Naomi R Wray

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

#	Paper	IF	Citations
399	Common polygenic variation contributes to risk of schizophrenia and bipolar disorder. <i>Nature</i> , 2009 , 460, 748-52	50.4	3568
398	Identification of risk loci with shared effects on five major psychiatric disorders: a genome-wide analysis. <i>Lancet, The</i> , 2013 , 381, 1371-1379	40	2112
397	10 Years of GWAS Discovery: Biology, Function, and Translation. <i>American Journal of Human Genetics</i> , 2017 , 101, 5-22	11	1651
396	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. <i>Nature Genetics</i> , 2013 , 45, 984-94	36.3	1628
395	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. <i>Nature Genetics</i> , 2018 , 50, 668-681	36.3	1301
394	Heritability in the genomics eraconcepts and misconceptions. <i>Nature Reviews Genetics</i> , 2008 , 9, 255-6	630.1	1155
393	Genome-wide association analysis identifies 13 new risk loci for schizophrenia. <i>Nature Genetics</i> , 2013 , 45, 1150-9	36.3	1153
392	Integration of summary data from GWAS and eQTL studies predicts complex trait gene targets. <i>Nature Genetics</i> , 2016 , 48, 481-7	36.3	929
391	A mega-analysis of genome-wide association studies for major depressive disorder. <i>Molecular Psychiatry</i> , 2013 , 18, 497-511	15.1	853
390	Common schizophrenia alleles are enriched in mutation-intolerant genes and in regions under strong background selection. <i>Nature Genetics</i> , 2018 , 50, 381-389	36.3	787
389	Estimating missing heritability for disease from genome-wide association studies. <i>American Journal of Human Genetics</i> , 2011 , 88, 294-305	11	737
388	DNA methylation age of blood predicts all-cause mortality in later life. <i>Genome Biology</i> , 2015 , 16, 25	18.3	670
387	Analysis of shared heritability in common disorders of the brain. <i>Science</i> , 2018 , 360,	33.3	666
386	Genome-wide association study identifies 30 loci associated with bipolar disorder. <i>Nature Genetics</i> , 2019 , 51, 793-803	36.3	662
385	A versatile gene-based test for genome-wide association studies. <i>American Journal of Human Genetics</i> , 2010 , 87, 139-45	11	648
384	Genome-wide meta-analysis of depression identifies 102 independent variants and highlights the importance of the prefrontal brain regions. <i>Nature Neuroscience</i> , 2019 , 22, 343-352	25.5	639
383	DNA methylation-based measures of biological age: meta-analysis predicting time to death. <i>Aging</i> , 2016 , 8, 1844-1865	5.6	531

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382	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. <i>Nature Genetics</i> , 2017 , 49, 27-35	36.3	530
381	Genetic variance estimation with imputed variants finds negligible missing heritability for human height and body mass index. <i>Nature Genetics</i> , 2015 , 47, 1114-20	36.3	522
380	Estimating the proportion of variation in susceptibility to schizophrenia captured by common SNPs. <i>Nature Genetics</i> , 2012 , 44, 247-50	36.3	471
379	Pitfalls of predicting complex traits from SNPs. <i>Nature Reviews Genetics</i> , 2013 , 14, 507-15	30.1	457
378	Epigenetic Signatures of Cigarette Smoking. Circulation: Cardiovascular Genetics, 2016, 9, 436-447		442
377	Prediction of individual genetic risk to disease from genome-wide association studies. <i>Genome Research</i> , 2007 , 17, 1520-8	9.7	436
376	Estimation of pleiotropy between complex diseases using single-nucleotide polymorphism-derived genomic relationships and restricted maximum likelihood. <i>Bioinformatics</i> , 2012 , 28, 2540-2	7.2	414
375	Partitioning heritability of regulatory and cell-type-specific variants across 11 common diseases. <i>American Journal of Human Genetics</i> , 2014 , 95, 535-52	11	411
374	Research review: Polygenic methods and their application to psychiatric traits. <i>Journal of Child Psychology and Psychiatry and Allied Disciplines</i> , 2014 , 55, 1068-87	7.9	410
