Patrick F Sullivan

List of Publications by Year in Descending Order

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	Genetic heterogeneity and subtypes of major depression.. *Molecular Psychiatry*, **2022**,	15.1	2
439	Sex-Dependent Shared and Nonshared Genetic Architecture Across Mood and Psychotic Disorders. *Biological Psychiatry*, **2022**, 91, 102-117	7.9	11
438	THUNDER: A reference-free deconvolution method to infer cell type proportions from bulk Hi-C data.. *PLoS Genetics*, **2022**, 18, e1010102	6	0
437	Characterizing mood disorders in the AFFECT study: a large, longitudinal, and phenotypically rich genetic cohort in the US.. *Translational Psychiatry*, **2022**, 12, 121	8.6	0
436	Acute COVID-19 severity and mental health morbidity trajectories in patient populations of six nations: an observational study.. *Lancet Public Health, The*, **2022**,	22.4	5
435	Mapping genomic loci implicates genes and synaptic biology in schizophrenia.. *Nature*, **2022**,	50.4	35
434	Rare coding variants in ten genes confer substantial risk for schizophrenia.. *Nature*, **2022**,	50.4	16
433	Transcriptome-wide association study for postpartum depression implicates altered B-cell activation and insulin resistance.. *Molecular Psychiatry*, **2022**,	15.1	1
432	Gene expression changes following chronic antipsychotic exposure in single cells from mouse striatum.. *Molecular Psychiatry*, **2022**,	15.1	2
431	Increased schizophrenia family history burden and reduced premorbid IQ in treatment-resistant schizophrenia: a Swedish National Register and Genomic Study. *Molecular Psychiatry*, **2021**, 26, 4487-4495	15.1	10
430	Genome-wide association study of panic disorder reveals genetic overlap with neuroticism and depression. *Molecular Psychiatry*, **2021**, 26, 4179-4190	15.1	8
429	Cohort Profile: COVIDMENT: COVID-19 cohorts on mental health across six nations.. *International Journal of Epidemiology*, **2021**,	7.8	2
428	The climate envelope of Alaska's northern treelines: implications for controlling factors and future treeline advance. *Ecography*, **2021**, 44, 1710	6.5	5
427	Conditional GWAS analysis to identify disorder-specific SNPs for psychiatric disorders. *Molecular Psychiatry*, **2021**, 26, 2070-2081	15.1	19
426	The association between family history and genomic burden with schizophrenia mortality: a Swedish population-based register and genetic sample study. *Translational Psychiatry*, **2021**, 11, 163	8.6	
425	HLA-DQB1 6672G>C (rs113332494) is associated with clozapine-induced neutropenia and agranulocytosis in individuals of European ancestry. *Translational Psychiatry*, **2021**, 11, 214	8.6	3
424	Comparative drought sensitivity of co-occurring white spruce and paper birch in interior Alaska. *Journal of Ecology*, **2021**, 109, 2448-2460	6	2

