Naomi R Wray

List of Publications by Year in Descending Order

399 papers	42,488 citations	93 h-index	201 g-index
472 ext. papers	55,930 ext. citations	10.6 avg, IF	7.65 L-index

#	Paper	IF	Citations
399	Impact of CYP2C19 metaboliser status on SSRI response: a retrospective study of 9500 participants of the Australian Genetics of Depression Study.. *Pharmacogenomics Journal*, **2022**,	3.5	1
398	Genome-wide identification of the genetic basis of amyotrophic lateral sclerosis.. *Neuron*, **2022**,	13.9	8
397	Functional characterisation of the amyotrophic lateral sclerosis risk locus GPX3/TNIP1.. *Genome Medicine*, **2022**, 14, 7	14.4	0
396	Investigating the phenotypic and genetic associations between personality traits and suicidal behavior across major mental health diagnoses.. *European Archives of Psychiatry and Clinical Neuroscience*, **2022**, 1	5.1	0
395	Genome-wide study of DNA methylation shows alterations in metabolic, inflammatory, and cholesterol pathways in ALS.. *Science Translational Medicine*, **2022**, 14, eabj0264	17.5	4
394	Mapping genomic loci implicates genes and synaptic biology in schizophrenia.. *Nature*, **2022**,	50.4	35
393	Comprehensive genetic analysis of the human lipidome identifies loci associated with lipid homeostasis with links to coronary artery disease. *Nature Communications*, **2022**, 13,	17.4	5
392	Common and rare variant association analyses in amyotrophic lateral sclerosis identify 15 risk loci with distinct genetic architectures and neuron-specific biology. *Nature Genetics*, **2021**, 53, 1636-1648	36.3	19
391	Understanding genetic risk factors for common side effects of antidepressant medications. *Communications Medicine*, **2021**, 1,		2
390	Autism-related dietary preferences mediate autism-gut microbiome associations. *Cell*, **2021**, 184, 5916-5931.e17	38.6	30
389	Polygenic burden could explain high rates of affective disorders in a community with restricted founder population. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2021**, 186, 367-375	3.5	
388	The Australian Genetics of Depression Study: New Risk Loci and Dissecting Heterogeneity Between Subtypes.. *Biological Psychiatry*, **2021**,	7.9	2
387	Conditional GWAS analysis to identify disorder-specific SNPs for psychiatric disorders. *Molecular Psychiatry*, **2021**, 26, 2070-2081	15.1	19
386	Meta-analysis of genome-wide DNA methylation identifies shared associations across neurodegenerative disorders. *Genome Biology*, **2021**, 22, 90	18.3	6
385	Genome-wide gene expression changes in postpartum depression point towards an altered immune landscape. *Translational Psychiatry*, **2021**, 11, 155	8.6	5
384	Polygenic risk score analysis for amyotrophic lateral sclerosis leveraging cognitive performance, educational attainment and schizophrenia. *European Journal of Human Genetics*, **2021**,	5.3	7
383	Comorbid Chronic Pain and Depression: Shared Risk Factors and Differential Antidepressant Effectiveness. *Frontiers in Psychiatry*, **2021**, 12, 643609	5	13

