David J Porteous

List of Publications by Year in descending order

459 papers	46,917 citations	2795 94 h-index	3173 186 g-index
569 all docs	569 docs citations	569 times ranked	49447 citing authors

#	Article	IF	Citations
1	Loss of SORCS2 is Associated with Neuronal DNA Double-Strand Breaks. Cellular and Molecular Neurobiology, 2023, 43, 237-249.	1.7	4
2	Additive Effects of Stress and Alcohol Exposure on Accelerated Epigenetic Aging in Alcohol Use Disorder. Biological Psychiatry, 2023, 93, 331-341.	0.7	10
3	Methylome-wide association study of early life stressors and adult mental health. Human Molecular Genetics, 2022, 31, 651-664.	1.4	7
4	Pre-pandemic mental health and disruptions to healthcare, economic and housing outcomes during the COVID-19 pandemic: evidence from 12 UK longitudinal studies. British Journal of Psychiatry, 2022, 220, 21-30.	1.7	29
5	Genomeâ€Wide Association Study of NAFLD Using Electronic Health Records. Hepatology Communications, 2022, 6, 297-308.	2.0	33
6	Dissecting the Shared Genetic Architecture of Suicide Attempt, Psychiatric Disorders, and Known Risk Factors. Biological Psychiatry, 2022, 91, 313-327.	0.7	114
7	Cohort Profile: COVIDMENT: COVID-19 cohorts on mental health across six nations. International Journal of Epidemiology, 2022, 51, e108-e122.	0.9	16
8	Genomeâ€wide analysis identifies gallstoneâ€susceptibility loci including genes regulating gastrointestinal motility. Hepatology, 2022, 75, 1081-1094.	3.6	12
9	Epigenome-wide association study of global cortical volumes in generation Scotland: Scottish family health study. Epigenetics, 2022, 17, 1143-1158.	1.3	3
10	Genome-wide interaction study with major depression identifies novel variants associated with cognitive function. Molecular Psychiatry, 2022, 27, 1111-1119.	4.1	24
11	Epigenome-wide association study of alcohol consumption in Nâ€‰=â€‰8161 individuals and relevance to alcohol use disorder pathophysiology: identification of the cystine/glutamate transporter SLC7A11 as a top target. Molecular Psychiatry, 2022, 27, 1754-1764.	4.1	18
12	A proteomic survival predictor for COVID-19 patients in intensive care. , 2022, 1, e0000007.		28
13	Blood-based epigenome-wide analyses of cognitive abilities. Genome Biology, 2022, 23, 26.	3.8	20
14	Epigenetic scores for the circulating proteome as tools for disease prediction. ELife, 2022, 11, .	2.8	37
15	Meta-GWAS Reveals Novel Genetic Variants Associated with Urinary Excretion of Uromodulin. Journal of the American Society of Nephrology: JASN, 2022, 33, 511-529.	3.0	14
16	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals. Nature Genetics, 2022, 54, 437-449.	9.4	215
17	Acute COVID-19 severity and mental health morbidity trajectories in patient populations of six nations: an observational study. Lancet Public Health, The, 2022, 7, e406-e416.	4.7	99
18	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508.	13.7	929

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19	Methylome-wide association study of antidepressant use in Generation Scotland and the Netherlands Twin Register implicates the innate immune system. Molecular Psychiatry, 2022, 27, 1647-1657.	4.1	10
20	Psychological Distress Before and During the COVID-19 Pandemic Among Adults in the United Kingdom Based on Coordinated Analyses of 11 Longitudinal Studies. JAMA Network Open, 2022, 5, e227629.	2.8	116
21	Genomeâ€•and epigenomeâ€wide studies of plasma protein biomarkers for Alzheimer's disease implicate TBCA and TREM2 in disease risk. Alzheimer's and Dementia: Diagnosis, Assessment and Disease Monitoring, 2022, 14, e12280.	1.2	4
22	Complex trait methylation scores in the prediction of major depressive disorder. EBioMedicine, 2022, 79, 104000.	2.7	4
23	Within-sibship genome-wide association analyses decrease bias in estimates of direct genetic effects. Nature Genetics, 2022, 54, 581-592.	9.4	142