373	The epigenetic clock is correlated with physical and cognitive fitness in the Lothian Birth Cohort 1936. <i>International Journal of Epidemiology</i> , 2015 , 44, 1388-96	7.8	357
372	Causal associations between risk factors and common diseases inferred from GWAS summary data. <i>Nature Communications</i> , 2018 , 9, 224	17.4	346
371	The neuroprogressive nature of major depressive disorder: pathways to disease evolution and resistance, and therapeutic implications. <i>Molecular Psychiatry</i> , 2013 , 18, 595-606	15.1	338
370	Genome-wide association study of major depressive disorder: new results, meta-analysis, and lessons learned. <i>Molecular Psychiatry</i> , 2012 , 17, 36-48	15.1	335
369	Genome-wide association analyses identify new risk variants and the genetic architecture of amyotrophic lateral sclerosis. <i>Nature Genetics</i> , 2016 , 48, 1043-8	36.3	328
368	Genome-wide association for major depressive disorder: a possible role for the presynaptic protein piccolo. <i>Molecular Psychiatry</i> , 2009 , 14, 359-75	15.1	322
367	Contrasting genetic architectures of schizophrenia and other complex diseases using fast variance-components analysis. <i>Nature Genetics</i> , 2015 , 47, 1385-92	36.3	299
366	Allele Frequencies and the r2 Measure of Linkage Disequilibrium: Impact on Design and Interpretation of Association Studies. <i>Twin Research and Human Genetics</i> , 2005 , 8, 87-94	2.2	276
365	Large-scale genomics unveils the genetic architecture of psychiatric disorders. <i>Nature Neuroscience</i> , 2014 , 17, 782-90	25.5	269

364	Brain age predicts mortality. <i>Molecular Psychiatry</i> , 2018 , 23, 1385-1392	15.1	260
363	The genetic interpretation of area under the ROC curve in genomic profiling. <i>PLoS Genetics</i> , 2010 , 6, e1000864	6	239
362	GWAS on family history of Alzheimer's disease. Translational Psychiatry, 2018, 8, 99	8.6	238
361	Harnessing the information contained within genome-wide association studies to improve individual prediction of complex disease risk. <i>Human Molecular Genetics</i> , 2009 , 18, 3525-31	5.6	237
360	Statistical power to detect genetic (co)variance of complex traits using SNP data in unrelated samples. <i>PLoS Genetics</i> , 2014 , 10, e1004269	6	236
359	Lifetime stress accelerates epigenetic aging in an urban, African American cohort: relevance of glucocorticoid signaling. <i>Genome Biology</i> , 2015 , 16, 266	18.3	234
358	Concepts, estimation and interpretation of SNP-based heritability. <i>Nature Genetics</i> , 2017 , 49, 1304-1310	036.3	217
357	Genetic variants associated with response to lithium treatment in bipolar disorder: a genome-wide association study. <i>Lancet, The</i> , 2016 , 387, 1085-1093	40	216
356	Meta-analysis of genome-wide association studies of anxiety disorders. <i>Molecular Psychiatry</i> , 2016 , 21, 1391-9	15.1	213
355	Simultaneous discovery, estimation and prediction analysis of complex traits using a bayesian mixture model. <i>PLoS Genetics</i> , 2015 , 11, e1004969	6	206
354	Partitioning the heritability of Tourette syndrome and obsessive compulsive disorder reveals differences in genetic architecture. <i>PLoS Genetics</i> , 2013 , 9, e1003864	6	189
353	Signatures of negative selection in the genetic architecture of human complex traits. <i>Nature Genetics</i> , 2018 , 50, 746-753	36.3	178
352	Polygenic Risk Score, Parental Socioeconomic Status, Family History of Psychiatric Disorders, and the Risk for Schizophrenia: A Danish Population-Based Study and Meta-analysis. <i>JAMA Psychiatry</i> , 2015 , 72, 635-41	14.5	177
351	A DNA methylation biomarker of alcohol consumption. <i>Molecular Psychiatry</i> , 2018 , 23, 422-433	15.1	164
350	Association of Body Mass Index with DNA Methylation and Gene Expression in Blood Cells and Relations to Cardiometabolic Disease: A Mendelian Randomization Approach. <i>PLoS Medicine</i> , 2017 , 14, e1002215	11.6	162
