Patrick F Sullivan

List of Publications by Citations

440 papers	60,378 citations	108 h-index	241 g-index
482 ext. papers	79,129 ext. citations	12.3 avg, IF	7.4 L-index

#	Paper	IF	Citations
440	Analysis of protein-coding genetic variation in 60,706 humans. *Nature*, **2016**, 536, 285-91	50.4	6940
439	Common polygenic variation contributes to risk of schizophrenia and bipolar disorder. *Nature*, **2009**, 460, 748-52	50.4	3568
438	The mutational constraint spectrum quantified from variation in 141,456 humans. *Nature*, **2020**, 581, 434-443	50.4	2278
437	Genetic epidemiology of major depression: review and meta-analysis. *American Journal of Psychiatry*, **2000**, 157, 1552-62	11.9	2142
436	Clonal hematopoiesis and blood-cancer risk inferred from blood DNA sequence. *New England Journal of Medicine*, **2014**, 371, 2477-87	59.2	1855
435	Schizophrenia as a complex trait: evidence from a meta-analysis of twin studies. *Archives of General Psychiatry*, **2003**, 60, 1187-92		1593
434	Common genetic determinants of schizophrenia and bipolar disorder in Swedish families: a population-based study. *Lancet, The*, **2009**, 373, 234-9	40	1467
433	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
432	Meta-analysis of the heritability of human traits based on fifty years of twin studies. *Nature Genetics*, **2015**, 47, 702-9	36.3	1184
431	Genome-wide association analysis identifies 13 new risk loci for schizophrenia. *Nature Genetics*, **2013**, 45, 1150-9	36.3	1153
430	A polygenic burden of rare disruptive mutations in schizophrenia. *Nature*, **2014**, 506, 185-90	50.4	1059
429	Genetic architectures of psychiatric disorders: the emerging picture and its implications. *Nature Reviews Genetics*, **2012**, 13, 537-51	30.1	866
428	A mega-analysis of genome-wide association studies for major depressive disorder. *Molecular Psychiatry*, **2013**, 18, 497-511	15.1	853
427	Integrative approaches for large-scale transcriptome-wide association studies. *Nature Genetics*, **2016**, 48, 245-52	36.3	843
426	Discovery of the first genome-wide significant risk loci for attention deficit/hyperactivity disorder. *Nature Genetics*, **2019**, 51, 63-75	36.3	826
425	Genome-wide meta-analysis identifies new loci and functional pathways influencing Alzheimer's disease risk. *Nature Genetics*, **2019**, 51, 404-413	36.3	771
424	Identification of common genetic risk variants for autism spectrum disorder. *Nature Genetics*, **2019**, 51, 431-444	36.3	746

423	Analysis of shared heritability in common disorders of the brain. *Science*, **2018**, 360,	33.3	666
422	Genome-wide association study identifies 30 loci associated with bipolar disorder. *Nature Genetics*, **2019**, 51, 793-803	36.3	662
421	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
420	Gene expression elucidates functional impact of polygenic risk for schizophrenia. *Nature Neuroscience*, **2016**, 19, 1442-1453	25.5	622
419	Microduplications of 16p11.2 are associated with schizophrenia. *Nature Genetics*, **2009**, 41, 1223-7	36.3	550
418	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
417	Genome-wide association meta-analysis in 269,867 individuals identifies new genetic and functional links to intelligence. *Nature Genetics*, **2018**, 50, 912-919	36.3	475
416	Estimating the proportion of variation in susceptibility to schizophrenia captured by common SNPs. *Nature Genetics*, **2012**, 44, 247-50	36.3	471
415	Partitioning heritability of regulatory and cell-type-specific variants across 11 common diseases. *American Journal of Human Genetics*, **2014**, 95, 535-52	11	411
414	Evaluating the comparability of gene expression in blood and brain. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2006**, 141B, 261-8	3.5	405
413	Discovery and statistical genotyping of copy-number variation from whole-exome sequencing depth. *American Journal of Human Genetics*, **2012**, 91, 597-607	11	391
412	Genomewide association studies: history, rationale, and prospects for psychiatric disorders. *American Journal of Psychiatry*, **2009**, 166, 540-56	11.9	355
411	Genome-wide association study of major depressive disorder: new results, meta-analysis, and lessons learned. *Molecular Psychiatry*, **2012**, 17, 36-48	15.1	335
410	Psychiatric Genomics: An Update and an Agenda. *American Journal of Psychiatry*, **2018**, 175, 15-27	11.9	328
409	Genome-wide association for major depressive disorder: a possible role for the presynaptic protein piccolo. *Molecular Psychiatry*, **2009**, 14, 359-75	15.1	322
408	Genome-wide association study of alcohol dependence. *Archives of General Psychiatry*, **2009**, 66, 773-84		318
407	Meta-analysis of genome-wide association studies for neuroticism in 449,484 individuals identifies novel genetic loci and pathways. *Nature Genetics*, **2018**, 50, 920-927	36.3	312
406	The genetic epidemiology of smoking. *Nicotine and Tobacco Research*, **1999**, 1 Suppl 2, S51-7; discussion S69-70	4.9	309