382	Risk of Early-Onset Depression Associated With Polygenic Liability, Parental Psychiatric History, and Socioeconomic Status. *JAMA Psychiatry*, **2021**, 78, 387-397	14.5	11
381	A Comparison of Ten Polygenic Score Methods for Psychiatric Disorders Applied Across Multiple Cohorts. *Biological Psychiatry*, **2021**, 90, 611-620	7.9	17
380	Genome-wide association study of more than 40,000 bipolar disorder cases provides new insights into the underlying biology. *Nature Genetics*, **2021**, 53, 817-829	36.3	83
379	Estimation of non-additive genetic variance in human complex traits from a large sample of unrelated individuals. *American Journal of Human Genetics*, **2021**, 108, 786-798	11	19
378	Gene action, genetic variation, and GWAS: A user-friendly web tool. *PLoS Genetics*, **2021**, 17, e1009548	6	0
377	Leveraging both individual-level genetic data and GWAS summary statistics increases polygenic prediction. *American Journal of Human Genetics*, **2021**, 108, 1001-1011	11	2
376	Examining Sex-Differentiated Genetic Effects Across Neuropsychiatric and Behavioral Traits. *Biological Psychiatry*, **2021**, 89, 1127-1137	7.9	12
375	Association of Antihypertensive Drug Target Genes With Psychiatric Disorders: A Mendelian Randomization Study. *JAMA Psychiatry*, **2021**, 78, 623-631	14.5	0
374	Genetic risk for chronic pain is associated with lower antidepressant effectiveness: Converging evidence for a depression subtype. *Australian and New Zealand Journal of Psychiatry*, **2021**, 486742110314 91	2.6	0
373	Genetic association study of childhood aggression across raters, instruments, and age. *Translational Psychiatry*, **2021**, 11, 413	8.6	7
372	Risk in Relatives, Heritability, SNP-Based Heritability, and Genetic Correlations in Psychiatric Disorders: A Review. *Biological Psychiatry*, **2021**, 89, 11-19	7.9	20
371	Cardiovascular disease, psychiatric diagnosis and sex differences in the multistep hypothesis of amyotrophic lateral sclerosis. *European Journal of Neurology*, **2021**, 28, 421-429	6	7
370	From Basic Science to Clinical Application of Polygenic Risk Scores: A Primer. *JAMA Psychiatry*, **2021** , 78, 101-109	14.5	49
369	Could Polygenic Risk Scores Be Useful in Psychiatry?: A Review. *JAMA Psychiatry*, **2021**, 78, 210-219	14.5	53
368	Genome-wide analyses of behavioural traits are subject to bias by misreports and longitudinal changes. *Nature Communications*, **2021**, 12, 20211	17.4	16
367	GWAS of peptic ulcer disease implicates Helicobacter pylori infection, other gastrointestinal disorders and depression. *Nature Communications*, **2021**, 12, 1146	17.4	20
366	Widespread signatures of natural selection across human complex traits and functional genomic categories. *Nature Communications*, **2021**, 12, 1164	17.4	12
365	Analysis of common genetic variation and rare CNVs in the Australian Autism Biobank. *Molecular Autism*, **2021**, 12, 12	6.5	4

364	Schizophrenia polygenic risk scores in youth mental health: preliminary associations with diagnosis, clinical stage and functioning. *BJPsych Open*, **2021**, 7, e58	5	1
363	Phenotypic covariance across the entire spectrum of relatedness for 86 billion pairs of individuals. *Nature Communications*, **2021**, 12, 1050	17.4	7
362	Genomic partitioning of inbreeding depression in humans. *American Journal of Human Genetics*, **2021**, 108, 1488-1501	11	3
361	Polygenic Risk Scores Derived From Varying Definitions of Depression and Risk of Depression. *JAMA Psychiatry*, **2021**, 78, 1152-1160	14.5	3
360	Continuity of Genetic Risk for Aggressive Behavior Across the Life-Course. *Behavior Genetics*, **2021**, 51, 592-606	3.2	2
359	Investigating Shared Genetic Basis Across Tourette Syndrome and Comorbid Neurodevelopmental Disorders Along the Impulsivity-Compulsivity Spectrum. *Biological Psychiatry*, **2021**, 90, 317-327	7.9	12
358	MiNDAUS partnership: a roadmap for the cure and management of motor Neurone disease. *Amyotrophic Lateral Sclerosis and Frontotemporal Degeneration*, **2021**, 1-8	3.6	0
357	Discovery and implications of polygenicity of common diseases. *Science*, **2021**, 373, 1468-1473	33.3	13
356	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. *Nature Genetics*, **2021**, 53, 1311-1321	36.3	27
355	The Genetic Architecture of Depression in Individuals of East Asian Ancestry: A Genome-Wide Association Study. *JAMA Psychiatry*, **2021**, 78, 1258-1269	14.5	7
354	Dissecting the Shared Genetic Architecture of Suicide Attempt, Psychiatric Disorders, and Known Risk Factors. *Biological Psychiatry*, **2021**,	7.9	11
353	Refining Attention-Deficit/Hyperactivity Disorder and Autism Spectrum Disorder Genetic Loci by Integrating Summary Data From Genome-wide Association, Gene Expression, and DNA Methylation Studies. *Biological Psychiatry*, **2020**, 88, 470-479	7.9	6
352	Nick Martin and the Genetics of Depression: Sample Size, Sample Size, Sample Size. *Twin Research and Human Genetics*, **2020**, 23, 109-111	2.2	
351	ALS in Danish Registries: Heritability and links to psychiatric and cardiovascular disorders. *Neurology: Genetics*, **2020**, 6, e398	3.8	15
350	Cohort profile: the Australian genetics of depression study. *BMJ Open*, **2020**, 10, e032580	3	13
349	Mutations in heat shock protein beta-1 (HSPB1) are associated with a range of clinical phenotypes related to different patterns of motor neuron dysfunction: A case series. *Journal of the Neurological Sciences*, **2020**, 413, 116809	3.2	3
348	Genetic stratification of depression in UK Biobank. *Translational Psychiatry*, **2020**, 10, 163	8.6	8
347	Bayesian reassessment of the epigenetic architecture of complex traits. *Nature Communications*, **2020**, 11, 2865	17.4	18

