List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	9.4	924
2	Age-associated cognitive decline. British Medical Bulletin, 2009, 92, 135-152.	2.7	857
3	Common genetic variants influence human subcortical brain structures. Nature, 2015, 520, 224-229.	13.7	772
4	The ENIGMA Consortium: large-scale collaborative analyses of neuroimaging and genetic data. Brain Imaging and Behavior, 2014, 8, 153-182.	1.1	696
5	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. Nature Genetics, 2013, 45, 145-154.	9.4	675
6	Identification of common variants associated with human hippocampal and intracranial volumes. Nature Genetics, 2012, 44, 552-561.	9.4	594
7	Genome-wide association studies establish that human intelligence is highly heritable and polygenic. Molecular Psychiatry, 2011, 16, 996-1005.	4.1	571
8	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. Nature Genetics, 2017, 49, 403-415.	9.4	492
9	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. Nature Genetics, 2011, 43, 1005-1011.	9.4	403
10	New gene functions in megakaryopoiesis and platelet formation. Nature, 2011, 480, 201-208.	13.7	401
11	Genome-wide association and large-scale follow up identifies 16 new loci influencing lung function. Nature Genetics, 2011, 43, 1082-1090.	9.4	367
12	Meta-analysis of genome-wide association studies for personality. Molecular Psychiatry, 2012, 17, 337-349.	4.1	340
13	Seventy-five genetic loci influencing the human red blood cell. Nature, 2012, 492, 369-375.	13.7	320
14	Meta-analyses identify 13 loci associated with age at menopause and highlight DNA repair and immune pathways. Nature Genetics, 2012, 44, 260-268.	9.4	303
15	Genetic foundations of human intelligence. Human Genetics, 2009, 126, 215-232.	1.8	302
16	Novel genetic loci associated with hippocampal volume. Nature Communications, 2017, 8, 13624.	5.8	250
17	Genetic contributions to stability and change in intelligence from childhood to old age. Nature, 2012, 482, 212-215.	13.7	228
18	Novel genetic loci underlying human intracranial volume identified through genome-wide association. Nature Neuroscience, 2016, 19, 1569-1582.	7.1	213

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19	Genetic influences on schizophrenia and subcortical brain volumes: large-scale proof of concept. Nature Neuroscience, 2016, 19, 420-431.	7.1	204
20	A Meta-Analysis of Thyroid-Related Traits Reveals Novel Loci and Gender-Specific Differences in the Regulation of Thyroid Function. PLoS Genetics, 2013, 9, e1003266.	1.5	194
21	Genome-Wide Association Studies Identify <i>CHRNA5/3</i> and <i>HTR4</i> in the Development of Airflow Obstruction. American Journal of Respiratory and Critical Care Medicine, 2012, 186, 622-632.	2.5	164
22	Multiethnic Genome-Wide Association Study of Cerebral White Matter Hyperintensities on MRI. Circulation: Cardiovascular Genetics, 2015, 8, 398-409.	5.1	162
23	Meta-Analysis of Genome-Wide Association Studies Identifies Six New Loci for Serum Calcium Concentrations. PLoS Genetics, 2013, 9, e1003796.	1.5	142
24	A genome-wide association study implicates the APOE locus in nonpathological cognitive ageing. Molecular Psychiatry, 2014, 19, 76-87.	4.1	142
25	Proteomic and genomic evidence implicates the postsynaptic density in schizophrenia. Molecular Psychiatry, 2015, 20, 424-432.	4.1	140
26	Genome-wide association analysis identifies six new loci associated with forced vital capacity. Nature Genetics, 2014, 46, 669-677.	9.4	131
27	Multiethnic Meta-Analysis of Genome-Wide Association Studies in >100 000 Subjects Identifies 23 Fibrinogen-Associated Loci but No Strong Evidence of a Causal Association Between Circulating Fibrinogen and Cardiovascular Disease. Circulation, 2013, 128, 1310-1324.	1.6	128
28	Multi-site study of additive genetic effects on fractional anisotropy of cerebral white matter: Comparing meta and megaanalytical approaches for data pooling. NeuroImage, 2014, 95, 136-150.	2.1	127
29	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. Hypertension, 2017, 70, .	1.3	123
30	Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation. Nature Communications, 2015, 6, 8658.	5.8	108
31	The genetic association between personality and major depression or bipolar disorder. A polygenic score analysis using genome-wide association data. Translational Psychiatry, 2011, 1, e50-e50.	2.4	90
32	Reduced protein synthesis in schizophrenia patient-derived olfactory cells. Translational Psychiatry, 2015, 5, e663-e663.	2.4	89
33	Genetic Associations for Activated Partial Thromboplastin Time and Prothrombin Time, their Gene Expression Profiles, and Risk of Coronary Artery Disease. American Journal of Human Genetics, 2012, 91, 152-162.	2.6	85
34	Common Variants of Large Effect in F12, KNG1, and HRG Are Associated with Activated Partial Thromboplastin Time. American Journal of Human Genetics, 2010, 86, 626-631.	2.6	81
35	Replication study of candidate genes for cognitive abilities: the Lothian Birth Cohort 1936. Genes, Brain and Behavior, 2009, 8, 238-247.	1.1	79
36	Evidence of Inbreeding Depression on Human Height. PLoS Genetics, 2012, 8, e1002655.	1.5	79