405	Genomewide association for schizophrenia in the CATIE study: results of stage 1. *Molecular Psychiatry*, **2008**, 13, 570-84	15.1	308
404	Genome-wide association study identifies eight risk loci and implicates metabo-psychiatric origins for anorexia nervosa. *Nature Genetics*, **2019**, 51, 1207-1214	36.3	303
403	Exome sequencing and the genetic basis of complex traits. *Nature Genetics*, **2012**, 44, 623-30	36.3	303
402	Genetic identification of brain cell types underlying schizophrenia. *Nature Genetics*, **2018**, 50, 825-833	36.3	295
401	Increased burden of ultra-rare protein-altering variants among 4,877 individuals with schizophrenia. *Nature Neuroscience*, **2016**, 19, 1433-1441	25.5	291
400	The Swedish Twin Registry in the Third Millennium: An Update. *Twin Research and Human Genetics*, **2006**, 9, 875-882	2.2	290
399	Rare loss-of-function variants in SETD1A are associated with schizophrenia and developmental disorders. *Nature Neuroscience*, **2016**, 19, 571-7	25.5	284
398	Integrative functional genomic analysis of human brain development and neuropsychiatric risks. *Science*, **2018**, 362,	33.3	277
397	Significant Locus and Metabolic Genetic Correlations Revealed in Genome-Wide Association Study of Anorexia Nervosa. *American Journal of Psychiatry*, **2017**, 174, 850-858	11.9	276
396	Genome-wide association analysis identifies 30 new susceptibility loci for schizophrenia. *Nature Genetics*, **2017**, 49, 1576-1583	36.3	272
395	Spurious genetic associations. *Biological Psychiatry*, **2007**, 61, 1121-6	7.9	268
394	No Support for Historical Candidate Gene or Candidate Gene-by-Interaction Hypotheses for Major Depression Across Multiple Large Samples. *American Journal of Psychiatry*, **2019**, 176, 376-387	11.9	266
393	Heritability and genomics of gene expression in peripheral blood. *Nature Genetics*, **2014**, 46, 430-7	36.3	258
392	Polygenic dissection of diagnosis and clinical dimensions of bipolar disorder and schizophrenia. *Molecular Psychiatry*, **2014**, 19, 1017-1024	15.1	258
391	New models of collaboration in genome-wide association studies: the Genetic Association Information Network. *Nature Genetics*, **2007**, 39, 1045-51	36.3	258
390	seeQTL: a searchable database for human eQTLs. *Bioinformatics*, **2012**, 28, 451-2	7.2	256
389	Genome-wide analysis of insomnia in 1,331,010 individuals identifies new risk loci and functional pathways. *Nature Genetics*, **2019**, 51, 394-403	36.3	246
388	The PsychENCODE project. *Nature Neuroscience*, **2015**, 18, 1707-12	25.5	226

