€02: CIRCULATING METABOLITESâ€™ ASSOCIATION WITH ALZHEIMER'S DISEASEâ€“ASSOCIATED GENETIC VARIANTS. Alzheimer's and Dementia, 2018, 14, P997.	0.8	0
79	P3â€134: CIRCULATING METABOLITES ARE ASSOCIATED WITH WHITE MATTER HYPERINTENSITIES. Alzheimer's and Dementia, 2018, 14, P1119.	0.8	0
80	P1â€298: CEREBROSPINAL FLUID AND PLASMA LEVELS OF LYSOPHOSPHATIDIC ACIDS (LPAS) ASSOCIATE WITH CEREBROSPINAL FLUID Aî²â€42 AND Pâ€TAU. Alzheimer's and Dementia, 2018, 14, P403.	0.8	0
81	From blood to lung tissue: effect of cigarette smoke on DNA methylation and lung function. Respiratory Research, 2018, 19, 212.	3.6	47
82	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
83	Genome-wide association study of 23,500 individuals identifies 7 loci associated with brain ventricular volume. Nature Communications, 2018, 9, 3945.	12.8	31
84	Whole-Genome Linkage Scan Combined With Exome Sequencing Identifies Novel Candidate Genes for Carotid Intima-Media Thickness. Frontiers in Genetics, 2018, 9, 420.	2.3	3
85	Large-scale whole-exome sequencing association studies identify rare functional variants influencing serum urate levels. Nature Communications, 2018, 9, 4228.	12.8	43
86	Occupational exposure to pesticides is associated with differential DNA methylation. Occupational and Environmental Medicine, 2018, 75, 427-435.	2.8	61
87	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
88	Genome-wide association meta-analysis highlights light-induced signaling as a driver for refractive error. Nature Genetics, 2018, 50, 834-848.	21.4	239
89	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. Nature Communications, 2018, 9, 2098.	12.8	484
90	A Genome-Wide Linkage Study for Chronic Obstructive Pulmonary Disease in a Dutch Genetic Isolate Identifies Novel Rare Candidate Variants. Frontiers in Genetics, 2018, 9, 133.	2.3	8

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91	DNA Methylation Signatures of Depressive Symptoms in Middle-aged and Elderly Persons. JAMA Psychiatry, 2018, 75, 949.	11.0	78
92	A combined linkage, microarray and exome analysis suggests MAP3K11 as a candidate gene for left ventricular hypertrophy. BMC Medical Genomics, 2018, 11, 22.	1.5	4
93	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. PLoS ONE, 2018, 13, e0198166.	2.5	94
94	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
95	Novel genetic loci associated with hippocampal volume. Nature Communications, 2017, 8, 13624.	12.8	250
96	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
97	Discovery and functional prioritization of Parkinsonâ€™s disease candidate genes from large-scale whole exome sequencing. Genome Biology, 2017, 18, 22.	8.8	96
98	Gray matter heritability in familyâ€based and populationâ€based studies using voxelâ€based morphometry. Human Brain Mapping, 2017, 38, 2408-2423.	3.6	9
99	New insights into the genetics of primary open-angle glaucoma based on meta-analyses of intraocular pressure and optic disc characteristics.. Human Molecular Genetics, 2017, 26, ddw399.	2.9	120
100	Haplotype reference consortium panel: Practical implications of imputations with large reference panels. Human Mutation, 2017, 38, 1025-1032.	2.5	43
101	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
102	Variants in TTC25 affect autistic trait in patients with autism spectrum disorder and general population. European Journal of Human Genetics, 2017, 25, 982-987.	2.8	5
103	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
104	Characterization of pathogenic SORL1 genetic variants for association with Alzheimerâ€™s disease: a clinical interpretation strategy. European Journal of Human Genetics, 2017, 25, 973-981.	2.8	102
105	Causal Effect of Plasminogen Activator Inhibitor Type 1 on Coronary Heart Disease. Journal of the American Heart Association, 2017, 6, .	3.7	89
106	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
107	Genome-wide meta-analysis associates HLA-DQA1/DRB1 and LPA and lifestyle factors with human longevity. Nature Communications, 2017, 8, 910.	12.8	118
108	New Blood Pressureâ€“Associated Loci Identified in Meta-Analyses of 475â€‰000 Individuals. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	48