24	Alcohol use disorder is associated with DNA methylation-based shortening of telomere length and regulated by TESPA1: implications for aging. Molecular Psychiatry, 2022, 27, 3875-3884.	4.1	7
25	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. Communications Biology, 2022, 5, .	2.0	17
26	Long COVID burden and risk factors in 10 UK longitudinal studies and electronic health records. Nature Communications, 2022, 13, .	5.8	243
27	Genetic and shared couple environmental contributions to smoking and alcohol use in the UK population. Molecular Psychiatry, 2021, 26, 4344-4354.	4.1	10
28	Birth weight associations with DNA methylation differences in an adult population. Epigenetics, 2021, 16, 783-796.	1.3	18
29	Epigenome-wide association study and multi-tissue replication of individuals with alcohol use disorder: evidence for abnormal glucocorticoid signaling pathway gene regulation. Molecular Psychiatry, 2021, 26, 2224-2237.	4.1	32
30	Epigenetic prediction of major depressive disorder. Molecular Psychiatry, 2021, 26, 5112-5123.	4.1	44
31	Polygenic contributions to alcohol use and alcohol use disorders across population-based and clinically ascertained samples. Psychological Medicine, 2021, 51, 1147-1156.	2.7	18
32	The influence of X chromosome variants on trait neuroticism. Molecular Psychiatry, 2021, 26, 483-491.	4.1	17
33	Mental health before and during the COVID-19 pandemic in two longitudinal UK population cohorts. British Journal of Psychiatry, 2021, 218, 334-343.	1.7	330
34	Structural brain correlates of serum and epigenetic markers of inflammation in major depressive disorder. Brain, Behavior, and Immunity, 2021, 92, 39-48.	2.0	53
35	Functional brain defects in a mouse model of a chromosomal t(1;11) translocation that disrupts DISC1 and confers increased risk of psychiatric illness. Translational Psychiatry, 2021, 11, 135.	2.4	3
36	Genome-wide association study of cardiac troponin I in the general population. Human Molecular Genetics, 2021, 30, 2027-2039.	1.4	11

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37	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	9.4	341
38	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. Genome Biology, 2021, 22, 194.	3.8	90
39	Contribution of common risk variants to multiple sclerosis in Orkney and Shetland. European Journal of Human Genetics, 2021, 29, 1701-1709.	1.4	6
40	Sex Differences in Cardiac Troponin I and T and the Prediction of Cardiovascular Events in the General Population. Clinical Chemistry, 2021, 67, 1351-1360.	1.5	30
41	Using symptom-based case predictions to identify host genetic factors that contribute to COVID-19 susceptibility. PLoS ONE, 2021, 16, e0255402.	1.1	6
42	A time-resolved proteomic and prognostic map of COVID-19. Cell Systems, 2021, 12, 780-794.e7.	2.9	125
43	The Genetic Architecture of Depression in Individuals of East Asian Ancestry. JAMA Psychiatry, 2021, 78, 1258.	6.0	88
44	Spectral clustering based on structural magnetic resonance imaging and its relationship with major depressive disorder and cognitive ability. European Journal of Neuroscience, 2021, 54, 6281-6303.	1.2	5
45	Genome-wide methylation data improves dissection of the effect of smoking on body mass index. PLoS Genetics, 2021, 17, e1009750.	1.5	7
46	Genome-wide analysis of gene dosage in 24,092 individuals estimates that 10,000 genes modulate cognitive ability. Molecular Psychiatry, 2021, 26, 2663-2676.	4.1	33
47	Identification of epigenome-wide DNA methylation differences between carriers of APOE Îµ4 and APOE Îµ2 alleles. Genome Medicine, 2021, 13, 1.	3.6	76
48	Genetic mechanisms of critical illness in COVID-19. Nature, 2021, 591, 92-98.	13.7	1,014
49	Hair glucocorticoids are associated with childhood adversity, depressive symptoms and reduced global and lobar grey matter in Generation Scotland. Translational Psychiatry, 2021, 11, 523.	2.4	13