387	Genome-wide association study of depression phenotypes in UK Biobank identifies variants in excitatory synaptic pathways. *Nature Communications*, **2018**, 9, 1470	17.4	226
386	A genome-wide association study of anorexia nervosa. *Molecular Psychiatry*, **2014**, 19, 1085-94	15.1	224
385	Transcriptome-wide association study of schizophrenia and chromatin activity yields mechanistic disease insights. *Nature Genetics*, **2018**, 50, 538-548	36.3	222
384	Evaluating historical candidate genes for schizophrenia. *Molecular Psychiatry*, **2015**, 20, 555-62	15.1	219
383	Poor replication of candidate genes for major depressive disorder using genome-wide association data. *Molecular Psychiatry*, **2011**, 16, 516-32	15.1	219
382	All SNPs are not created equal: genome-wide association studies reveal a consistent pattern of enrichment among functionally annotated SNPs. *PLoS Genetics*, **2013**, 9, e1003449	6	209
381	Quantifying prion disease penetrance using large population control cohorts. *Science Translational Medicine*, **2016**, 8, 322ra9	17.5	205
380	Twin studies of eating disorders: a review. *International Journal of Eating Disorders*, **2000**, 27, 1-20	6.3	205
379	Genome-wide association study in a Swedish population yields support for greater CNV and MHC involvement in schizophrenia compared with bipolar disorder. *Molecular Psychiatry*, **2012**, 17, 880-6	15.1	196
378	Single nucleotide polymorphism genotyping: biochemistry, protocol, cost and throughput. *Pharmacogenomics Journal*, **2003**, 3, 77-96	3.5	196
377	Copy number variation in schizophrenia in Sweden. *Molecular Psychiatry*, **2014**, 19, 762-73	15.1	191
376	The psychiatric GWAS consortium: big science comes to psychiatry. *Neuron*, **2010**, 68, 182-6	13.9	185
375	Comparative genetic architectures of schizophrenia in East Asian and European populations. *Nature Genetics*, **2019**, 51, 1670-1678	36.3	185
374	Extremely low-coverage sequencing and imputation increases power for genome-wide association studies. *Nature Genetics*, **2012**, 44, 631-5	36.3	184
373	The genetics of schizophrenia. *PLoS Medicine*, **2005**, 2, e212	11.6	182
372	Polygenic Risk Score, Parental Socioeconomic Status, Family History of Psychiatric Disorders, and the Risk for Schizophrenia: A Danish Population-Based Study and Meta-analysis. *JAMA Psychiatry*, **2015**, 72, 635-41	14.5	177
371	Methylome-wide association study of schizophrenia: identifying blood biomarker signatures of environmental insults. *JAMA Psychiatry*, **2014**, 71, 255-64	14.5	172
370	Family history of schizophrenia and bipolar disorder as risk factors for autism. *Archives of General Psychiatry*, **2012**, 69, 1099-1103		167

369	Defining the Genetic, Genomic, Cellular, and Diagnostic Architectures of Psychiatric Disorders. *Cell*, **2019**, 177, 162-183	56.2	166
368	Genetic influences on schizophrenia and subcortical brain volumes: large-scale proof of concept. *Nature Neuroscience*, **2016**, 19, 420-431	25.5	163
367	Cross-disorder genomewide analysis of schizophrenia, bipolar disorder, and depression. *American Journal of Psychiatry*, **2010**, 167, 1254-63	11.9	157
366	zCall: a rare variant caller for array-based genotyping: genetics and population analysis. *Bioinformatics*, **2012**, 28, 2543-5	7.2	154
365	Common Disease Is More Complex Than Implied by the Core Gene Omnigenic Model. *Cell*, **2018**, 173, 1573-1580	56.2	151
364	A population-based twin study of functional somatic syndromes. *Psychological Medicine*, **2009**, 39, 497-505	6.9	150
363	Outcome of anorexia nervosa: eating attitudes, personality, and parental bonding. *International Journal of Eating Disorders*, **2000**, 28, 139-47	6.3	147
362	Genome-wide Association Studies in Ancestrally Diverse Populations: Opportunities, Methods, Pitfalls, and Recommendations. *Cell*, **2019**, 179, 589-603	56.2	145
361	The Swedish Twin Registry in the third millennium: an update. *Twin Research and Human Genetics*, **2006**, 9, 875-82	2.2	145
360	Transcriptome and epigenome landscape of human cortical development modeled in organoids. *Science*, **2018**, 362,	33.3	142
359	Susceptibility genes for nicotine dependence: a genome scan and followup in an independent sample suggest that regions on chromosomes 2, 4, 10, 16, 17 and 18 merit further study. *Molecular Psychiatry*, **1999**, 4, 129-44	15.1	138
358	Clinical phenotypes of perinatal depression and time of symptom onset: analysis of data from an international consortium. *Lancet Psychiatry,the*, **2017**, 4, 477-485	23.3	137
357	Analyses of allele-specific gene expression in highly divergent mouse crosses identifies pervasive allelic imbalance. *Nature Genetics*, **2015**, 47, 353-60	36.3	136
356	Gene expression in major depressive disorder. *Molecular Psychiatry*, **2016**, 21, 339-47	15.1	133
355	Effect of polygenic risk scores on depression in childhood trauma. *British Journal of Psychiatry*, **2014** , 205, 113-9	5.4	133
354	The contribution of rare variants to risk of schizophrenia in individuals with and without intellectual disability. *Nature Genetics*, **2017**, 49, 1167-1173	36.3	132
353	Genome-wide association of major depression: description of samples for the GAIN Major Depressive Disorder Study: NTR and NESDA biobank projects. *European Journal of Human Genetics*, **2008**, 16, 335-42	5.3	131
352	Evidence that duplications of 22q11.2 protect against schizophrenia. *Molecular Psychiatry*, **2014**, 19, 37-40	15.1	130