349	Joint analysis of psychiatric disorders increases accuracy of risk prediction for schizophrenia, bipolar disorder, and major depressive disorder. <i>American Journal of Human Genetics</i> , 2015 , 96, 283-94	11	161
348	A better coefficient of determination for genetic profile analysis. <i>Genetic Epidemiology</i> , 2012 , 36, 214-2	4 2.6	158
347	The epigenetic clock and telomere length are independently associated with chronological age and mortality. <i>International Journal of Epidemiology</i> , 2018 , 45, 424-432	7.8	153

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346	A comparative study of techniques for differential expression analysis on RNA-Seq data. <i>PLoS ONE</i> , 2014 , 9, e103207	3.7	152	
345	Common Disease Is More Complex Than Implied by the Core Gene Omnigenic Model. <i>Cell</i> , 2018 , 173, 1573-1580	56.2	151	
344	Association between the TRAX/DISC locus and both bipolar disorder and schizophrenia in the Scottish population. <i>Molecular Psychiatry</i> , 2005 , 10, 657-68, 616	15.1	149	
343	Identifying gene targets for brain-related traits using transcriptomic and methylomic data from blood. <i>Nature Communications</i> , 2018 , 9, 2282	17.4	147	
342	Estimation and partitioning of polygenic variation captured by common SNPs for Alzheimer's disease, multiple sclerosis and endometriosis. <i>Human Molecular Genetics</i> , 2013 , 22, 832-41	5.6	147	
341	COPD education and cognitive behavioral therapy group treatment for clinically significant symptoms of depression and anxiety in COPD patients: a randomized controlled trial. <i>Psychological Medicine</i> , 2008 , 38, 385-96	6.9	145	
340	Using summary data from the danish national registers to estimate heritabilities for schizophrenia, bipolar disorder, and major depressive disorder. <i>Frontiers in Genetics</i> , 2012 , 3, 118	4.5	140	
339	Common SNPs explain some of the variation in the personality dimensions of neuroticism and extraversion. <i>Translational Psychiatry</i> , 2012 , 2, e102	8.6	137	
338	Genetic predisposition to schizophrenia associated with increased use of cannabis. <i>Molecular Psychiatry</i> , 2014 , 19, 1201-4	15.1	136	
337	Prediction of rates of inbreeding in selected populations. <i>Genetical Research</i> , 1990 , 55, 41-54	1.1	133	
336	Genome-wide Association for Major Depression Through Age at Onset Stratification: Major Depressive Disorder Working Group of the Psychiatric Genomics Consortium. <i>Biological Psychiatry</i> , 2017 , 81, 325-335	7.9	129	
335	Synthetic associations created by rare variants do not explain most GWAS results. <i>PLoS Biology</i> , 2011 , 9, e1000579	9.7	129	
334	Prediction of individual genetic risk of complex disease. <i>Current Opinion in Genetics and Development</i> , 2008 , 18, 257-63	4.9	129	
333	A genome-wide association study of Cloninger's temperament scales: implications for the evolutionary genetics of personality. <i>Biological Psychology</i> , 2010 , 85, 306-17	3.2	128	
332	A whole genome association study of neuroticism using DNA pooling. <i>Molecular Psychiatry</i> , 2008 , 13, 302-12	15.1	127	
331	Genetic studies of major depressive disorder: why are there no genome-wide association study findings and what can we do about it?. <i>Biological Psychiatry</i> , 2014 , 76, 510-2	7.9	125	
330	Polygenic transmission and complex neuro developmental network for attention deficit hyperactivity disorder: genome-wide association study of both common and rare variants. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2013 , 162B, 419-430	3.5	125	
329	Genetic and environmental exposures constrain epigenetic drift over the human life course. Genome Research, 2014, 24, 1725-33	9.7	123	

328	Genetic risk profiles for depression and anxiety in adult and elderly cohorts. <i>Molecular Psychiatry</i> , 2011 , 16, 773-83	15.1	116
327	A direct test of the diathesis-stress model for depression. <i>Molecular Psychiatry</i> , 2018 , 23, 1590-1596	15.1	114