423	The Eating Disorders Genetics Initiative (EDGI): study protocol. *BMC Psychiatry*, **2021**, 21, 234	4.2	7
422	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
421	Lack of Support for the Genes by Early Environment Interaction Hypothesis in the Pathogenesis of Schizophrenia. *Schizophrenia Bulletin*, **2021**,	1.3	6
420	Transcriptome-wide association analysis of brain structures yields insights into pleiotropy with complex neuropsychiatric traits. *Nature Communications*, **2021**, 12, 2878	17.4	2
419	Neuronal and glial 3D chromatin architecture informs the cellular etiology of brain disorders. *Nature Communications*, **2021**, 12, 3968	17.4	2
418	Combined cellomics and proteomics analysis reveals shared neuronal morphology and molecular pathway phenotypes for multiple schizophrenia risk genes. *Molecular Psychiatry*, **2021**, 26, 784-799	15.1	10
417	Genome-wide association study of patients with a severe major depressive episode treated with electroconvulsive therapy. *Molecular Psychiatry*, **2021**, 26, 2429-2439	15.1	8
416	DNA methylation meta-analysis reveals cellular alterations in psychosis and markers of treatment-resistant schizophrenia. *ELife*, **2021**, 10,	8.9	15
415	Swedish large-scale schizophrenia study: Why do patients and healthy controls participate?. *Schizophrenia Research*, **2021**, 228, 360-366	3.6	
414	Herbivory and warming interact in opposing patterns of covariation between arctic shrub species at large and local scales. *Proceedings of the National Academy of Sciences of the United States of America*, **2021**, 118,	11.5	2
413	Technological readiness and implementation of genomic-driven precision medicine for complex diseases. *Journal of Internal Medicine*, **2021**, 290, 602-620	10.8	6
412	The epidemiology of psychiatric disorders in Africa: a scoping review. *Lancet Psychiatry,the*, **2021**, 8, 717-731	13.3	0
411	Identifying the Common Genetic Basis of Antidepressant Response. *Biological Psychiatry Global Open Science*, **2021**,		4
410	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
409	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
408	Investigating rare pathogenic/likely pathogenic exonic variation in bipolar disorder. *Molecular Psychiatry*, **2021**, 26, 5239-5250	15.1	3
407	Familial risk and heritability of intellectual disability: a population-based cohort study in Sweden.. *Journal of Child Psychology and Psychiatry and Allied Disciplines*, **2021**,	7.9	1
406	The Relationship Between Polygenic Risk Scores and Cognition in Schizophrenia. *Schizophrenia Bulletin*, **2020**, 46, 336-344	1.3	38

405	Divergence of Arctic shrub growth associated with sea ice decline. *Proceedings of the National Academy of Sciences of the United States of America*, **2020**, 117, 33334-33344	11.5	17
404	Association test using Copy Number Profile Curves (CONCUR) enhances power in rare copy number variant analysis. *PLoS Computational Biology*, **2020**, 16, e1007797	5	1
403	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
402	Test-statistic inflation in methylome-wide association studies. *Epigenetics*, **2020**, 15, 1163-1166	5.7	5
401	Genetic stratification of depression in UK Biobank. *Translational Psychiatry*, **2020**, 10, 163	8.6	8
400	The mutational constraint spectrum quantified from variation in 141,456 humans. *Nature*, **2020**, 581, 434-443	50.4	2278
399	The effect of LRRK2 loss-of-function variants in humans. *Nature Medicine*, **2020**, 26, 869-877	50.5	47
398	mTADA is a framework for identifying risk genes from de novo mutations in multiple traits. *Nature Communications*, **2020**, 11, 2929	17.4	2
397	Functional annotation of rare structural variation in the human brain. *Nature Communications*, **2020**, 11, 2990	17.4	18
396	Chronicity and Sex Affect Genetic Risk Prediction in Schizophrenia. *Frontiers in Psychiatry*, **2020**, 11, 313	5	2
395	Increasing the Clinical Psychiatric Knowledge Base About Pathogenic Copy Number Variation. *American Journal of Psychiatry*, **2020**, 177, 204-209	11.9	14
394	Robust Hi-C Maps of Enhancer-Promoter Interactions Reveal the Function of Non-coding Genome in Neural Development and Diseases. *Molecular Cell*, **2020**, 79, 521-534.e15	17.6	38
393	Stitching the synapse: Cross-linking mass spectrometry into resolving synaptic protein interactions. *Science Advances*, **2020**, 6, eaax5783	14.3	35
392	A Munc18-1 mutant mimicking phosphorylation by Down Syndrome-related kinase Dyrk1a supports normal synaptic transmission and promotes recovery after intense activity. *Scientific Reports*, **2020**, 10, 3181	4.9	
391	Pathways of tundra encroachment by trees and tall shrubs in the western Brooks Range of Alaska. *Ecography*, **2020**, 43, 769-778	6.5	8
390	Robust kernel association testing (RobKAT). *Genetic Epidemiology*, **2020**, 44, 272-282	2.6	1
389	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
388	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