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109	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
110	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
111	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. Nature Communications, 2017, 8, 80.	12.8	147
112	Common variants at 2q11.2, 8q21.3, and 11q13.2 are associated with major mood disorders. Translational Psychiatry, 2017, 7, 1273.	4.8	9
113	Large-scale GWAS identifies multiple loci for hand grip strength providing biological insights into muscular fitness. Nature Communications, 2017, 8, 16015.	12.8	149
114	Lack of evidence for a role of genetic variation in TMEM230 in the risk for Parkinson's disease in the Caucasian population. Neurobiology of Aging, 2017, 50, 167.e11-167.e13.	3.1	24
115	Nonsynonymous Variation in NKPD1 Increases Depressive Symptoms in European Populations. Biological Psychiatry, 2017, 81, 702-707.	1.3	26
116	Genome-wide association study on the FEV 1 /FVC ratio in never-smokers identifies HHIP and FAM13A. Journal of Allergy and Clinical Immunology, 2017, 139, 533-540.	2.9	45
117	Exome-sequencing in a large population-based study reveals a rare Asn396Ser variant in the LIPG gene associated with depressive symptoms. Molecular Psychiatry, 2017, 22, 537-543.	7.9	49
118	[P1â€“139]: PATHWAYâ€SPECIFIC GENETIC RISK SCORE ASSOCIATED WITH ALZHEIMER's DISEASE AND WHITE MATTER LESIONS IN COGNITIVELY NORMAL SUBJECTS. Alzheimer's and Dementia, 2017, 13, P295.	0.8	0
119	Exome-Wide Meta-Analysis Identifies Rare 3â€²-UTR Variant in ERCC1/CD3EAP Associated with Symptoms of Sleep Apnea. Frontiers in Genetics, 2017, 8, 151.	2.3	7
120	Genome-wide physical activity interactions in adiposity â€• A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	3.5	158
121	A Combined Linkage and Exome Sequencing Analysis for Electrocardiogram Parameters in the Erasmus Rucphen Family Study. Frontiers in Genetics, 2016, 7, 190.	2.3	5
122	An Empirical Comparison of Joint and Stratified Frameworks for Studying G Ã— E Interactions: Systolic Blood Pressure and Smoking in the CHARGE Geneâ€Lifestyle Interactions Working Group. Genetic Epidemiology, 2016, 40, 404-415.	1.3	18
123	P1â€381: Evaluation of The Absolute Genetic Risk of Alzheimer's Disease in The Aging Population. Alzheimer's and Dementia, 2016, 12, P578.	0.8	1
124	F1-02-03: Metabolites Associated with Cognitive Function in the Rotterdam Study and Erasmus Rucphen Family Study. , 2016, 12, P165-P165.		4
125	O1-09-01: Genomewide Linkage Analysis Identifies Novel Candidate Genes for Alzheimerâ€™s Disease. , 2016, 12, P196-P196.		0
126	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

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127	A Genome-Wide Association Study in isolated populations reveals new genes associated to common food likings. Reviews in Endocrine and Metabolic Disorders, 2016, 17, 209-219.	5.7	22
128	Genetic variants in RBFOX3 are associated with sleep latency. European Journal of Human Genetics, 2016, 24, 1488-1495.	2.8	27
129	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	27.8	1,204
130	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. Nature Genetics, 2016, 48, 1303-1312.	21.4	66
131	Novel genetic loci underlying human intracranial volume identified through genome-wide association. Nature Neuroscience, 2016, 19, 1569-1582.	14.8	213
132	Shared genetic contribution to ischemic stroke and Alzheimer's disease. Annals of Neurology, 2016, 79, 739-747.	5.3	56
133	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
134	Multiethnic Exome-Wide Association Study of Subclinical Atherosclerosis. Circulation: Cardiovascular Genetics, 2016, 9, 511-520.	5.1	54
135	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
136	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. Nature Genetics, 2016, 48, 1171-1184.	21.4	362
137	Meta-analysis of geneâ€“environment-wide association scans accounting for education level identifies additional loci for refractive error. Nature Communications, 2016, 7, 11008.	12.8	104
138	Genome-wide study for circulating metabolites identifies 62 loci and reveals novel systemic effects of LPA. Nature Communications, 2016, 7, 11122.	12.8	576
139	Non-additive genome-wide association scan reveals a new gene associated with habitual coffee consumption. Scientific Reports, 2016, 6, 31590.	3.3	25
140	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. Nature Genetics, 2016, 48, 1462-1472.	21.4	284
141	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
142	Rare Exome Sequence Variants in CLCN6 Reduce Blood Pressure Levels and Hypertension Risk. Circulation: Cardiovascular Genetics, 2016, 9, 64-70.	5.1	44
143	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. Nature Communications, 2016, 7, 10494.	12.8	153
144	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