351	Meta-analysis of genome-wide association data of bipolar disorder and major depressive disorder. *Molecular Psychiatry*, **2011**, 16, 2-4	15.1	130
350	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
349	Recurrence risks for schizophrenia in a Swedish national cohort. *Psychological Medicine*, **2006**, 36, 1417-26	6.9	127
348	Genetic studies of major depressive disorder: why are there no genome-wide association study findings and what can we do about it?. *Biological Psychiatry*, **2014**, 76, 510-2	7.9	125
347	Genome-wide pharmacogenomic analysis of response to treatment with antipsychotics. *Molecular Psychiatry*, **2011**, 16, 76-85	15.1	124
346	Genomewide pharmacogenomic study of metabolic side effects to antipsychotic drugs. *Molecular Psychiatry*, **2011**, 16, 321-32	15.1	123
345	Functional gene group analysis identifies synaptic gene groups as risk factor for schizophrenia. *Molecular Psychiatry*, **2012**, 17, 996-1006	15.1	123
344	Patterns of remission, continuation and incidence of broadly defined eating disorders during early pregnancy in the Norwegian Mother and Child Cohort Study (MoBa). *Psychological Medicine*, **2007**, 37, 1109-18	6.9	120
343	Identification of a high-risk haplotype for the dystrobrevin binding protein 1 (DTNBP1) gene in the Irish study of high-density schizophrenia families. *Molecular Psychiatry*, **2003**, 8, 499-510	15.1	119
342	Clozapine-induced agranulocytosis is associated with rare HLA-DQB1 and HLA-B alleles. *Nature Communications*, **2014**, 5, 4757	17.4	118
341	Genetic risk profiles for depression and anxiety in adult and elderly cohorts. *Molecular Psychiatry*, **2011**, 16, 773-83	15.1	116
340	Genome-wide association study of smoking initiation and current smoking. *American Journal of Human Genetics*, **2009**, 84, 367-79	11	116
339	A comprehensive family-based replication study of schizophrenia genes. *JAMA Psychiatry*, **2013**, 70, 573-81	14.5	115
338	False discoveries and models for gene discovery. *Trends in Genetics*, **2003**, 19, 537-42	8.5	114
337	The use of race variables in genetic studies of complex traits and the goal of reducing health disparities: a transdisciplinary perspective. *American Psychologist*, **2005**, 60, 77-103	9.5	114
336	Genome-wide association study of suicide attempts in mood disorder patients. *American Journal of Psychiatry*, **2010**, 167, 1499-507	11.9	113
335	Genetic epidemiology of binging and vomiting. *British Journal of Psychiatry*, **1998**, 173, 75-9	5.4	112
334	Deletion of TOP3β, a component of FMRP-containing mRNPs, contributes to neurodevelopmental disorders. *Nature Neuroscience*, **2013**, 16, 1228-1237	25.5	110