50	SNP and Haplotype Regional Heritability Mapping (SNHap-RHM): Joint Mapping of Common and Rare Variation Affecting Complex Traits. Frontiers in Genetics, 2021, 12, 791712.	1.1	2
51	Lifestyle and Genetic Factors Modify Parent-of-Origin Effects on the Human Methylome. EBioMedicine, 2021, 74, 103730.	2.7	5
52	Association of low-frequency and rare coding variants with information processing speed. Translational Psychiatry, 2021, 11, 613.	2.4	2
53	Genome-wide association study of antidepressant treatment resistance in a population-based cohort using health service prescription data and meta-analysis with GENDEP. Pharmacogenomics Journal, 2020, 20, 329-341.	0.9	45
54	Genetic contributions to two special factors of neuroticism are associated with affluence, higher intelligence, better health, and longer life. Molecular Psychiatry, 2020, 25, 3034-3052.	4.1	60

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55	Genetic stratification of depression by neuroticism: revisiting a diagnostic tradition. Psychological Medicine, 2020, 50, 2526-2535.	2.7	27
56	Factors associated with sharing e-mail information and mental health survey participation in large population cohorts. International Journal of Epidemiology, 2020, 49, 410-421.	0.9	67
57	Classical Human Leukocyte Antigen Alleles and C4 Haplotypes Are Not Significantly Associated With Depression. Biological Psychiatry, 2020, 87, 419-430.	0.7	27
58	Prescreening for European Prevention of Alzheimer Dementia (EPAD) trial-ready cohort: impact of AD risk factors and recruitment settings. Alzheimer's Research and Therapy, 2020, 12, 8.	3.0	12
59	An epigenome-wide association study of sex-specific chronological ageing. Genome Medicine, 2020, 12, 1.	3.6	117
60	Genome-Wide Association Study of Suicide Death and Polygenic Prediction of Clinical Antecedents. American Journal of Psychiatry, 2020, 177, 917-927.	4.0	66
61	Epigenome-Wide Association Study and Multi-Tissue Replication of Individuals With Alcohol Use Disorder: Evidence for Abnormal Glucocorticoid Signaling Pathway Gene Regulation. Biological Psychiatry, 2020, 87, S113.	0.7	3
62	Genetic comorbidity between major depression and cardioâ€metabolic traits, stratified by age at onset of major depression. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2020, 183, 309-330.	1.1	33
63	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. Nature Genetics, 2020, 52, 1314-1332.	9.4	91
64	Chronic obstructive pulmonary disease and related phenotypes: polygenic risk scores in population-based and case-control cohorts. Lancet Respiratory Medicine,the, 2020, 8, 696-708.	5.2	69
65	Epigenetic measures of ageing predict the prevalence and incidence of leading causes of death and disease burden. Clinical Epigenetics, 2020, 12, 115.	1.8	109
66	Epigenomeâ€wide analyses identify DNA methylation signatures of dementia risk. Alzheimer's and Dementia: Diagnosis, Assessment and Disease Monitoring, 2020, 12, e12078.	1.2	8
67	Estimating the effects of copyâ€number variants on intelligence using hierarchical Bayesian models. Genetic Epidemiology, 2020, 44, 825-840.	0.6	1
68	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. Molecular Psychiatry, 2020, 26, 2111-2125.	4.1	17
69	DNA methylation in APOE: The relationship with Alzheimer's and with cardiovascular health. Alzheimer's and Dementia: Translational Research and Clinical Interventions, 2020, 6, e12026.	1.8	14
70	Ultra-High-Throughput Clinical Proteomics Reveals Classifiers of COVID-19 Infection. Cell Systems, 2020, 11, 11-24.e4.	2.9	439
71	Genetic stratification of depression in UK Biobank. Translational Psychiatry, 2020, 10, 163.	2.4	19
72	Blunted medial prefrontal cortico-limbic reward-related effective connectivity and depression. Brain, 2020, 143, 1946-1956.	3.7	54

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73	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	5.8	59
74	Bayesian reassessment of the epigenetic architecture of complex traits. Nature Communications, 2020, 11, 2865.	5.8	43