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145	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
146	Rare, low frequency and common coding variants in CHRNA5 and their contribution to nicotine dependence in European and African Americans. Molecular Psychiatry, 2016, 21, 601-607.	7.9	32
147	GWAS for executive function and processing speed suggests involvement of the CADM2 gene. Molecular Psychiatry, 2016, 21, 189-197.	7.9	134
148	A novel Alzheimer disease locus located near the gene encoding tau protein. Molecular Psychiatry, 2016, 21, 108-117.	7.9	260
149	Rare Functional Variant in TM2D3 is Associated with Late-Onset Alzheimer's Disease. PLoS Genetics, 2016, 12, e1006327.	3.5	47
150	O4-05-02: Genome-wide association study of lobar brain volumes. , 2015, 11, P278-P278.		0
151	Heritabilities, proportions of heritabilities explained by GWAS findings, and implications of cross-phenotype effects on PR interval. Human Genetics, 2015, 134, 1211-1219.	3.8	20
152	Large-Scale Genomic Analyses Link Reproductive Aging to Hypothalamic Signaling, Breast Cancer Susceptibility, and BRCA1-Mediated DNA Repair. Obstetrical and Gynecological Survey, 2015, 70, 758-762.	0.4	0
153	Parent-of-Origin Effects of the APOB Gene on Adiposity in Young Adults. PLoS Genetics, 2015, 11, e1005573.	3.5	16
154	Meta-analysis of Genome-wide Association Studies for Neuroticism, and the Polygenic Association With Major Depressive Disorder. JAMA Psychiatry, 2015, 72, 642.	11.0	289
155	The association between lower educational attainment and depression owing to shared genetic effects? Results in ~25â€‰000 subjects. Molecular Psychiatry, 2015, 20, 735-743.	7.9	59
156	Genome-wide association study identifies novel genetic variants contributing to variation in blood metabolite levels. Nature Communications, 2015, 6, 7208.	12.8	178
157	P2-024: Whole-exome sequencing in dutch families with Alzheimer's disease. , 2015, 11, P490-P490.		0
158	O3-13-01: Whole genome sequencing of late-onset Alzheimer's disease patients from genetic isolate. , 2015, 11, P250-P251.		0
159	Genome wide association study identifies variants in NBEA associated with migraine in bipolar disorder. Journal of Affective Disorders, 2015, 172, 453-461.	4.1	15
160	ARHGEF12 influences the risk of glaucoma by increasing intraocular pressure. Human Molecular Genetics, 2015, 24, 2689-2699.	2.9	79
161	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	27.8	1,328
162	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823

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163	The dystrophin gene and cognitive function in the general population. European Journal of Human Genetics, 2015, 23, 837-843.	2.8	6
164	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. Nature Communications, 2015, 6, 5897.	12.8	173
165	Metaâ€analysis of Genomeâ€Wide Association Studies Identifies Novel Loci Associated With Optic Disc Morphology. Genetic Epidemiology, 2015, 39, 207-216.	1.3	72
166	Genetic contributions to variation in general cognitive function: a meta-analysis of genome-wide association studies in the CHARGE consortium (N=53â€‰949). Molecular Psychiatry, 2015, 20, 183-192.	7.9	344
167	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	27.8	173
168	Insight in Genome-Wide Association of Metabolite Quantitative Traits by Exome Sequence Analyses. PLoS Genetics, 2015, 11, e1004835.	3.5	70
169	Genome-wide association study for refractive astigmatism reveals genetic co-determination with spherical equivalent refractive error: the CREAM consortium. Human Genetics, 2015, 134, 131-146.	3.8	24
170	Characteristics of de novo structural changes in the human genome. Genome Research, 2015, 25, 792-801.	5.5	115
171	Genome-wide association analysis on five isolated populations identifies variants of the HLA-DOA gene associated with white wine liking. European Journal of Human Genetics, 2015, 23, 1717-1722.	2.8	12
172	PLD3 variants in population studies. Nature, 2015, 520, E2-E3.	27.8	49
173	Expression and Gene Variation Studies Deny Association of Human HSD3B1 Gene With Aldosterone Production or Blood Pressure. American Journal of Hypertension, 2015, 28, 113-120.	2.0	7
174	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
175	Wholeâ€genome sequencing identifies EN1 as a determinant of bone density and fracture. Nature, 2015, 526, 112-117.	27.8	483
176	Genetic analysis for a shared biological basis between migraine and coronary artery disease. Neurology: Genetics, 2015, 1, e10.	1.9	61
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178	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
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