## David J Porteous

List of Publications by Year in descending order

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459 papers 46,917 citations

94 h-index 186 g-index

569 all docs 569 does citations

569 times ranked 49447 citing authors

#	Article	IF	CITATIONS
1	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
2	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
3	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
4	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
5	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	13.7	1,204
6	Analysis of shared heritability in common disorders of the brain. Science, 2018, 360, .	6.0	1,085
7	The UK10K project identifies rare variants in health and disease. Nature, 2015, 526, 82-90.	13.7	1,014
8	Genetic mechanisms of critical illness in COVID-19. Nature, 2021, 591, 92-98.	13.7	1,014
9	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508.	13.7	929
10	The candidate Wilms' tumour gene is involved in genitourinary development. Nature, 1990, 346, 194-197.	13.7	814
10	The candidate Wilms' tumour gene is involved in genitourinary development. Nature, 1990, 346, 194-197.  Liposome-mediated CFTR gene transfer to the nasal epithelium of patients with cystic fibrosis. Nature Medicine, 1995, 1, 39-46.	13.7	814 736
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11	Liposome-mediated CFTR gene transfer to the nasal epithelium of patients with cystic fibrosis. Nature Medicine, 1995, 1, 39-46.  DISC1 and PDE4B Are Interacting Genetic Factors in Schizophrenia That Regulate cAMP Signaling.	15.2	736
11 12	Liposome-mediated CFTR gene transfer to the nasal epithelium of patients with cystic fibrosis. Nature Medicine, 1995, 1, 39-46.  DISC1 and PDE4B Are Interacting Genetic Factors in Schizophrenia That Regulate cAMP Signaling. Science, 2005, 310, 1187-1191.	15.2 6.0	736 605
11 12 13	Liposome-mediated CFTR gene transfer to the nasal epithelium of patients with cystic fibrosis. Nature Medicine, 1995, 1, 39-46.  DISC1 and PDE4B Are Interacting Genetic Factors in Schizophrenia That Regulate cAMP Signaling. Science, 2005, 310, 1187-1191.  Identification of common variants associated with human hippocampal and intracranial volumes. Nature Genetics, 2012, 44, 552-561.  Genome-wide association studies establish that human intelligence is highly heritable and polygenic.	15.2 6.0 9.4	736 605 594
11 12 13 14	Liposome-mediated CFTR gene transfer to the nasal epithelium of patients with cystic fibrosis. Nature Medicine, 1995, 1, 39-46.  DISC1 and PDE4B Are Interacting Genetic Factors in Schizophrenia That Regulate cAMP Signaling. Science, 2005, 310, 1187-1191.  Identification of common variants associated with human hippocampal and intracranial volumes. Nature Genetics, 2012, 44, 552-561.  Genome-wide association studies establish that human intelligence is highly heritable and polygenic. Molecular Psychiatry, 2011, 16, 996-1005.	15.2 6.0 9.4 4.1	736 605 594 571
11 12 13 14	Liposome-mediated CFTR gene transfer to the nasal epithelium of patients with cystic fibrosis. Nature Medicine, 1995, 1, 39-46.  DISC1 and PDE4B Are Interacting Genetic Factors in Schizophrenia That Regulate cAMP Signaling. Science, 2005, 310, 1187-1191.  Identification of common variants associated with human hippocampal and intracranial volumes. Nature Genetics, 2012, 44, 552-561.  Genome-wide association studies establish that human intelligence is highly heritable and polygenic. Molecular Psychiatry, 2011, 16, 996-1005.  The DISC locus in psychiatric illness. Molecular Psychiatry, 2008, 13, 36-64.	15.2 6.0 9.4 4.1	736 605 594 571