75	Genome-wide gene-environment analyses of major depressive disorder and reported lifetime traumatic experiences in UK Biobank. Molecular Psychiatry, 2020, 25, 1430-1446.	4.1	116
76	Molecular Genetic Risk for Psychosis Is Associated With Psychosis Risk Symptoms in a Population-Based UK Cohort: Findings From Generation Scotland. Schizophrenia Bulletin, 2020, 46, 1045-1052.	2.3	12
77	The Dementias Platform UK (DPUK) Data Portal. European Journal of Epidemiology, 2020, 35, 601-611.	2.5	45
78	Variants associated with HHIP expression have sex-differential effects on lung function. Wellcome Open Research, 2020, 5, 111.	0.9	3
79	Using a knowledge exchange event to assess study participantsâ€™ attitudes to research in a rapidly evolving research context. Wellcome Open Research, 2020, 5, 24.	0.9	3
80	Using a knowledge exchange event to assess study participantsâ€™ attitudes to research in a rapidly evolving research context. Wellcome Open Research, 2020, 5, 24.	0.9	4
81	Variants associated with HHIP expression have sex-differential effects on lung function. Wellcome Open Research, 2020, 5, 111.	0.9	4
82	Using tree-based methods for detection of geneâ€“gene interactions in the presence of a polygenic signal: simulation study with application to educational attainment in the Generation Scotland Cohort Study. Bioinformatics, 2019, 35, 181-188.	1.8	10
83	New alcohol-related genes suggest shared genetic mechanisms with neuropsychiatric disorders. Nature Human Behaviour, 2019, 3, 950-961.	6.2	75
84	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	5.8	84
85	Investigating genetic links between graphemeâ€“colour synaesthesia and neuropsychiatric traits. Philosophical Transactions of the Royal Society B: Biological Sciences, 2019, 374, 20190026.	1.8	12
86	SU42COMMONALITIES AND DIFFERENCES IN THE GENETIC ARCHITECTURE OF NEUROTICISM AND DEPRESSION. European Neuropsychopharmacology, 2019, 29, S1290.	0.3	0
87	Improved precision of epigenetic clock estimates across tissues and its implication for biological ageing. Genome Medicine, 2019, 11, 54.	3.6	191
88	The genetic landscape of Scotland and the Isles. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 19064-19070.	3.3	24
89	SA91A GENOME-WIDE ASSOCIATION STUDY OF COMPLETED SUICIDE IN UTAH. European Neuropsychopharmacology, 2019, 29, S1238.	0.3	0
90	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	9.4	251

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91	SU51INTERACTIONS BETWEEN OBSTETRIC COMPLICATIONS AND GENETIC LOAD FOR PSYCHIATRIC DISORDERS IMPACT PSYCHOPATHOLOGY IN ADULTHOOD. European Neuropsychopharmacology, 2019, 29, S1294-S1295.	0.3	0
92	SA25RISK FACTORS FOR ENDOPHENOTYPES FOR MDD: INTERACTION DETECTION USING MACHINE LEARNING. European Neuropsychopharmacology, 2019, 29, S1201-S1202.	0.3	0
93	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	5.8	64
94	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	9.4	549
95	THE IDENTIFICATION OF HETEROGENEOUS GENETIC SUBGROUPS FOR MAJOR DEPRESSIVE DISORDER. European Neuropsychopharmacology, 2019, 29, S846.	0.3	2
96	Cardiac Troponin T and Troponin I in the General Population. Circulation, 2019, 139, 2754-2764.	1.6	200
97	Parent of origin genetic effects on methylation in humans are common and influence complex trait variation. Nature Communications, 2019, 10, 1383.	5.8	37
98	An epigenetic score for BMI based on DNA methylation correlates with poor physical health and major disease in the Lothian Birth Cohort. International Journal of Obesity, 2019, 43, 1795-1802.	1.6	25
99	Pharmaco-epidemiology of antidepressant exposure in a UK cohort record-linkage study. Journal of Psychopharmacology, 2019, 33, 482-493.	2.0	11
100	Insulin resistance: Genetic associations with depression and cognition in population based cohorts. Experimental Neurology, 2019, 316, 20-26.	2.0	10
101	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.	1.4	31