346	What do we know about the variability in survival of patients with amyotrophic lateral sclerosis?. *Expert Review of Neurotherapeutics*, **2020**, 20, 921-941	4.3	4
345	Analysis of DNA methylation associates the cystine-glutamate antiporter SLC7A11 with risk of Parkinson's disease. *Nature Communications*, **2020**, 11, 1238	17.4	25
344	Significant out-of-sample classification from methylation profile scoring for amyotrophic lateral sclerosis. *Npj Genomic Medicine*, **2020**, 5, 10	6.2	11
343	Association of Mental Disorder in Childhood and Adolescence With Subsequent Educational Achievement. *JAMA Psychiatry*, **2020**, 77, 797-805	14.5	31
342	Multi-method genome- and epigenome-wide studies of inflammatory protein levels in healthy older adults. *Genome Medicine*, **2020**, 12, 60	14.4	9
341	Progression and survival of patients with motor neuron disease relative to their fecal microbiota. *Amyotrophic Lateral Sclerosis and Frontotemporal Degeneration*, **2020**, 21, 549-562	3.6	11
340	Genome-wide association study of dietary intake in the UK biobank study and its associations with schizophrenia and other traits. *Translational Psychiatry*, **2020**, 10, 51	8.6	10
339	Genome-wide gene-environment analyses of major depressive disorder and reported lifetime traumatic experiences in UK Biobank. *Molecular Psychiatry*, **2020**, 25, 1430-1446	15.1	47
338	Promoter-anchored chromatin interactions predicted from genetic analysis of epigenomic data. *Nature Communications*, **2020**, 11, 2061	17.4	1
337	Genome-wide association study identifies 143 loci associated with 25 hydroxyvitamin D concentration. *Nature Communications*, **2020**, 11, 1647	17.4	58
336	Blood DNA methylation sites predict death risk in a longitudinal study of 12, 300 individuals. *Aging*, **2020**, 12, 14092-14124	5.6	6
335	repeat expansions confer risk for amyotrophic lateral sclerosis and contribute to TDP-43 mislocalization. *Brain Communications*, **2020**, 2, fcaa064	4.5	12
334	A unified framework for association and prediction from vertex-wise grey-matter structure. *Human Brain Mapping*, **2020**, 41, 4062-4076	5.9	3
333	Genetic comorbidity between major depression and cardio-metabolic traits, stratified by age at onset of major depression. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2020**, 183, 309-330	3.5	8
332	Rare Variant Burden Analysis within Enhancers Identifies CAV1 as an ALS Risk Gene. *Cell Reports*, **2020**, 33, 108456	10.6	6
331	Genome-wide Meta-analysis Finds the ACSL5-ZDHHC6 Locus Is Associated with ALS and Links Weight Loss to the Disease Genetics. *Cell Reports*, **2020**, 33, 108323	10.6	18
330	Risk prediction of late-onset Alzheimer's disease implies an oligogenic architecture. *Nature Communications*, **2020**, 11, 4799	17.4	41
329	Genetic control of temperament traits across species: association of autism spectrum disorder risk genes with cattle temperament. *Genetics Selection Evolution*, **2020**, 52, 51	4.9	9