333	The Mouse Universal Genotyping Array: From Substrains to Subspecies. *G3: Genes, Genomes, Genetics*, **2015**, 6, 263-79	3.2	109
332	Genomes of the Mouse Collaborative Cross. *Genetics*, **2017**, 206, 537-556	4	108
331	Genomewide association study of movement-related adverse antipsychotic effects. *Biological Psychiatry*, **2010**, 67, 279-82	7.9	107
330	The subtypes of major depression in a twin registry. *Journal of Affective Disorders*, **2002**, 68, 273-84	6.6	103
329	Meta-analysis of genome-wide association studies with overlapping subjects. *American Journal of Human Genetics*, **2009**, 85, 862-72	11	101
328	Gene expression imputation across multiple brain regions provides insights into schizophrenia risk. *Nature Genetics*, **2019**, 51, 659-674	36.3	99
327	Genomewide linkage study in the Irish affected sib pair study of alcohol dependence: evidence for a susceptibility region for symptoms of alcohol dependence on chromosome 4. *Molecular Psychiatry* , **2006**, 11, 603-11	15.1	98
326	The antipsychotic olanzapine interacts with the gut microbiome to cause weight gain in mouse. *PLoS ONE*, **2014**, 9, e115225	3.7	97
325	A Genetic Investigation of Sex Bias in the Prevalence of Attention-Deficit/Hyperactivity Disorder. *Biological Psychiatry*, **2018**, 83, 1044-1053	7.9	93
324	Genome-wide association study of post-traumatic stress disorder reexperiencing symptoms in >165,000 US veterans. *Nature Neuroscience*, **2019**, 22, 1394-1401	25.5	92
323	Runs of homozygosity implicate autozygosity as a schizophrenia risk factor. *PLoS Genetics*, **2012**, 8, e1002656		91
322	Genome-wide association study of exercise behavior in Dutch and American adults. *Medicine and Science in Sports and Exercise*, **2009**, 41, 1887-95	1.2	89
321	Genome-wide pharmacogenomic study of neurocognition as an indicator of antipsychotic treatment response in schizophrenia. *Neuropsychopharmacology*, **2011**, 36, 616-26	8.7	87
320	Genetic case-control association studies in neuropsychiatry. *Archives of General Psychiatry*, **2001**, 58, 1015-24		87
319	Sequencing and de novo assembly of 150 genomes from Denmark as a population reference. *Nature*, **2017**, 548, 87-91	50.4	87
318	Translating genome-wide association findings into new therapeutics for psychiatry. *Nature Neuroscience*, **2016**, 19, 1392-1396	25.5	86
317	High density methylation QTL analysis in human blood via next-generation sequencing of the methylated genomic DNA fraction. *Genome Biology*, **2015**, 16, 291	18.3	86
316	Estimation of SNP heritability from dense genotype data. *American Journal of Human Genetics*, **2013**, 93, 1151-5	11	85

315	Schizophrenia genetics: where next?. *Schizophrenia Bulletin*, **2011**, 37, 456-63	1.3	84
314	The genetic association between personality and major depression or bipolar disorder. A polygenic score analysis using genome-wide association data. *Translational Psychiatry*, **2011**, 1, e50	8.6	83
313	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
312	Specific glial functions contribute to schizophrenia susceptibility. *Schizophrenia Bulletin*, **2014**, 40, 925-35	1.3	82
311	Analysis of protein-coding genetic variation in 60,706 humans		81
310	Genetic identification of cell types underlying brain complex traits yields insights into the etiology of Parkinson's disease. *Nature Genetics*, **2020**, 52, 482-493	36.3	79
309	Author's Response to Dr. Leo. *PLoS Medicine*, **2006**, 3, e376	11.6	78
308	Polygenic overlap between schizophrenia risk and antipsychotic response: a genomic medicine approach. *Lancet Psychiatry,the*, **2016**, 3, 350-7	23.3	77
307	LifeGene--a large prospective population-based study of global relevance. *European Journal of Epidemiology*, **2011**, 26, 67-77	12.1	77
306	Evaluation of analyses of univariate discrete twin data. *Behavior Genetics*, **2002**, 32, 221-7	3.2	75
305	Evaluation of chromatin accessibility in prefrontal cortex of individuals with schizophrenia. *Nature Communications*, **2018**, 9, 3121	17.4	74
304	Haplotypes of four novel single nucleotide polymorphisms in the nicotinic acetylcholine receptor 2-subunit (CHRNB2) gene show no association with smoking initiation or nicotine dependence. *American Journal of Medical Genetics Part A*, **2000**, 96, 646-653		74
303	Converging genetic and functional brain imaging evidence links neuronal excitability to working memory, psychiatric disease, and brain activity. *Neuron*, **2014**, 81, 1203-1213	13.9	73
302	The genomics of schizophrenia: update and implications. *Journal of Clinical Investigation*, **2013**, 123, 4557-63	13.9	73
301	Genome-wide association studies: a primer. *Psychological Medicine*, **2010**, 40, 1063-77	6.9	73
300	Landscape of Conditional eQTL in Dorsolateral Prefrontal Cortex and Co-localization with Schizophrenia GWAS. *American Journal of Human Genetics*, **2018**, 102, 1169-1184	11	73
299	NCAM1 and neurocognition in schizophrenia. *Biological Psychiatry*, **2007**, 61, 902-10	7.9	70
298	Hypothesis-driven candidate genes for schizophrenia compared to genome-wide association results. *Psychological Medicine*, **2012**, 42, 607-16	6.9	69