102	BEYOND THE TRANSLOCATION: WHOLE GENOME SEQUENCING ANALYSIS OF THE SCOTTISH T(1;11) FAMILY. European Neuropsychopharmacology, 2019, 29, S890.	0.3	0
103	Identification of novel differentially methylated sites with potential as clinical predictors of impaired respiratory function and COPD. EBioMedicine, 2019, 43, 576-586.	2.7	21
104	New genetic signals for lung function highlight pathways and chronic obstructive pulmonary disease associations across multiple ancestries. Nature Genetics, 2019, 51, 481-493.	9.4	350
105	A meta-analysis of genome-wide association studies of epigenetic age acceleration. PLoS Genetics, 2019, 15, e1008104.	1.5	83
106	SA66EPIGENOME-WIDE ASSOCIATION STUDY OF ANTIDEPRESSANT USE. European Neuropsychopharmacology, 2019, 29, S1224.	0.3	0
107	Genome-wide analysis identifies molecular systems and 149 genetic loci associated with income. Nature Communications, 2019, 10, 5741.	5.8	110
108	Association of Whole-Genome and NETRIN1 Signaling Pathwayâ€“Derived Polygenic Risk Scores for Major Depressive Disorder and White Matter Microstructure in the UK Biobank. Biological Psychiatry: Cognitive Neuroscience and Neuroimaging, 2019, 4, 91-100.	1.1	16

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109	Genome-wide meta-analysis of depression identifies 102 independent variants and highlights the importance of the prefrontal brain regions. Nature Neuroscience, 2019, 22, 343-352.	7.1	1,589
110	Assessment of dried blood spots for DNA methylation profiling. Wellcome Open Research, 2019, 4, 44.	0.9	20
111	Cohort profile for the STratifying Resilience and Depression Longitudinally (STRADL) study: A depression-focused investigation of Generation Scotland, using detailed clinical, cognitive, and neuroimaging assessments. Wellcome Open Research, 2019, 4, 185.	0.9	27
112	1461-P: Cardiac Troponin T and Troponin I and Incident Diabetes in the General Population: Generation Scotland Scottish Family Health Study. Diabetes, 2019, 68, .	0.3	0
113	Generation Scotland participant survey on data collection. Wellcome Open Research, 2019, 4, 111.	0.9	2
114	Common schizophrenia alleles are enriched in mutation-intolerant genes and in regions under strong background selection. Nature Genetics, 2018, 50, 381-389.	9.4	1,332
115	Self-reported medication use validated through record linkage to national prescribing data. Journal of Clinical Epidemiology, 2018, 94, 132-142.	2.4	75
116	Genome-wide meta-analyses of stratified depression in Generation Scotland and UK Biobank. Translational Psychiatry, 2018, 8, 9.	2.4	66
117	Genomic analysis of family data reveals additional genetic effects on intelligence and personality. Molecular Psychiatry, 2018, 23, 2347-2362.	4.1	131
118	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. Nature Genetics, 2018, 50, 668-681.	9.4	2,224
119	European Prevention of Alzheimer's Dementia Registry: Recruitment and prescreening approach for a longitudinal cohort and prevention trials. Alzheimer's and Dementia, 2018, 14, 837-842.	0.4	20
120	Phenotypic and genetic analysis of cognitive performance in Major Depressive Disorder in the Generation Scotland: Scottish Family Health Study. Translational Psychiatry, 2018, 8, 63.	2.4	11
121	Altered DNA methylation associated with a translocation linked to major mental illness. NPJ Schizophrenia, 2018, 4, 5.	2.0	9
122	Does Childhood Trauma Moderate Polygenic Risk for Depression? A Meta-analysis of 5765 Subjects From the Psychiatric Genomics Consortium. Biological Psychiatry, 2018, 84, 138-147.	0.7	87
123	Association Between Schizophrenia-Related Polygenic Liability and the Occurrence and Level of Mood-Incongruent Psychotic Symptoms in Bipolar Disorder. JAMA Psychiatry, 2018, 75, 28.	6.0	91
124	Epigenetic signatures of starting and stopping smoking. EBioMedicine, 2018, 37, 214-220.	2.7	67
125	Epigenetic prediction of complex traits and death. Genome Biology, 2018, 19, 136.	3.8	146