387	Clinical phenotypes of peripartum depression and time of onset **2020**, 1-14		2
386	Treatment-resistant psychotic symptoms and the 15q11.2 BP1-BP2 (Burnside-Butler) deletion syndrome: case report and review of the literature. *Translational Psychiatry*, **2020**, 10, 42	8.6	6
385	Characterization of Single Gene Copy Number Variants in Schizophrenia. *Biological Psychiatry*, **2020**, 87, 736-744	7.9	8
384	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
383	The Psychiatric Genomics Consortium: History, development, and the future **2020**, 91-101		3
382	International Consortium on the Genetics of Electroconvulsive Therapy and Severe Depressive Disorders (Gen-ECT-ic). *European Archives of Psychiatry and Clinical Neuroscience*, **2020**, 270, 921-932	5.1	8
381	Treatment-resistant psychotic symptoms and early-onset dementia: A case report of the 3q29 deletion syndrome. *Schizophrenia Research*, **2020**, 224, 195-197	3.6	2
380	Large eQTL meta-analysis reveals differing patterns between cerebral cortical and cerebellar brain regions. *Scientific Data*, **2020**, 7, 340	8.2	26
379	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
378	PCM1 is necessary for focal ciliary integrity and is a candidate for severe schizophrenia. *Nature Communications*, **2020**, 11, 5903	17.4	4
377	Antipsychotic Behavioral Phenotypes in the Mouse Collaborative Cross Recombinant Inbred Inter-Crosses (RIX). *G3: Genes, Genomes, Genetics*, **2020**, 10, 3165-3177	3.2	1
376	Labile carbon limits late winter microbial activity near Arctic treeline. *Nature Communications*, **2020**, 11, 4024	17.4	6
375	A shared genetic contribution to breast cancer and schizophrenia. *Nature Communications*, **2020**, 11, 4637	17.4	11
374	Contributions of common genetic variants to risk of schizophrenia among individuals of African and Latino ancestry. *Molecular Psychiatry*, **2020**, 25, 2455-2467	15.1	41
373	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
372	Classical Human Leukocyte Antigen Alleles and C4 Haplotypes Are Not Significantly Associated With Depression. *Biological Psychiatry*, **2020**, 87, 419-430	7.9	9
371	Increased burden of ultra-rare structural variants localizing to boundaries of topologically associated domains in schizophrenia. *Nature Communications*, **2020**, 11, 1842	17.4	22
370	Unraveling the genetic architecture of major depressive disorder: merits and pitfalls of the approaches used in genome-wide association studies. *Psychological Medicine*, **2019**, 49, 2646-2656	6.9	12

369	CommonMind Consortium provides transcriptomic and epigenomic data for Schizophrenia and Bipolar Disorder. *Scientific Data*, **2019**, 6, 180	8.2	52
368	The Genomics of Electroconvulsive Therapy International Consortium (GenECT-ic). *Lancet Psychiatry,the*, **2019**, 6, e23	23.3	3
367	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
366	Methylation age acceleration does not predict mortality in schizophrenia. *Translational Psychiatry*, **2019**, 9, 157	8.6	9
365	Associations Between Attention-Deficit/Hyperactivity Disorder and Various Eating Disorders: A Swedish Nationwide Population Study Using Multiple Genetically Informative Approaches. *Biological Psychiatry*, **2019**, 86, 577-586	7.9	24
364	A Single-Cell Model for Synaptic Transmission and Plasticity in Human iPSC-Derived Neurons. *Cell Reports*, **2019**, 27, 2199-2211.e6	10.6	40
363	Experimentally warmer and drier conditions in an Arctic plant community reveal microclimatic controls on senescence. *Ecosphere*, **2019**, 10, e02677	3.1	7
362	Genome-wide association study identifies 30 loci associated with bipolar disorder. *Nature Genetics*, **2019**, 51, 793-803	36.3	662
361	The international postpartum depression: action towards causes and treatment (PACT) consortium. *International Review of Psychiatry*, **2019**, 31, 229-236	3.6	6
360	Defining the Genetic, Genomic, Cellular, and Diagnostic Architectures of Psychiatric Disorders. *Cell*, **2019**, 177, 162-183	56.2	166
359	Gene expression imputation across multiple brain regions provides insights into schizophrenia risk. *Nature Genetics*, **2019**, 51, 659-674	36.3	99
358	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
357	Roadmap for a precision-medicine initiative in the Nordic region. *Nature Genetics*, **2019**, 51, 924-930	36.3	12
356	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
355	Uncovering the Genetic Architecture of Major Depression. *Neuron*, **2019**, 102, 91-103	13.9	66
354	The genomics of major psychiatric disorders in a large pedigree from Northern Sweden. *Translational Psychiatry*, **2019**, 9, 60	8.6	11
353	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
352	Identification of common genetic risk variants for autism spectrum disorder. *Nature Genetics*, **2019**, 51, 431-444	36.3	746