326	Improved polygenic prediction by Bayesian multiple regression on summary statistics. <i>Nature Communications</i> , 2019 , 10, 5086	17.4	114
325	Assessment of Response to Lithium Maintenance Treatment in Bipolar Disorder: A Consortium on Lithium Genetics (ConLiGen) Report. <i>PLoS ONE</i> , 2013 , 8, e65636	3.7	113
324	Integrative analysis of omics summary data reveals putative mechanisms underlying complex traits. <i>Nature Communications</i> , 2018 , 9, 918	17.4	110
323	Estimation and partition of heritability in human populations using whole-genome analysis methods. <i>Annual Review of Genetics</i> , 2013 , 47, 75-95	14.5	110
322	Explaining additional genetic variation in complex traits. <i>Trends in Genetics</i> , 2014 , 30, 124-32	8.5	110
321	Translation elongation factor eEF1A2 is a potential oncoprotein that is overexpressed in two-thirds of breast tumours. <i>BMC Cancer</i> , 2005 , 5, 113	4.8	110
320	Genetic Association of Major Depression With Atypical Features and Obesity-Related Immunometabolic Dysregulations. <i>JAMA Psychiatry</i> , 2017 , 74, 1214-1225	14.5	109
319	Evidence-based psychiatric genetics, AKA the false dichotomy between common and rare variant hypotheses. <i>Molecular Psychiatry</i> , 2012 , 17, 474-85	15.1	108
318	GWAS of epigenetic aging rates in blood reveals a critical role for TERT. <i>Nature Communications</i> , 2018 , 9, 387	17.4	106
317	The contribution of genetic variants to disease depends on the ruler. <i>Nature Reviews Genetics</i> , 2014 , 15, 765-76	30.1	105
316	Estimating Effects and Making Predictions from Genome-Wide Marker Data. <i>Statistical Science</i> , 2009 , 24,	2.4	105
315	GWAS of Suicide Attempt in Psychiatric Disorders and Association With Major Depression Polygenic Risk Scores. <i>American Journal of Psychiatry</i> , 2019 , 176, 651-660	11.9	103
314	A resource-efficient tool for mixed model association analysis of large-scale data. <i>Nature Genetics</i> , 2019 , 51, 1749-1755	36.3	102
313	Genome-wide association study of borderline personality disorder reveals genetic overlap with bipolar disorder, major depression and schizophrenia. <i>Translational Psychiatry</i> , 2017 , 7, e1155	8.6	100
312	Genetic correlations of polygenic disease traits: from theory to practice. <i>Nature Reviews Genetics</i> , 2019 , 20, 567-581	30.1	98
311	Hypermetabolism in ALS is associated with greater functional decline and shorter survival. <i>Journal of Neurology, Neurosurgery and Psychiatry</i> , 2018 , 89, 1016-1023	5.5	96

310	Genetic signatures of high-altitude adaptation in Tibetans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 4189-4194	11.5	93
309	A genome-wide association study of shared risk across psychiatric disorders implicates gene regulation during fetal neurodevelopment. <i>Nature Neuroscience</i> , 2019 , 22, 353-361	25.5	93
308	Genome-wide association analysis of coffee drinking suggests association with CYP1A1/CYP1A2 and NRCAM. <i>Molecular Psychiatry</i> , 2012 , 17, 1116-29	15.1	93
307	Accurate, Large-Scale Genotyping of 5HTTLPR and Flanking Single Nucleotide Polymorphisms in an Association Study of Depression, Anxiety, and Personality Measures. <i>Biological Psychiatry</i> , 2009 , 66, 468	3 <i>-7</i> -8	93
306	A Genetic Investigation of Sex Bias in the Prevalence of Attention-Deficit/Hyperactivity Disorder. <i>Biological Psychiatry</i> , 2018 , 83, 1044-1053	7.9	93
305	Association between ORMDL3, IL1RL1 and a deletion on chromosome 17q21 with asthma risk in Australia. <i>European Journal of Human Genetics</i> , 2011 , 19, 458-64	5.3	92
304	Narrowing the boundaries of the genetic architecture of schizophrenia. <i>Schizophrenia Bulletin</i> , 2010 , 36, 14-23	1.3	86
303	Improving Phenotypic Prediction by Combining Genetic and Epigenetic Associations. <i>American Journal of Human Genetics</i> , 2015 , 97, 75-85	11	85