328	RICOPILI: Rapid Imputation for COnsortias PIpeLIne. *Bioinformatics*, **2020**, 36, 930-933	7.2	72
327	Evaluating the Impact of Nonrandom Mating: Psychiatric Outcomes Among the Offspring of Pairs Diagnosed With Schizophrenia and Bipolar Disorder. *Biological Psychiatry*, **2020**, 87, 253-262	7.9	4
326	Classical Human Leukocyte Antigen Alleles and C4 Haplotypes Are Not Significantly Associated With Depression. *Biological Psychiatry*, **2020**, 87, 419-430	7.9	9
325	Improved precision of epigenetic clock estimates across tissues and its implication for biological ageing. *Genome Medicine*, **2019**, 11, 54	14.4	81
324	Extreme inbreeding in a European ancestry sample from the contemporary UK population. *Nature Communications*, **2019**, 10, 3719	17.4	14
323	A genome-wide association study of shared risk across psychiatric disorders implicates gene regulation during fetal neurodevelopment. *Nature Neuroscience*, **2019**, 22, 353-361	25.5	93
322	Quantifying between-cohort and between-sex genetic heterogeneity in major depressive disorder. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2019**, 180, 439-447	3.5	16
321	Sleep Disorders and Risk of Incident Depression: A Population Case-Control Study. *Twin Research and Human Genetics*, **2019**, 22, 140-146	2.2	12
320	Genetic correlations of polygenic disease traits: from theory to practice. *Nature Reviews Genetics*, **2019**, 20, 567-581	30.1	98
319	OSCA: a tool for omic-data-based complex trait analysis. *Genome Biology*, **2019**, 20, 107	18.3	40
318	GWAS of Suicide Attempt in Psychiatric Disorders and Association With Major Depression Polygenic Risk Scores. *American Journal of Psychiatry*, **2019**, 176, 651-660	11.9	103
317	Gut microbiota in ALS: possible role in pathogenesis?. *Expert Review of Neurotherapeutics*, **2019**, 19, 785-805	4.5	21
316	Examining the Impact of Imputation Errors on Fine-Mapping Using DNA Methylation QTL as a Model Trait. *Genetics*, **2019**, 212, 577-586	4	1
315	Genotype-covariate correlation and interaction disentangled by a whole-genome multivariate reaction norm model. *Nature Communications*, **2019**, 10, 2239	17.4	23
314	Genome-wide association study of medication-use and associated disease in the UK Biobank. *Nature Communications*, **2019**, 10, 1891	17.4	48
313	Genome-wide association study identifies 30 loci associated with bipolar disorder. *Nature Genetics*, **2019**, 51, 793-803	36.3	662
312	Complex Trait Prediction from Genome Data: Contrasting EBV in Livestock to PRS in Humans: Genomic Prediction. *Genetics*, **2019**, 211, 1131-1141	4	47
311	A DIRECT TEST OF THE DIATHESIS-STRESS MODEL FOR DEPRESSION. *European Neuropsychopharmacology*, **2019**, 29, S805-S806	1.2	2

310	Evidence of causal effect of major depression on alcohol dependence: findings from the psychiatric genomics consortium. *Psychological Medicine*, **2019**, 49, 1218-1226	6.9	33
309	Attention deficit hyperactivity disorder symptoms as antecedents of later psychotic outcomes in 22q11.2 deletion syndrome. *Schizophrenia Research*, **2019**, 204, 320-325	3.6	11
308	Genotype-by-environment interactions inferred from genetic effects on phenotypic variability in the UK Biobank. *Science Advances*, **2019**, 5, eaaw3538	14.3	59
307	Assortative Mating in Autism Spectrum Disorder: Toward an Evidence Base From DNA Data, but Not There Yet. *Biological Psychiatry*, **2019**, 86, 250-252	7.9	1
306	Genome and epigenome wide studies of neurological protein biomarkers in the Lothian Birth Cohort 1936. *Nature Communications*, **2019**, 10, 3160	17.4	21
305	"Arte et Labore"-A Blackburn Rovers fan's legacy in human complex trait genetics. *Journal of Animal Breeding and Genetics*, **2019**, 136, 273-278	2.9	0
304	Association of Schizophrenia Risk With Disordered Niacin Metabolism in an Indian Genome-wide Association Study. *JAMA Psychiatry*, **2019**, 76, 1026-1034	14.5	24
303	Genetic risk scores for major psychiatric disorders and the risk of postpartum psychiatric disorders. *Translational Psychiatry*, **2019**, 9, 288	8.6	10
302	Genetic correlates of social stratification in Great Britain. *Nature Human Behaviour*, **2019**, 3, 1332-1342	12.8	83
301	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	25.5	639
300	Improved polygenic prediction by Bayesian multiple regression on summary statistics. *Nature Communications*, **2019**, 10, 5086	17.4	114
299	A resource-efficient tool for mixed model association analysis of large-scale data. *Nature Genetics*, **2019**, 51, 1749-1755	36.3	102
298	Association of Whole-Genome and NETRIN1 Signaling Pathway-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	3.4	12
297	Cumulative influence of parity-related genomic changes in multiple sclerosis. *Journal of Neuroimmunology*, **2019**, 328, 38-49	3.5	4
296	Is Schizophrenia a Risk Factor for Breast Cancer?-Evidence From Genetic Data. *Schizophrenia Bulletin*, **2019**, 45, 1251-1256	1.3	11
295	Improving genetic prediction by leveraging genetic correlations among human diseases and traits. *Nature Communications*, **2018**, 9, 989	17.4	76
294	Reply to Kardos et al.: Estimation of inbreeding depression from SNP data. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, E2494-E2495	11.5	4
293	Common schizophrenia alleles are enriched in mutation-intolerant genes and in regions under strong background selection. *Nature Genetics*, **2018**, 50, 381-389	36.3	787