351	Environmental pollution is associated with increased risk of psychiatric disorders in the US and Denmark. *PLoS Biology*, **2019**, 17, e3000353	9.7	68
350	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
349	Single cell analysis of autism patient with bi-allelic NRXN1-alpha deletion reveals skewed fate choice in neural progenitors and impaired neuronal functionality. *Experimental Cell Research*, **2019**, 383, 111469	4.2	22
348	Non-coding variability at the APOE locus contributes to the Alzheimer's risk. *Nature Communications*, **2019**, 10, 3310	17.4	42
347	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
346	Obesity remodels activity and transcriptional state of a lateral hypothalamic brake on feeding. *Science*, **2019**, 364, 1271-1274	33.3	58
345	Genome-wide Association Studies in Ancestrally Diverse Populations: Opportunities, Methods, Pitfalls, and Recommendations. *Cell*, **2019**, 179, 589-603	56.2	145
344	Genetic risk scores for major psychiatric disorders and the risk of postpartum psychiatric disorders. *Translational Psychiatry*, **2019**, 9, 288	8.6	10
343	A Combined Cellomics and Proteomics Approach to Uncover Neuronal Pathways to Psychiatric Disorder. *Neuromethods*, **2019**, 199-215	0.4	
342	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
341	Comparative genetic architectures of schizophrenia in East Asian and European populations. *Nature Genetics*, **2019**, 51, 1670-1678	36.3	185
340	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
339	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
338	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
337	Discovery of the first genome-wide significant risk loci for attention deficit/hyperactivity disorder. *Nature Genetics*, **2019**, 51, 63-75	36.3	826
336	Genome-wide meta-analysis identifies new loci and functional pathways influencing Alzheimer's disease risk. *Nature Genetics*, **2019**, 51, 404-413	36.3	771
335	Common-variant associations with fragile X syndrome. *Molecular Psychiatry*, **2019**, 24, 338-344	15.1	4
334	Biological annotation of genetic loci associated with intelligence in a meta-analysis of 87,740 individuals. *Molecular Psychiatry*, **2019**, 24, 182-197	15.1	31

333	Genome-wide association study of depression phenotypes in UK Biobank identifies variants in excitatory synaptic pathways. *Nature Communications*, **2018**, 9, 1470	17.4	226
332	Transcriptome-wide association study of schizophrenia and chromatin activity yields mechanistic disease insights. *Nature Genetics*, **2018**, 50, 538-548	36.3	222
331	MIR137 schizophrenia-associated locus controls synaptic function by regulating synaptogenesis, synapse maturation and synaptic transmission. *Human Molecular Genetics*, **2018**, 27, 1879-1891	5.6	36
330	Pamela Sklar 1959-2017. *Nature Neuroscience*, **2018**, 21, 151	25.5	
329	Inference on phenotype-specific effects of genes using multivariate kernel machine regression. *Genetic Epidemiology*, **2018**, 42, 64-79	2.6	0
328	Developmental Delay, Treatment-Resistant Psychosis, and Early-Onset Dementia in a Man With 22q11 Deletion Syndrome and Huntington's Disease. *American Journal of Psychiatry*, **2018**, 175, 400-407	11.9	7
327	Genetic variation in 117 myelination-related genes in schizophrenia: Replication of association to lipid biosynthesis genes. *Scientific Reports*, **2018**, 8, 6915	4.9	7
326	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
325	A Comprehensive Analysis of Nuclear-Encoded Mitochondrial Genes in Schizophrenia. *Biological Psychiatry*, **2018**, 83, 780-789	7.9	14
324	Comparative genomic evidence for the involvement of schizophrenia risk genes in antipsychotic effects. *Molecular Psychiatry*, **2018**, 23, 708-712	15.1	20
323	A Powerful Test for SNP Effects on Multivariate Binary Outcomes using Kernel Machine Regression. *Statistics in Biosciences*, **2018**, 10, 117-138	1.5	3
322	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
321	Psychiatric Genomics: An Update and an Agenda. *American Journal of Psychiatry*, **2018**, 175, 15-27	11.9	328
320	Declining growth of deciduous shrubs in the warming climate of continental western Greenland. *Journal of Ecology*, **2018**, 106, 640-654	6	37
319	Genetic risk scores and family history as predictors of schizophrenia in Nordic registers. *Psychological Medicine*, **2018**, 48, 1201-1208	6.9	18
318	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
317	Evaluation of chromatin accessibility in prefrontal cortex of individuals with schizophrenia. *Nature Communications*, **2018**, 9, 3121	17.4	74
316	Analysis of shared heritability in common disorders of the brain. *Science*, **2018**, 360,	33.3	666