302	Estimation of SNP heritability from dense genotype data. <i>American Journal of Human Genetics</i> , 2013 , 93, 1151-5	11	85
301	A genome-wide meta-analysis of association studies of Cloninger's Temperament Scales. <i>Translational Psychiatry</i> , 2012 , 2, e116	8.6	85
300	Sex-specific association between bipolar affective disorder in women and GPR50, an X-linked orphan G protein-coupled receptor. <i>Molecular Psychiatry</i> , 2005 , 10, 470-8	15.1	84
299	Genetic correlates of social stratification in Great Britain. <i>Nature Human Behaviour</i> , 2019 , 3, 1332-1342	12.8	83
298	The genetic association between personality and major depression or bipolar disorder. A polygenic score analysis using genome-wide association data. <i>Translational Psychiatry</i> , 2011 , 1, e50	8.6	83
297	Genome-wide association study of more than 40,000 bipolar disorder cases provides new insights into the underlying biology. <i>Nature Genetics</i> , 2021 , 53, 817-829	36.3	83
296	Cohort Profile Update: The Mater-University of Queensland Study of Pregnancy (MUSP). <i>International Journal of Epidemiology</i> , 2015 , 44, 78-78f	7.8	82
295	Improved precision of epigenetic clock estimates across tissues and its implication for biological ageing. <i>Genome Medicine</i> , 2019 , 11, 54	14.4	81
294	A genome-wide association study of sleep habits and insomnia. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2013 , 162B, 439-51	3.5	81
293	Large-scale GWAS identifies multiple loci for hand grip strength providing biological insights into muscular fitness. <i>Nature Communications</i> , 2017 , 8, 16015	17.4	80

292	Monozygotic twins affected with major depressive disorder have greater variance in methylation than their unaffected co-twin. <i>Translational Psychiatry</i> , 2013 , 3, e269	8.6	78
291	Sporadic cases are the norm for complex disease. European Journal of Human Genetics, 2010, 18, 1039-4	13 5.3	78
2 90	Identification of 55,000 Replicated DNA Methylation QTL. Scientific Reports, 2018, 8, 17605	4.9	78
289	Epigenetic prediction of complex traits and death. <i>Genome Biology</i> , 2018 , 19, 136	18.3	77
288	Improving genetic prediction by leveraging genetic correlations among human diseases and traits. <i>Nature Communications</i> , 2018 , 9, 989	17.4	76
287	Evidence of CNIH3 involvement in opioid dependence. <i>Molecular Psychiatry</i> , 2016 , 21, 608-14	15.1	74
286	Genetic and environmental influences on the co-morbidity between depression, panic disorder, agoraphobia, and social phobia: a twin study. <i>Depression and Anxiety</i> , 2009 , 26, 1004-11	8.4	74
285	Risk of psychiatric illness from advanced paternal age is not predominantly from de novo mutations. <i>Nature Genetics</i> , 2016 , 48, 718-24	36.3	74
284	Estimation and partitioning of (co)heritability of inflammatory bowel disease from GWAS and immunochip data. <i>Human Molecular Genetics</i> , 2014 , 23, 4710-20	5.6	73
283	Hypermethylation in the ZBTB20 gene is associated with major depressive disorder. <i>Genome Biology</i> , 2014 , 15, R56	18.3	73
282	RICOPILI: Rapid Imputation for COnsortias PlpeLine. <i>Bioinformatics</i> , 2020 , 36, 930-933	7.2	72
281	Asymptotic rates of response from index selection. <i>Animal Science</i> , 1989 , 49, 217-227		71
280	Shared temperament risk factors for anorexia nervosa: a twin study. <i>Psychosomatic Medicine</i> , 2008 , 70, 239-44	3.7	70
279	Research review: the role of cytokines in depression in adolescents: a systematic review. <i>Journal of Child Psychology and Psychiatry and Allied Disciplines</i> , 2013 , 54, 816-35	7.9	65
278	Interpreting the role of de novo protein-coding mutations in neuropsychiatric disease. <i>Nature Genetics</i> , 2013 , 45, 234-8	36.3	64
277	Genetic co-morbidity between neuroticism, anxiety/depression and somatic distress in a population sample of adolescent and young adult twins. <i>Psychological Medicine</i> , 2012 , 42, 1249-60	6.9	64