292	Integrative analysis of omics summary data reveals putative mechanisms underlying complex traits. *Nature Communications*, **2018**, 9, 918	17.4	110
291	Sizing up whole-genome sequencing studies of common diseases. *Nature Genetics*, **2018**, 50, 635-637	36.3	10
290	Signatures of negative selection in the genetic architecture of human complex traits. *Nature Genetics*, **2018**, 50, 746-753	36.3	178
289	GWAS of epigenetic aging rates in blood reveals a critical role for TERT. *Nature Communications*, **2018**, 9, 387	17.4	106
288	Causal associations between risk factors and common diseases inferred from GWAS summary data. *Nature Communications*, **2018**, 9, 224	17.4	346
287	Hypermetabolism in ALS is associated with greater functional decline and shorter survival. *Journal of Neurology, Neurosurgery and Psychiatry*, **2018**, 89, 1016-1023	5.5	96
286	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. *Nature Genetics*, **2018**, 50, 668-681	36.3	1301
285	A DNA methylation biomarker of alcohol consumption. *Molecular Psychiatry*, **2018**, 23, 422-433	15.1	164
284	Brain age predicts mortality. *Molecular Psychiatry*, **2018**, 23, 1385-1392	15.1	260
283	A direct test of the diathesis-stress model for depression. *Molecular Psychiatry*, **2018**, 23, 1590-1596	15.1	114
282	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	7.9	48
281	Embracing polygenicity: a review of methods and tools for psychiatric genetics research. *Psychological Medicine*, **2018**, 48, 1055-1067	6.9	48
280	The epigenetic clock and telomere length are independently associated with chronological age and mortality. *International Journal of Epidemiology*, **2018**, 45, 424-432	7.8	153
279	Accuracy of Inferred APOE Genotypes for a Range of Genotyping Arrays and Imputation Reference Panels. *Journal of Alzheimer's Disease*, **2018**, 64, 49-54	4.3	5
278	Analysis of the Influence of microRNAs in Lithium Response in Bipolar Disorder. *Frontiers in Psychiatry*, **2018**, 9, 207	5	15
277	Analysis of shared heritability in common disorders of the brain. *Science*, **2018**, 360,	33.3	666
276	DNA Methylation Signatures of Depressive Symptoms in Middle-aged and Elderly Persons: Meta-analysis of Multiethnic Epigenome-wide Studies. *JAMA Psychiatry*, **2018**, 75, 949-959	14.5	51
275	Familiality of Psychiatric Disorders and Risk of Postpartum Psychiatric Episodes: A Population-Based Cohort Study. *American Journal of Psychiatry*, **2018**, 175, 783-791	11.9	14