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37	A meta-analysis of 120 246 individuals identifies 18 new loci for fibrinogen concentration. Human Molecular Genetics, 2016, 25, 358-370.	1.4	73
38	Discovery and Fine Mapping of Serum Protein Loci through Transethnic Meta-analysis. American Journal of Human Genetics, 2012, 91, 744-753.	2.6	69
39	Modulation of Genetic Associations with Serum Urate Levels by Body-Mass-Index in Humans. PLoS ONE, 2015, 10, e0119752.	1.1	64
40	Genetic Predictors of Fibrin D-Dimer Levels in Healthy Adults. Circulation, 2011, 123, 1864-1872.	1.6	60
41	KNG1 lle581Thr and susceptibility to venous thrombosis. Blood, 2011, 117, 3692-3694.	0.6	53
42	Blood-Based Protein Changes in Childhood Are Associated With Increased Risk for Later Psychotic Disorder: Evidence From a Nested Case–Control Study of the ALSPAC Longitudinal Birth Cohort. Schizophrenia Bulletin, 2018, 44, 297-306.	2.3	53
43	<scp>GWAS</scp> analysis of handgrip and lower body strength in older adults in the <scp>CHARCE</scp> consortium. Aging Cell, 2016, 15, 792-800.	3.0	51
44	Proteomic analysis of the postsynaptic density implicates synaptic function and energy pathways in bipolar disorder. Translational Psychiatry, 2016, 6, e959-e959.	2.4	49
45	Genome-wide association studies identify genetic loci for low von Willebrand factor levels. European Journal of Human Genetics, 2016, 24, 1035-1040.	1.4	45
46	Association of Existing and New Candidate Genes for Anxiety, Depression and Personality Traits in Older People. Behavior Genetics, 2010, 40, 518-532.	1.4	44
47	Causal and Synthetic Associations of Variants in the SERPINA Gene Cluster with Alpha1-antitrypsin Serum Levels. PLoS Genetics, 2013, 9, e1003585.	1.5	43
48	A genome-wide search for genetic influences and biological pathways related to the brain's white matter integrity. Neurobiology of Aging, 2012, 33, 1847.e1-1847.e14.	1.5	37
49	White Matter Integrity in the Splenium of the Corpus Callosum is Related to Successful Cognitive Aging and Partly Mediates the Protective Effect of an Ancestral Polymorphism in ADRB2. Behavior Genetics, 2010, 40, 146-156.	1.4	35
50	Differential expression of the inflammation marker IL12p40 in the at-risk mental state for psychosis: a predictor of transition to psychotic disorder?. BMC Psychiatry, 2016, 16, 326.	1.1	34
51	Variation in the uric acid transporter gene (SLC2A9) and memory performance. Human Molecular Genetics, 2010, 19, 2321-2330.	1.4	33
52	Genes From a Translational Analysis Support a Multifactorial Nature of White Matter Hyperintensities. Stroke, 2015, 46, 341-347.	1.0	33
53	Comparison of HapMap and 1000 Genomes Reference Panels in a Large-Scale Genome-Wide Association Study. PLoS ONE, 2017, 12, e0167742.	1.1	29
54	Evolutionary conserved longevity genes and human cognitive abilities in elderly cohorts. European Journal of Human Genetics, 2012, 20, 341-347.	1.4	24

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55	Haplotype Analysis and a Novel Allele-Sharing Method Refines a Chromosome 4p Locus Linked to Bipolar Affective Disorder. Biological Psychiatry, 2007, 61, 797-805.	0.7	23
56	Genetic Copy Number Variation and General Cognitive Ability. PLoS ONE, 2012, 7, e37385.	1.1	21
57	Genetic Variants Associated With Altered Plasma Levels of C-Reactive Protein are not Associated With Late-Life Cognitive Ability in Four Scottish Samples. Behavior Genetics, 2010, 40, 3-11.	1.4	18
58	A Functional Polymorphism under Positive Evolutionary Selection in ADRB2 is Associated with Human Intelligence with Opposite Effects in the Young and the Elderly. Behavior Genetics, 2009, 39, 15-23.	1.4	16
59	Genetic Associations Between Fibrinogen and Cognitive Performance in Three Scottish Cohorts. Behavior Genetics, 2011, 41, 691-699.	1.4	13
60	Longevity candidate genes and their association with personality traits in the elderly. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2012, 159B, 192-200.	1.1	12
61	A case-control association study and family-based expression analysis of the bipolar disorder candidate gene PI4K2B. Journal of Psychiatric Research, 2009, 43, 1272-1277.	1.5	10
62	A pilot study of urinary peptides as biomarkers for intelligence in old age. Intelligence, 2011, 39, 46-53.	1.6	10
63	ADRB2, brain white matter integrity and cognitive ageing in the Lothian Birth Cohort 1936. Behavior Genetics, 2013, 43, 13-23.	1.4	9
64	No Evidence for Genome-Wide Interactions on Plasma Fibrinogen by Smoking, Alcohol Consumption and Body Mass Index: Results from Meta-Analyses of 80,607 Subjects. PLoS ONE, 2014, 9, e111156.	1.1	8
65	Replication association analysis of S100B and cognitive ageing. Psychiatric Genetics, 2010, 20, 133-134.	0.6	1
66	Combining meta- and mega- analytic approaches for multi-site diffusion imaging based genetic studies: From the ENIGMA-DTI working group. , 2014, , .		0
67	O1.1 ALTERED COMPLEMENT PATHWAY PROTEIN EXPRESSION IS ASSOCIATED WITH PSYCHOTIC EXPERIENCES AT AGE 11 WHICH PERSIST AT AGE 18. Schizophrenia Bulletin, 2018, 44, S72-S72.	2.3	0
68	32.4 ALTERED COMPLEMENT PATHWAY PROTEIN EXPRESSION IS ASSOCIATED WITH PSYCHOTIC EXPERIENCES AT AGE 11 WHICH PERSIST AT AGE 18. Schizophrenia Bulletin, 2018, 44, S53-S53.	2.3	0