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19	Timing, rates and spectra of human germline mutation. Nature Genetics, 2016, 48, 126-133.	9.4	502
20	Behavioral Phenotypes of Disc1 Missense Mutations in Mice. Neuron, 2007, 54, 387-402.	3.8	499
21	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
22	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. Nature Communications, 2018, 9, 2098.	5.8	484
23	Ultra-High-Throughput Clinical Proteomics Reveals Classifiers of COVID-19 Infection. Cell Systems, 2020, 11, 11-24.e4.	2.9	439
24	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
25	Non–invasive liposome–mediated gene delivery can correct the ion transport defect in cystic fibrosis mutant mice. Nature Genetics, 1993, 5, 135-142.	9.4	425
26	GWAS on family history of Alzheimer's disease. Translational Psychiatry, 2018, 8, 99.	2.4	406
27	New gene functions in megakaryopoiesis and platelet formation. Nature, 2011, 480, 201-208.	13.7	401
28	The Lothian Birth Cohort 1936: a study to examine influences on cognitive ageing from age 11 to age 70 and beyond. BMC Geriatrics, 2007, 7, 28.	1.1	399
29	Genome-wide association and large-scale follow up identifies 16 new loci influencing lung function. Nature Genetics, 2011, 43, 1082-1090.	9.4	367
30	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. Nature Genetics, 2015, 47, 1294-1303.	9.4	357
31	Cohort Profile: Generation Scotland: Scottish Family Health Study (GS:SFHS). The study, its participants and their potential for genetic research on health and illness. International Journal of Epidemiology, 2013, 42, 689-700.	0.9	353
32	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
33	Repeated nebulisation of non-viral CFTR gene therapy in patients with cystic fibrosis: a randomised, double-blind, placebo-controlled, phase 2b trial. Lancet Respiratory Medicine, the, 2015, 3, 684-691.	5.2	344
34	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	9.4	341
35	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
36	Cystic fibrosis in the mouse by targeted insertional mutagenesis. Nature, 1992, 359, 211-215.	13.7	294

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37	Meta-analysis of Genome-wide Association Studies for Neuroticism, and the Polygenic Association With Major Depressive Disorder. JAMA Psychiatry, 2015, 72, 642.	6.0	289
38	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
39	CpG-free plasmids confer reduced inflammation and sustained pulmonary gene expression. Nature Biotechnology, 2008, 26, 549-551.	9.4	269
40	Identification of polymorphic and off-target probe binding sites on the Illumina Infinium MethylationEPIC BeadChip. Genomics Data, 2016, 9, 22-24.	1.3	264
41	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	9.4	261
42	A locus for bipolar affective disorder on chromosome 4p. Nature Genetics, 1996, 12, 427-430.	9.4	258
43	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
44	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	9.4	251
45	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.	3.3	244
46	Long COVID burden and risk factors in 10 UK longitudinal studies and electronic health records. Nature Communications, 2022, 13, .	5.8	243
47	Genetic contributions to stability and change in intelligence from childhood to old age. Nature, 2012, 482, 212-215.	13.7	228
48	Generation Scotland: the Scottish Family Health Study; a new resource for researching genes and heritability. BMC Medical Genetics, 2006, 7, 74.	2.1	227
49	A neuregulin 1 variant associated with abnormal cortical function and psychotic symptoms. Nature Neuroscience, 2006, 9, 1477-1478.	7.1	226
50	SUSPECTS: enabling fast and effective prioritization of positional candidates. Bioinformatics, 2006, 22, 773-774.	1.8	222
51	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
52	Speeding disease gene discovery by sequence based candidate prioritization. BMC Bioinformatics, 2005, 6, 55.	1.2	208
53	Cardiac Troponin T and Troponin I in the General Population. Circulation, 2019, 139, 2754-2764.	1.6	200
54	Splinkerettesâ€"improved vectorettes for greater efficiency in PCR walking. Nucleic Acids Research, 1995, 23, 1644-1645.	6.5	192