276	Unraveling the genetic etiology of adult antisocial behavior: a genome-wide association study. <i>PLoS ONE</i> , 2012 , 7, e45086	3.7	63
275	Multi-locus genome-wide association analysis supports the role of glutamatergic synaptic transmission in the etiology of major depressive disorder. <i>Translational Psychiatry</i> , 2012 , 2, e184	8.6	62

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274	Genetic and phenotypic stability of measures of neuroticism over 22 years. <i>Twin Research and Human Genetics</i> , 2007 , 10, 695-702	2.2	61
273	Genotype-by-environment interactions inferred from genetic effects on phenotypic variability in the UK Biobank. <i>Science Advances</i> , 2019 , 5, eaaw3538	14.3	59
272	Where GWAS and epidemiology meet: opportunities for the simultaneous study of genetic and environmental risk factors in schizophrenia. <i>Schizophrenia Bulletin</i> , 2013 , 39, 955-9	1.3	59
271	Association of OPRD1 polymorphisms with heroin dependence in a large case-control series. <i>Addiction Biology</i> , 2014 , 19, 111-21	4.6	59
270	Predicting gene targets from integrative analyses of summary data from GWAS and eQTL studies for 28 human complex traits. <i>Genome Medicine</i> , 2016 , 8, 84	14.4	59
269	Genome-wide association study identifies 143 loci associated with 25 hydroxyvitamin D concentration. <i>Nature Communications</i> , 2020 , 11, 1647	17.4	58
268	Additive genetic variation in schizophrenia risk is shared by populations of African and European descent. <i>American Journal of Human Genetics</i> , 2013 , 93, 463-70	11	55
267	Estimation of Genetic Correlation via Linkage Disequilibrium Score Regression and Genomic Restricted Maximum Likelihood. <i>American Journal of Human Genetics</i> , 2018 , 102, 1185-1194	11	55
266	Multi-locus models of genetic risk of disease. <i>Genome Medicine</i> , 2010 , 2, 10	14.4	54
265	NFIB-mediated repression of the epigenetic factor Ezh2 regulates cortical development. <i>Journal of Neuroscience</i> , 2014 , 34, 2921-30	6.6	53
264	Spatial clustering of childhood leukaemia: summary results from the EUROCLUS project. <i>British Journal of Cancer</i> , 1998 , 77, 818-24	8.7	53
263	Could Polygenic Risk Scores Be Useful in Psychiatry?: A Review. <i>JAMA Psychiatry</i> , 2021 , 78, 210-219	14.5	53
262	DNA Methylation Signatures of Depressive Symptoms in Middle-aged and Elderly Persons: Meta-analysis of Multiethnic Epigenome-wide Studies. <i>JAMA Psychiatry</i> , 2018 , 75, 949-959	14.5	51
261	Comparing apples and oranges: equating the power of case-control and quantitative trait association studies. <i>Genetic Epidemiology</i> , 2010 , 34, 254-7	2.6	51
260	Impact of diagnostic misclassification on estimation of genetic correlations using genome-wide genotypes. <i>European Journal of Human Genetics</i> , 2012 , 20, 668-74	5.3	51
259	DNA modification study of major depressive disorder: beyond locus-by-locus comparisons. <i>Biological Psychiatry</i> , 2015 , 77, 246-255	7.9	49
258	Applying polygenic risk scores to postpartum depression. <i>Archives of Womends Mental Health</i> , 2014 , 17, 519-28	5	49
257	From Basic Science to Clinical Application of Polygenic Risk Scores: A Primer. <i>JAMA Psychiatry</i> , 2021 , 78, 101-109	14.5	49

256	The association between neonatal vitamin D status and risk of schizophrenia. <i>Scientific Reports</i> , 2018 , 8, 17692	4.9	49
255	Genetic effects influencing risk for major depressive disorder in China and Europe. <i>Translational Psychiatry</i> , 2017 , 7, e1074	8.6	48
254	Genome-wide association study of medication-use and associated disease in the UK Biobank. <i>Nature Communications</i> , 2019 , 10, 1891	17.4	48
253	Does Childhood Trauma Moderate Polygenic Risk for Depression? A Meta-analysis of 5765 Subjects From the Psychiatric Genomics Consortium. <i>Biological Psychiatry</i> , 2018 , 84, 138-147	7.9	48
252	Embracing polygenicity: a review of methods and tools for psychiatric genetics research. <i>Psychological Medicine</i> , 2018 , 48, 1055-1067	6.9	48