297	Candidate genes for nicotine dependence via linkage, epistasis, and bioinformatics. *American Journal of Medical Genetics Part A*, **2004**, 126B, 23-36		69
296	An Analysis of Two Genome-wide Association Meta-analyses Identifies a New Locus for Broad Depression Phenotype. *Biological Psychiatry*, **2017**, 82, 322-329	7.9	68
295	Environmental pollution is associated with increased risk of psychiatric disorders in the US and Denmark. *PLoS Biology*, **2019**, 17, e3000353	9.7	68
294	Food cravers: characteristics of those who binge. *International Journal of Eating Disorders*, **1998**, 23, 353-60	6.9	68
293	Uncovering the Genetic Architecture of Major Depression. *Neuron*, **2019**, 102, 91-103	13.9	66
292	Adverse life events, psychiatric history, and biological predictors of postpartum depression in an ethnically diverse sample of postpartum women. *Psychological Medicine*, **2018**, 48, 1190-1200	6.9	66
291	Cigarettes and oral snuff use in Sweden: Prevalence and transitions. *Addiction*, **2006**, 101, 1509-15	4.6	65
290	Association of the tryptophan hydroxylase gene with smoking initiation but not progression to nicotine dependence. *American Journal of Medical Genetics Part A*, **2001**, 105, 479-84		65
289	TAMAL: an integrated approach to choosing SNPs for genetic studies of human complex traits. *Bioinformatics*, **2006**, 22, 626-7	7.2	64
288	Is Swedish snus associated with smoking initiation or smoking cessation?. *Tobacco Control*, **2005**, 14, 422-3	5.3	64
287	Reproducible Genetic Risk Loci for Anxiety: Results From ~200,000 Participants in the Million Veteran Program. *American Journal of Psychiatry*, **2020**, 177, 223-232	11.9	64
286	Ultra-rare disruptive and damaging mutations influence educational attainment in the general population. *Nature Neuroscience*, **2016**, 19, 1563-1565	25.5	63
285	Heritability of Perinatal Depression and Genetic Overlap With Nonperinatal Depression. *American Journal of Psychiatry*, **2016**, 173, 158-65	11.9	62
284	Discovery of the first genome-wide significant risk loci for ADHD		62
283	CNV analysis in a large schizophrenia sample implicates deletions at 16p12.1 and SLC1A1 and duplications at 1p36.33 and CGNL1. *Human Molecular Genetics*, **2014**, 23, 1669-76	5.6	61
282	Puzzling over schizophrenia: schizophrenia as a pathway disease. *Nature Medicine*, **2012**, 18, 210-1	50.5	61
281	Genome-wide association study of antipsychotic-induced QTc interval prolongation. *Pharmacogenomics Journal*, **2012**, 12, 165-72	3.5	61
280	Latent class analysis of functional somatic symptoms in a population-based sample of twins. *Journal of Psychosomatic Research*, **2010**, 68, 447-53	4.1	60