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55	Improved precision of epigenetic clock estimates across tissues and its implication for biological ageing. Genome Medicine, 2019, 11, 54.	3.6	191
56	The effects of a neuregulin 1 variant on white matter density and integrity. Molecular Psychiatry, 2008, 13, 1054-1059.	4.1	190
57	Genomic structure and localisation within a linkage hotspot of Disrupted In Schizophrenia 1, a gene disrupted by a translocation segregating with schizophrenia. Molecular Psychiatry, 2001, 6, 173-178.	4.1	184
58	Meta-analysis of Genome-Wide Association Studies for Extraversion: Findings from the Genetics of Personality Consortium. Behavior Genetics, 2016, 46, 170-182.	1.4	178
59	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
60	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	13.7	173
61	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
62	DISC1-binding proteins in neural development, signalling and schizophrenia. Neuropharmacology, 2012, 62, 1230-1241.	2.0	168
63	Sputum Proteomics in Inflammatory and Suppurative Respiratory Diseases. American Journal of Respiratory and Critical Care Medicine, 2008, 178, 444-452.	2.5	166
64	Association between the TRAX/DISC locus and both bipolar disorder and schizophrenia in the Scottish population. Molecular Psychiatry, 2005, 10, 657-668.	4.1	165
65	The Genetics and Biology of Disc1—An Emerging Role in Psychosis and Cognition. Biological Psychiatry, 2006, 60, 123-131.	0.7	164
66	Genome-wide physical activity interactions in adiposity ― A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	1.5	158
67	Molecular genetic contributions to socioeconomic status and intelligence. Intelligence, 2014, 44, 26-32.	1.6	156
68	Yeast two-hybrid screens implicate DISC1 in brain development and function. Biochemical and Biophysical Research Communications, 2003, 311, 1019-1025.	1.0	153
69	Investigating the possible causal association of smoking with depression and anxiety using Mendelian randomisation meta-analysis: the CARTA consortium. BMJ Open, 2014, 4, e006141.	0.8	150
70	Isoform-Selective Susceptibility of DISC1/Phosphodiesterase-4 Complexes to Dissociation by Elevated Intracellular cAMP Levels. Journal of Neuroscience, 2007, 27, 9513-9524.	1.7	149
71	Epigenetic prediction of complex traits and death. Genome Biology, 2018, 19, 136.	3.8	146
72	Within-sibship genome-wide association analyses decrease bias in estimates of direct genetic effects. Nature Genetics, 2022, 54, 581-592.	9.4	142

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73	DISC1 association, heterogeneity and interplay in schizophrenia and bipolar disorder. Molecular Psychiatry, 2009, 14, 865-873.	4.1	140
74	Disrupted in Schizophrenia 1 (DISC1) is a multicompartmentalized protein that predominantly localizes to mitochondria. Molecular and Cellular Neurosciences, 2004, 26, 112-122.	1.0	137
75	Lung disease in the cystic fibrosis mouse exposed to bacterial pathogens. Nature Genetics, 1995, 9, 351-357.	9.4	131
76	Genome-wide association analysis identifies six new loci associated with forced vital capacity. Nature Genetics, 2014, 46, 669-677.	9.4	131
77	Systems genetics identifies a convergent gene network for cognition and neurodevelopmental disease. Nature Neuroscience, 2016, 19, 223-232.	7.1	131
78	Genomic analysis of family data reveals additional genetic effects on intelligence and personality. Molecular Psychiatry, 2018, 23, 2347-2362.	4.1	131
79	DISC1 at 10: connecting psychiatric genetics and neuroscience. Trends in Molecular Medicine, 2011, 17, 699-706.	3.5	126
80	A time-resolved proteomic and prognostic map of COVID-19. Cell Systems, 2021, 12, 780-794.e7.	2.9	125
81	Changes in physiological, functional and structural markers of cystic fibrosis lung disease with treatment of a pulmonary exacerbation. Thorax, 2013, 68, 532-539.	2.7	121
82	Polygenic Risk for Schizophrenia Is Associated with Cognitive Change Between Childhood and Old Age. Biological Psychiatry, 2013, 73, 938-943.	0.7	118
83	Sputum and serum calprotectin are useful biomarkers during CF exacerbation. Journal of Cystic Fibrosis, 2010, 9, 193-198.	0.3	117
84	An epigenome-wide association study of sex-specific chronological ageing. Genome Medicine, 2020, 12, 1.	3.6	117
85	Identification of polymorphisms within Disrupted in Schizophrenia 1 and Disrupted in Schizophrenia 2, and an investigation of their association with schizophrenia and bipolar affective disorder. Psychiatric Genetics, 2001, 11, 71-78.	0.6	116
86	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
87	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
88	SNP genotyping on pooled DNAs: comparison of genotyping technologies and a semi automated method for data storage and analysis. Nucleic Acids Research, 2002, 30, 74e-74.	<b>6.</b> 5	114
89	Dissecting the Shared Genetic Architecture of Suicide Attempt, Psychiatric Disorders, and Known Risk Factors. Biological Psychiatry, 2022, 91, 313-327.	0.7	114
90	Role of DISC1 in neural development and schizophrenia. Current Opinion in Neurobiology, 2007, 17, 95-102.	2.0	113