126	DISC1 regulates N-methyl-D-aspartate receptor dynamics: abnormalities induced by a Disc1 mutation modelling a translocation linked to major mental illness. Translational Psychiatry, 2018, 8, 184.	2.4	21

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127	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. Nature Communications, 2018, 9, 2098.	5.8	484
128	GWAS on family history of Alzheimerâ€™s disease. Translational Psychiatry, 2018, 8, 99.	2.4	406
129	Investigating the relationship between DNA methylation age acceleration and risk factors for Alzheimer's disease. Alzheimer's and Dementia: Diagnosis, Assessment and Disease Monitoring, 2018, 10, 429-437.	1.2	93
130	Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals. Nature Genetics, 2018, 50, 1112-1121.	9.4	1,835
131	Analysis of shared heritability in common disorders of the brain. Science, 2018, 360, .	6.0	1,085
132	DNA Methylation Signatures of Depressive Symptoms in Middle-aged and Elderly Persons. JAMA Psychiatry, 2018, 75, 949.	6.0	78
133	Common variants on 6q16.2, 12q24.31 and 16p13.3 are associated with major depressive disorder. Neuropsychopharmacology, 2018, 43, 2146-2153.	2.8	36
134	Comparison between High-Sensitivity Cardiac Troponin T and Cardiac Troponin I in a Large General Population Cohort. Clinical Chemistry, 2018, 64, 1607-1616.	1.5	101
135	Exploring causality in the association between circulating 25-hydroxyvitamin D and colorectal cancer risk: a large Mendelian randomisation study. BMC Medicine, 2018, 16, 142.	2.3	62
136	DNA sequence-level analyses reveal potential phenotypic modifiers in a large family with psychiatric disorders. Molecular Psychiatry, 2018, 23, 2254-2265.	4.1	19
137	Multi-ethnic genome-wide association study for atrial fibrillation. Nature Genetics, 2018, 50, 1225-1233.	9.4	552
138	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. PLoS ONE, 2018, 13, e0198166.	1.1	94
139	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 2018, 3, 4.	0.9	19
140	Genetic and environmental determinants of stressful life events and their overlap with depression and neuroticism. Wellcome Open Research, 2018, 3, 11.	0.9	15
141	Genetic and environmental determinants of stressful life events and their overlap with depression and neuroticism. Wellcome Open Research, 2018, 3, 11.	0.9	19
142	A Combined Pathway and Regional Heritability Analysis Indicates NETRIN1 Pathway Is Associated With Major Depressive Disorder. Biological Psychiatry, 2017, 81, 336-346.	0.7	32
143	Genome-wide Association for Major Depression Through Age at Onset Stratification: Major Depressive Disorder Working Group of the Psychiatric Genomics Consortium. Biological Psychiatry, 2017, 81, 325-335.	0.7	175
144	Evidence for large-scale gene-by-smoking interaction effects on pulmonary function. International Journal of Epidemiology, 2017, 46, dyw318.	0.9	36

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145	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
146	Exploration of haplotype research consortium imputation for genome-wide association studies in 20,032 Generation Scotland participants. Genome Medicine, 2017, 9, 23.	3.6	110
147	Genome-wide association analyses for lung function and chronic obstructive pulmonary disease identify new loci and potential druggable targets. Nature Genetics, 2017, 49, 416-425.	9.4	257
148	Discovery of novel heart rate-associated loci using the Exome Chip. Human Molecular Genetics, 2017, 26, 2346-2363.	1.4	29
149	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.	9.4	426
150	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. Nature Genetics, 2017, 49, 946-952.	9.4	279
151	911. Gene-By-Environment Analyses Reveal Obstetric Complications Interact with Genetics to Influence Psychopathology and Personality. Biological Psychiatry, 2017, 81, S368.	0.7	1
152	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. Nature Communications, 2017, 8, 14977.	5.8	169