274	Comparison of Genotypic and Phenotypic Correlations: Cheverud's Conjecture in Humans. *Genetics*, **2018**, 209, 941-948	4	48
273	Common Disease Is More Complex Than Implied by the Core Gene Omnigenic Model. *Cell*, **2018**, 173, 1573-1580	56.2	151
272	Identifying gene targets for brain-related traits using transcriptomic and methylomic data from blood. *Nature Communications*, **2018**, 9, 2282	17.4	147
271	Genome-wide gene-environment interaction in depression: A systematic evaluation of candidate genes: The childhood trauma working-group of PGC-MDD. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2018**, 177, 40-49	3.5	43
270	A Genetic Investigation of Sex Bias in the Prevalence of Attention-Deficit/Hyperactivity Disorder. *Biological Psychiatry*, **2018**, 83, 1044-1053	7.9	93
269	Identification of 55,000 Replicated DNA Methylation QTL. *Scientific Reports*, **2018**, 8, 17605	4.9	78
268	Imprint of assortative mating on the human genome. *Nature Human Behaviour*, **2018**, 2, 948-954	12.8	45
267	Trajectories of inflammatory biomarkers over the eighth decade and their associations with immune cell profiles and epigenetic ageing. *Clinical Epigenetics*, **2018**, 10, 159	7.7	17
266	Dissection of genetic variation and evidence for pleiotropy in male pattern baldness. *Nature Communications*, **2018**, 9, 5407	17.4	37
265	The association between neonatal vitamin D status and risk of schizophrenia. *Scientific Reports*, **2018**, 8, 17692	4.9	49
264	PPD ACT: an app-based genetic study of postpartum depression. *Translational Psychiatry*, **2018**, 8, 260	8.6	10
263	Epigenetic prediction of complex traits and death. *Genome Biology*, **2018**, 19, 136	18.3	77
262	Genotype effects contribute to variation in longitudinal methylome patterns in older people. *Genome Medicine*, **2018**, 10, 75	14.4	21
261	Study protocol for the Australian autism biobank: an international resource to advance autism discovery research. *BMC Pediatrics*, **2018**, 18, 284	2.6	9
260	GWAS on family history of Alzheimer's disease. *Translational Psychiatry*, **2018**, 8, 99	8.6	238
259	Estimation of Genetic Correlation via Linkage Disequilibrium Score Regression and Genomic Restricted Maximum Likelihood. *American Journal of Human Genetics*, **2018**, 102, 1185-1194	11	55
258	Age at first birth in women is genetically associated with increased risk of schizophrenia. *Scientific Reports*, **2018**, 8, 10168	4.9	11
257	Trans-eQTLs identified in whole blood have limited influence on complex disease biology. *European Journal of Human Genetics*, **2018**, 26, 1361-1368	5.3	1

256	Misestimation of heritability and prediction accuracy of male-pattern baldness. *Nature Communications*, **2018**, 9, 2537	17.4	14
255	A Combined Pathway and Regional Heritability Analysis Indicates NETRIN1 Pathway Is Associated With Major Depressive Disorder. *Biological Psychiatry*, **2017**, 81, 336-346	7.9	25
254	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	7.9	129
253	Using information of relatives in genomic prediction to apply effective stratified medicine. *Scientific Reports*, **2017**, 7, 42091	4.9	31
252	Genome-wide association study of borderline personality disorder reveals genetic overlap with bipolar disorder, major depression and schizophrenia. *Translational Psychiatry*, **2017**, 7, e1155	8.6	100
251	Genetic signatures of high-altitude adaptation in Tibetans. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, 4189-4194	11.5	93
250	Genetic effects influencing risk for major depressive disorder in China and Europe. *Translational Psychiatry*, **2017**, 7, e1074	8.6	48
249	Extra-motor abnormalities in amyotrophic lateral sclerosis: another layer of heterogeneity. *Expert Review of Neurotherapeutics*, **2017**, 17, 561-577	4.3	14
248	Genome-wide Regional Heritability Mapping Identifies a Locus Within the TOX2 Gene Associated With Major Depressive Disorder. *Biological Psychiatry*, **2017**, 82, 312-321	7.9	17
247	CNV-association meta-analysis in 191,161 European adults reveals new loci associated with anthropometric traits. *Nature Communications*, **2017**, 8, 744	17.4	37
246	Inference in Psychiatry via 2-Sample Mendelian Randomization-From Association to Causal Pathway?. *JAMA Psychiatry*, **2017**, 74, 1191-1192	14.5	11
245	Genetic Association of Major Depression With Atypical Features and Obesity-Related Immunometabolic Dysregulations. *JAMA Psychiatry*, **2017**, 74, 1214-1225	14.5	109
244	Association of Body Mass Index with DNA Methylation and Gene Expression in Blood Cells and Relations to Cardiometabolic Disease: A Mendelian Randomization Approach. *PLoS Medicine*, **2017**, 14, e1002215	11.6	162
243	Performance of risk prediction for inflammatory bowel disease based on genotyping platform and genomic risk score method. *BMC Medical Genetics*, **2017**, 18, 94	2.1	20
242	Whole-exome sequencing in amyotrophic lateral sclerosis suggests NEK1 is a risk gene in Chinese. *Genome Medicine*, **2017**, 9, 97	14.4	17
241	Concepts, estimation and interpretation of SNP-based heritability. *Nature Genetics*, **2017**, 49, 1304-1310	36.3	217
240	Comparison of faecal microbe diversity between motor neurone disease (mnd) and control participants. *Journal of Neurology, Neurosurgery and Psychiatry*, **2017**, 88, e1.83-e1	5.5	
239	Cross-ethnic meta-analysis identifies association of the GPX3-TNIP1 locus with amyotrophic lateral sclerosis. *Nature Communications*, **2017**, 8, 611	17.4	45