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91	Association of Neuregulin 1 with schizophrenia and bipolar disorder in a second cohort from the Scottish population. Molecular Psychiatry, 2007, 12, 94-104.	4.1	112
92	Genomeâ€wide association uncovers shared genetic effects among personality traits and mood states. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2012, 159B, 684-695.	1.1	112
93	Chromosomal abnormalities and mental illness. Molecular Psychiatry, 2003, 8, 275-287.	4.1	111
94	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
95	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
96	Genome-wide analysis identifies molecular systems and 149 genetic loci associated with income. Nature Communications, 2019, 10, 5741.	5.8	110
97	Relationship of Catechol-O-Methyltransferase Variants to Brain Structure and Function in a Population at High Risk of Psychosis. Biological Psychiatry, 2007, 61, 1127-1134.	0.7	109
98	DISC1: Structure, Function, and Therapeutic Potential for Major Mental Illness. ACS Chemical Neuroscience, 2011, 2, 609-632.	1.7	109
99	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
100	HIV-1 Tat protein transduction domain peptide facilitates gene transfer in combination with cationic liposomes. Journal of Controlled Release, 2004, 99, 435-444.	4.8	107
101	Chromosomal Location and Genomic Structure of the Human Translin-Associated Factor X Gene (TRAX; TSNAX) Revealed by Intergenic Splicing to DISC1, a Gene Disrupted by a Translocation Segregating with Schizophrenia. Genomics, 2000, 67, 69-77.	1.3	106
102	Cytogenetic and genetic evidence supports a role for the kainate-type glutamate receptor gene, GRIK4, in schizophrenia and bipolar disorder. Molecular Psychiatry, 2006, 11, 847-857.	4.1	105
103	A Cytogenetic Abnormality and Rare Coding Variants Identify ABCA13 as a Candidate Gene in Schizophrenia, Bipolar Disorder, and Depression. American Journal of Human Genetics, 2009, 85, 833-846.	2.6	102
104	Epidemiology and Heritability of Major Depressive Disorder, Stratified by Age of Onset, Sex, and Illness Course in Generation Scotland: Scottish Family Health Study (GS:SFHS). PLoS ONE, 2015, 10, e0142197.	1.1	101
105	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
106	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
107	Sex-specific association between bipolar affective disorder in women and GPR50, an X-linked orphan G protein-coupled receptor. Molecular Psychiatry, 2005, 10, 470-478.	4.1	98
108	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