153	Validation of Surrogates of Urine Osmolality in Population Studies. American Journal of Nephrology, 2017, 46, 26-36.	1.4	18
154	SOS2 and ACP1 Loci Identified through Large-Scale Exome Chip Analysis Regulate Kidney Development and Function. Journal of the American Society of Nephrology: JASN, 2017, 28, 981-994.	3.0	39
155	Genome-wide Regional Heritability Mapping Identifies a Locus Within the TOX2 Gene Associated With Major Depressive Disorder. Biological Psychiatry, 2017, 82, 312-321.	0.7	26
156	CNV-association meta-analysis in 191,161 European adults reveals new loci associated with anthropometric traits. Nature Communications, 2017, 8, 744.	5.8	64
157	Regional variation in health is predominantly driven by lifestyle rather than genetics. Nature Communications, 2017, 8, 801.	5.8	15
158	Inherited Chromosomally Integrated Human Herpesvirus 6 Genomes Are Ancient, Intact, and Potentially Able To Reactivate from Telomeres. Journal of Virology, 2017, 91, .	1.5	36
159	536. Cognitive Performance in Major Depressive Disorder in Generation Scotland: The Scottish Family Health Study (GS:SFHS). Biological Psychiatry, 2017, 81, S217.	0.7	0
160	Genome-wide haplotype-based association analysis of major depressive disorder in Generation Scotland and UK Biobank. Translational Psychiatry, 2017, 7, 1263.	2.4	23
161	Investigating shared aetiology between type 2 diabetes and major depressive disorder in a population based cohort. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2017, 174, 227-234.	1.1	27
162	Genetic Stratification to Identify Risk Groups for Alzheimerâ€™s Disease. Journal of Alzheimer's Disease, 2017, 57, 275-283.	1.2	33

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163	Genetic prediction of male pattern baldness. PLoS Genetics, 2017, 13, e1006594.	1.5	89
164	Haplotype-based association analysis of general cognitive ability in Generation Scotland, the English Longitudinal Study of Ageing, and UK Biobank. Wellcome Open Research, 2017, 2, 61.	0.9	4
165	Electronic health record and genome-wide genetic data in Generation Scotland participants. Wellcome Open Research, 2017, 2, 85.	0.9	14
166	Genome-wide physical activity interactions in adiposity â€• A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	1.5	158
167	Chronic pain, depression and cardiovascular disease linked through a shared genetic predisposition: Analysis of a family-based cohort and twin study. PLoS ONE, 2017, 12, e0170653.	1.1	71
168	Balanced translocation linked to psychiatric disorder, glutamate, and cortical structure/function. NPJ Schizophrenia, 2016, 2, 16024.	2.0	41
169	Differential effects of the APOE e4 allele on different domains of cognitive ability across the life-course. European Journal of Human Genetics, 2016, 24, 919-923.	1.4	54
170	Identification of polymorphic and off-target probe binding sites on the Illumina Infinium MethylationEPIC BeadChip. Genomics Data, 2016, 9, 22-24.	1.3	264
171	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	13.7	1,204
172	Data science for mental health: a UK perspective on a global challenge. Lancet Psychiatry,the, 2016, 3, 993-998.	3.7	47
173	Polygenic risk for alcohol dependence associates with alcohol consumption, cognitive function and social deprivation in a populationâ€based cohort. Addiction Biology, 2016, 21, 469-480.	1.4	27
174	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	9.4	261
175	Shared Genetics and Couple-Associated Environment Are Major Contributors to the Risk of Both Clinical and Self-Declared Depression. EBioMedicine, 2016, 14, 161-167.	2.7	32
176	Genetic variants linked to education predict longevity. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13366-13371.	3.3	110
177	Timing, rates and spectra of human germline mutation. Nature Genetics, 2016, 48, 126-133.	9.4	502
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