251	Comparison of Genotypic and Phenotypic Correlations: Cheverud's Conjecture in Humans. <i>Genetics</i> , 2018 , 209, 941-948	4	48
250	Complex Trait Prediction from Genome Data: Contrasting EBV in Livestock to PRS in Humans: Genomic Prediction. <i>Genetics</i> , 2019 , 211, 1131-1141	4	47
249	Genome-wide gene-environment analyses of major depressive disorder and reported lifetime traumatic experiences in UK Biobank. <i>Molecular Psychiatry</i> , 2020 , 25, 1430-1446	15.1	47
248	Don't give up on GWAS. <i>Molecular Psychiatry</i> , 2012 , 17, 2-3	15.1	46
247	Allele frequencies and the r2 measure of linkage disequilibrium: impact on design and interpretation of association studies. <i>Twin Research and Human Genetics</i> , 2005 , 8, 87-94	2.2	46
246	Cross-ethnic meta-analysis identifies association of the GPX3-TNIP1 locus with amyotrophic lateral sclerosis. <i>Nature Communications</i> , 2017 , 8, 611	17.4	45
245	ANKK1, TTC12, and NCAM1 polymorphisms and heroin dependence: importance of considering drug exposure. <i>JAMA Psychiatry</i> , 2013 , 70, 325-33	14.5	45
244	Anxiety and comorbid measures associated with PLXNA2. Archives of General Psychiatry, 2007, 64, 318-	26	45
243	A method to decipher pleiotropy by detecting underlying heterogeneity driven by hidden subgroups applied to autoimmune and neuropsychiatric diseases. <i>Nature Genetics</i> , 2016 , 48, 803-10	36.3	45
242	Imprint of assortative mating on the human genome. <i>Nature Human Behaviour</i> , 2018 , 2, 948-954	12.8	45
241	High loading of polygenic risk in cases with chronic schizophrenia. <i>Molecular Psychiatry</i> , 2016 , 21, 969-7	415.1	44
240	Association study of candidate variants of COMT with neuroticism, anxiety and depression. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2008 , 147B, 1314-8	3.5	44
239	New data and an old puzzle: the negative association between schizophrenia and rheumatoid arthritis. <i>International Journal of Epidemiology</i> , 2015 , 44, 1706-21	7.8	43

238	Genetic Basis of Complex Genetic Disease: The Contribution of Disease Heterogeneity to Missing Heritability. <i>Current Epidemiology Reports</i> , 2014 , 1, 220-227	2.9	43
237	Genome-wide gene-environment interaction in depression: A systematic evaluation of candidate genes: The childhood trauma working-group of PGC-MDD. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2018 , 177, 40-49	3.5	43
236	Overlap of expression quantitative trait loci (eQTL) in human brain and blood. <i>BMC Medical Genomics</i> , 2014 , 7, 31	3.7	41
235	Risk prediction of late-onset Alzheimer's disease implies an oligogenic architecture. <i>Nature Communications</i> , 2020 , 11, 4799	17.4	41
234	OSCA: a tool for omic-data-based complex trait analysis. <i>Genome Biology</i> , 2019 , 20, 107	18.3	40
233	C9orf72 hexanucleotide repeat expansions in Chinese sporadic amyotrophic lateral sclerosis. <i>Neurobiology of Aging</i> , 2015 , 36, 2660.e1-8	5.6	40
232	Evidence for Genetic Overlap Between Schizophrenia and Age at First Birth in Women. <i>JAMA Psychiatry</i> , 2016 , 73, 497-505	14.5	40
231	The association between lower educational attainment and depression owing to shared genetic effects? Results in ~25,000 subjects. <i>Molecular Psychiatry</i> , 2015 , 20, 735-43	15.1	39
230	Prediction of long-term contributions and inbreeding in populations undergoing mass selection. <i>Genetical Research</i> , 1993 , 62, 231-242	1.1	39
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55	Examining sex-differentiated genetic effects across neuropsychiatric and behavioral traits		3
54	Estimation of non-additive genetic variance in human complex traits from a large sample of unrelated individuals		3
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23	GWAS of epigenetic ageing rates in blood reveals a critical role forTERT		1

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