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109	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
110	A genome scan and follow-up study identify a bipolar disorder susceptibility locus on chromosome 1q42. Molecular Psychiatry, 2004, 9, 1083-1090.	4.1	92
111	Disrupted In Schizophrenia 1 (DISC1): Subcellular targeting and induction of ring mitochondria. Molecular and Cellular Neurosciences, 2005, 30, 477-484.	1.0	92
112	Are some genetic risk factors common to schizophrenia, bipolar disorder and depression? evidence from DISC1, GRIK4 and NRG1. Neurotoxicity Research, 2007, $11$ , $73-83$ .	1.3	91
113	Interacting haplotypes at the NPAS3 locus alter risk of schizophrenia and bipolar disorder. Molecular Psychiatry, 2009, 14, 874-884.	4.1	91
114	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
115	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
116	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. Genome Biology, 2021, 22, 194.	3.8	90
117	Sputum Trace Metals Are Biomarkers of Inflammatory and Suppurative Lung Disease. Chest, 2010, 137, 635-641.	0.4	89
118	DISC1 in Schizophrenia: Genetic Mouse Models and Human Genomic Imaging. Schizophrenia Bulletin, 2011, 37, 14-20.	2.3	89
119	Genetic prediction of male pattern baldness. PLoS Genetics, 2017, 13, e1006594.	1.5	89
120	The PDE4B gene confers sex-specific protection against schizophrenia. Psychiatric Genetics, 2007, 17, 129-133.	0.6	88
121	Disrupted in schizophrenia 1 and phosphodiesterase 4B: towards an understanding of psychiatric illness. Journal of Physiology, 2007, 584, 401-405.	1.3	88
122	The Genetic Architecture of Depression in Individuals of East Asian Ancestry. JAMA Psychiatry, 2021, 78, 1258.	6.0	88
123	The genomic organisation of the metabotropic glutamate receptor subtype 5 gene, and its association with schizophrenia. Molecular Psychiatry, 2001, 6, 311-314.	4.1	87
124	DISC1, PDE4B, and NDE1 at the centrosome and synapse. Biochemical and Biophysical Research Communications, 2008, 377, 1091-1096.	1.0	87
125	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
126	Adenoviral Augmentation of Elafin Protects the Lung Against Acute Injury Mediated by Activated Neutrophils and Bacterial Infection. Journal of Immunology, 2001, 167, 1778-1786.	0.4	86

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127	Assessment of F/HN-Pseudotyped Lentivirus as a Clinically Relevant Vector for Lung Gene Therapy. American Journal of Respiratory and Critical Care Medicine, 2012, 186, 846-856.	2.5	86
128	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
129	Genes and Schizophrenia: Beyond Schizophrenia: The Role of DISC1 in Major Mental Illness. Schizophrenia Bulletin, 2005, 32, 409-416.	2.3	84
130	DISC1 complexes with TRAK1 and Miro1 to modulate anterograde axonal mitochondrial trafficking. Human Molecular Genetics, 2014, 23, 906-919.	1.4	84
131	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	5.8	84
132	Evolutionary constraints on the Disrupted in Schizophrenia locus. Genomics, 2003, 81, 67-77.	1.3	83
133	A meta-analysis of genome-wide association studies of epigenetic age acceleration. PLoS Genetics, 2019, 15, e1008104.	1.5	83
134	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
135	Novel Approach Identifies SNPs in SLC2A10 and KCNK9 with Evidence for Parent-of-Origin Effect on Body Mass Index. PLoS Genetics, 2014, 10, e1004508.	1.5	80
136	Evidence of Inbreeding Depression on Human Height. PLoS Genetics, 2012, 8, e1002655.	1.5	79
137	DNA Methylation Signatures of Depressive Symptoms in Middle-aged and Elderly Persons. JAMA Psychiatry, 2018, 75, 949.	6.0	78
138	Identification of epigenome-wide DNA methylation differences between carriers of APOE $\hat{l}\mu4$ and APOE $\hat{l}\mu2$ alleles. Genome Medicine, 2021, 13, 1.	3.6	76
139	Heritability of chronic pain in 2195 extended families. European Journal of Pain, 2012, 16, 1053-1063.	1.4	75
140	Self-reported medication use validated through record linkage to national prescribing data. Journal of Clinical Epidemiology, 2018, 94, 132-142.	2.4	75
141	New alcohol-related genes suggest shared genetic mechanisms with neuropsychiatric disorders. Nature Human Behaviour, 2019, 3, 950-961.	6.2	75
142	Disruption of a brain transcription factor, NPAS3, is associated with schizophrenia and learning disability. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2005, 136B, 26-32.	1.1	74
143	Enhanced Lung Gene Expression After Aerosol Delivery of Concentrated pDNA/PEI Complexes. Molecular Therapy, 2008, 16, 1283-1290.	3.7	73
144	The DISC1 Pathway Modulates Expression of Neurodevelopmental, Synaptogenic and Sensory Perception Genes. PLoS ONE, 2009, 4, e4906.	1.1	72