238	Whole exome sequencing and DNA methylation analysis in a clinical amyotrophic lateral sclerosis cohort. *Molecular Genetics & Genomic Medicine*, **2017**, 5, 418-428	2.3	8
237	Detection and quantification of inbreeding depression for complex traits from SNP data. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, 8602-8607	11.5	20
236	Large-scale GWAS identifies multiple loci for hand grip strength providing biological insights into muscular fitness. *Nature Communications*, **2017**, 8, 16015	17.4	80
235	10 Years of GWAS Discovery: Biology, Function, and Translation. *American Journal of Human Genetics*, **2017**, 101, 5-22	11	1651
234	Investigating the relationship between iron and depression. *Journal of Psychiatric Research*, **2017**, 94, 148-155	5.2	3
233	Rare DNA variants in the brain-derived neurotrophic factor gene increase risk for attention-deficit hyperactivity disorder: a next-generation sequencing study. *Molecular Psychiatry*, **2017**, 22, 580-584	15.1	25
232	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. *Nature Genetics*, **2017**, 49, 27-35	36.3	530
231	High loading of polygenic risk in cases with chronic schizophrenia. *Molecular Psychiatry*, **2016**, 21, 969-74	15.1	44
230	Evidence of CNIH3 involvement in opioid dependence. *Molecular Psychiatry*, **2016**, 21, 608-14	15.1	74
229	GCTA-GREML accounts for linkage disequilibrium when estimating genetic variance from genome-wide SNPs. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, E4579-80	11.5	25
228	Epigenetic Signatures of Cigarette Smoking. *Circulation: Cardiovascular Genetics*, **2016**, 9, 436-447		442
227	Genome-wide association analyses identify new risk variants and the genetic architecture of amyotrophic lateral sclerosis. *Nature Genetics*, **2016**, 48, 1043-8	36.3	328
226	Exploring Boundaries for the Genetic Consequences of Assortative Mating for Psychiatric Traits. *JAMA Psychiatry*, **2016**, 73, 1189-1195	14.5	36
225	Genome-wide association study reveals greater polygenic loading for schizophrenia in cases with a family history of illness. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2016**, 171B, 276-89	3.5	23
224	Meta-analysis of genome-wide association studies of anxiety disorders. *Molecular Psychiatry*, **2016**, 21, 1391-9	15.1	213
223	Genetic variants associated with response to lithium treatment in bipolar disorder: a genome-wide association study. *Lancet, The*, **2016**, 387, 1085-1093	40	216
222	Evidence for Genetic Overlap Between Schizophrenia and Age at First Birth in Women. *JAMA Psychiatry*, **2016**, 73, 497-505	14.5	40
221	Integration of summary data from GWAS and eQTL studies predicts complex trait gene targets. *Nature Genetics*, **2016**, 48, 481-7	36.3	929

220	Disease and Polygenic Architecture: Avoid Trio Design and Appropriately Account for Unscreened Control Subjects for Common Disease. *American Journal of Human Genetics*, **2016**, 98, 382-91	11	27
219	Across-cohort QC analyses of GWAS summary statistics from complex traits. *European Journal of Human Genetics*, **2016**, 25, 137-146	5.3	13
218	DNA methylation-based measures of biological age: meta-analysis predicting time to death. *Aging*, **2016**, 8, 1844-1865	5.6	531
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