279	Predictors of rapid and sustained response to cognitive-behavioral therapy for bulimia nervosa. *International Journal of Eating Disorders*, **1999**, 26, 137-44	6.3	60
278	Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. *Nature Genetics*, **2021**, 53, 1300-1310	36.3	60
277	Multivariate phenotype association analysis by marker-set kernel machine regression. *Genetic Epidemiology*, **2012**, 36, 686-95	2.6	59
276	Joint Contributions of Rare Copy Number Variants and Common SNPs to Risk for Schizophrenia. *American Journal of Psychiatry*, **2019**, 176, 29-35	11.9	59
275	Quantifying the Impact of Rare and Ultra-rare Coding Variation across the Phenotypic Spectrum. *American Journal of Human Genetics*, **2018**, 102, 1204-1211	11	59
274	Obesity remodels activity and transcriptional state of a lateral hypothalamic brake on feeding. *Science*, **2019**, 364, 1271-1274	33.3	58
273	GWA study data mining and independent replication identify cardiomyopathy-associated 5 (CMYA5) as a risk gene for schizophrenia. *Molecular Psychiatry*, **2011**, 16, 1117-29	15.1	58
272	A meta-analysis of gene expression quantitative trait loci in brain. *Translational Psychiatry*, **2014**, 4, e459	8.6	56
271	Chronic fatigue in a population sample: definitions and heterogeneity. *Psychological Medicine*, **2005** , 35, 1337-48	6.9	56
270	The epidemiology of chronic fatigue in the Swedish Twin Registry. *Psychological Medicine*, **2005**, 35, 1317-26	6.9	56
269	Latent class analysis of symptoms associated with chronic fatigue syndrome and fibromyalgia. *Psychological Medicine*, **2002**, 32, 881-8	6.9	55
268	Reciprocal duplication of the Williams-Beuren syndrome deletion on chromosome 7q11.23 is associated with schizophrenia. *Biological Psychiatry*, **2014**, 75, 371-7	7.9	54
267	Ethnic stratification of the association of RGS4 variants with antipsychotic treatment response in schizophrenia. *Biological Psychiatry*, **2008**, 63, 32-41	7.9	54
266	A genome-wide association study of kynurenic acid in cerebrospinal fluid: implications for psychosis and cognitive impairment in bipolar disorder. *Molecular Psychiatry*, **2016**, 21, 1342-50	15.1	53
265	The genetic structure of the Swedish population. *PLoS ONE*, **2011**, 6, e22547	3.7	53
264	Typology of common psychiatric syndromes. An empirical study. *British Journal of Psychiatry*, **1998**, 173, 312-9	5.4	53
263	CommonMind Consortium provides transcriptomic and epigenomic data for Schizophrenia and Bipolar Disorder. *Scientific Data*, **2019**, 6, 180	8.2	52
262	Allelic differences between Europeans and Chinese for CREB1 SNPs and their implications in gene expression regulation, hippocampal structure and function, and bipolar disorder susceptibility. *Molecular Psychiatry*, **2014**, 19, 452-61	15.1	52

261	Genetic influences on eight psychiatric disorders based on family data of 4 408 646 full and half-siblings, and genetic data of 333 748 cases and controls. *Psychological Medicine*, **2019**, 49, 1166-1173	6.9	52
260	Functional Architectures of Local and Distal Regulation of Gene Expression in Multiple Human Tissues. *American Journal of Human Genetics*, **2017**, 100, 605-616	11	50
259	Modeling psychiatric disorders: from genomic findings to cellular phenotypes. *Molecular Psychiatry*, **2016**, 21, 1167-79	15.1	49
258	Applying polygenic risk scores to postpartum depression. *Archives of Womens Mental Health*, **2014**, 17, 519-28	5	49
257	Genetic modifiers and subtypes in schizophrenia: investigations of age at onset, severity, sex and family history. *Schizophrenia Research*, **2014**, 154, 48-53	3.6	49
256	Genetic effects influencing risk for major depressive disorder in China and Europe. *Translational Psychiatry*, **2017**, 7, e1074	8.6	48
255	Integrated Bayesian analysis of rare exonic variants to identify risk genes for schizophrenia and neurodevelopmental disorders. *Genome Medicine*, **2017**, 9, 114	14.4	48
254	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
253	CNS-restricted Transduction and CRISPR/Cas9-mediated Gene Deletion with an Engineered AAV Vector. *Molecular Therapy - Nucleic Acids*, **2016**, 5, e338	10.7	48
252	The impact of education, country, race and ethnicity on the self-report of postpartum depression using the Edinburgh Postnatal Depression Scale. *Psychological Medicine*, **2017**, 47, 787-799	6.9	47
251	The effect of LRRK2 loss-of-function variants in humans. *Nature Medicine*, **2020**, 26, 869-877	50.5	47
250	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
249	A multi-megabase copy number gain causes maternal transmission ratio distortion on mouse chromosome 2. *PLoS Genetics*, **2015**, 11, e1004850	6	46
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