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145	PKA Phosphorylation of NDE1 Is DISC1/PDE4 Dependent and Modulates Its Interaction with LIS1 and NDEL1. Journal of Neuroscience, 2011, 31, 9043-9054.	1.7	72
146	Pedigree- and SNP-Associated Genetics and Recent Environment are the Major Contributors to Anthropometric and Cardiometabolic Trait Variation. PLoS Genetics, 2016, 12, e1005804.	1.5	72
147	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
148	Whole genome association scan for genetic polymorphisms influencing information processing speed. Biological Psychology, 2011, 86, 193-202.	1.1	70
149	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
150	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.	0.7	67
151	Epigenetic signatures of starting and stopping smoking. EBioMedicine, 2018, 37, 214-220.	2.7	67
152	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
153	A randomised, double-blind, placebo-controlled phase IIB clinical trial of repeated application of gene therapy in patients with cystic fibrosis: TableÂ1. Thorax, 2013, 68, 1075-1077.	2.7	66
154	Genome-wide meta-analyses of stratified depression in Generation Scotland and UK Biobank. Translational Psychiatry, 2018, 8, 9.	2.4	66
155	Genome-Wide Association Study of Suicide Death and Polygenic Prediction of Clinical Antecedents. American Journal of Psychiatry, 2020, 177, 917-927.	4.0	66
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	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	5.8	64
158	Polygenic Risk for Alzheimer's Disease is not Associated with Cognitive Ability or Cognitive Aging in Non-Demented Older People. Journal of Alzheimer's Disease, 2014, 39, 565-574.	1.2	63
159	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
160	A t(1;11) translocation linked to schizophrenia and affective disorders gives rise to aberrant chimeric DISC1 transcripts that encode structurally altered, deleterious mitochondrial proteins. Human Molecular Genetics, 2012, 21, 3374-3386.	1.4	61
161	Cardiovascular risk factors associated with the metabolic syndrome are more prevalent in people reporting chronic pain: Results from a cross-sectional general population study. Pain, 2013, 154, 1595-1602.	2.0	61
162	Structural Models of Human eEF1A1 and eEF1A2 Reveal Two Distinct Surface Clusters of Sequence Variation and Potential Differences in Phosphorylation. PLoS ONE, 2009, 4, e6315.	1.1	60

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163	Genetic Predictors of Fibrin D-Dimer Levels in Healthy Adults. Circulation, 2011, 123, 1864-1872.	1.6	60
164	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
165	Genetic and Environmental Risk for Chronic Pain and the Contribution of Risk Variants for Major Depressive Disorder: A Family-Based Mixed-Model Analysis. PLoS Medicine, 2016, 13, e1002090.	3.9	60
166	Subcellular targeting of DISC1 is dependent on a domain independent from the Nudel binding site. Molecular and Cellular Neurosciences, 2005, 28, 613-624.	1.0	59
167	Differential global gene expression in cystic fibrosis nasal and bronchial epithelium. Genomics, 2011, 98, 327-336.	1.3	59
168	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	5.8	59
169	Alzheimer's disease susceptibility genes APOE and TOMM40, and brain white matter integrity in the Lothian Birth Cohort 1936. Neurobiology of Aging, 2014, 35, 1513.e25-1513.e33.	1.5	58
170	YAC mapping by FISH using Alu-PCR-generated probes. Genomics, 1992, 13, 726-730.	1.3	55
171	Optimizing Aerosol Gene Delivery and Expression in the Ovine Lung. Molecular Therapy, 2007, 15, 348-354.	3.7	54
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