315	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
314	Common Disease Is More Complex Than Implied by the Core Gene Omnigenic Model. *Cell*, **2018**, 173, 1573-1580	56.2	151
313	Building a schizophrenia genetic network: transcription factor 4 regulates genes involved in neuronal development and schizophrenia risk. *Human Molecular Genetics*, **2018**, 27, 3246-3256	5.6	20
312	Examining the role of common and rare mitochondrial variants in schizophrenia. *PLoS ONE*, **2018**, 13, e0191153	3.7	14
311	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
310	Improved ethical guidance for the return of results from psychiatric genomics research. *Molecular Psychiatry*, **2018**, 23, 15-23	15.1	23
309	A Genetic Investigation of Sex Bias in the Prevalence of Attention-Deficit/Hyperactivity Disorder. *Biological Psychiatry*, **2018**, 83, 1044-1053	7.9	93
308	National-scale precision medicine for psychiatric disorders in Sweden. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2018**, 177, 630-634	3.5	6
307	Investigation of common, low-frequency and rare genome-wide variation in anorexia nervosa. *Molecular Psychiatry*, **2018**, 23, 1169-1180	15.1	24
306	Transcriptome and epigenome landscape of human cortical development modeled in organoids. *Science*, **2018**, 362,	33.3	142
305	Integrative functional genomic analysis of human brain development and neuropsychiatric risks. *Science*, **2018**, 362,	33.3	277
304	PPD ACT: an app-based genetic study of postpartum depression. *Translational Psychiatry*, **2018**, 8, 260	8.6	10
303	The Anorexia Nervosa Genetics Initiative (ANGI): Overview and methods. *Contemporary Clinical Trials*, **2018**, 74, 61-69	2.3	36
302	Addendum: Genome-wide association study of depression phenotypes in UK Biobank identifies variants in excitatory synaptic pathways. *Nature Communications*, **2018**, 9, 3578	17.4	3
301	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
300	Enhancing Psychosis-Spectrum Nosology Through an International Data Sharing Initiative. *Schizophrenia Bulletin*, **2018**, 44, S460-S467	1.3	9
299	Genetic identification of brain cell types underlying schizophrenia. *Nature Genetics*, **2018**, 50, 825-833	36.3	295
298	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

297	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
296	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
295	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
294	Schizophrenia and the dynamic genome. *Genome Medicine*, **2017**, 9, 22	14.4	5
293	Deep Sequencing of 71 Candidate Genes to Characterize Variation Associated with Alcohol Dependence. *Alcoholism: Clinical and Experimental Research*, **2017**, 41, 711-718	3.7	8
292	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
291	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
290	HUGIn: Hi-C Unifying Genomic Interrogator. *Bioinformatics*, **2017**, 33, 3793-3795	7.2	41
289	Genomes of the Mouse Collaborative Cross. *Genetics*, **2017**, 206, 537-556	4	108
288	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
287	Genetic effects influencing risk for major depressive disorder in China and Europe. *Translational Psychiatry*, **2017**, 7, e1074	8.6	48
286	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
285	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
284	Genome-wide association analysis identifies 30 new susceptibility loci for schizophrenia. *Nature Genetics*, **2017**, 49, 1576-1583	36.3	272
283	How Good Were Candidate Gene Guesses in Schizophrenia Genetics?. *Biological Psychiatry*, **2017**, 82, 696-697	7.9	16
282	Integrated Bayesian analysis of rare exonic variants to identify risk genes for schizophrenia and neurodevelopmental disorders. *Genome Medicine*, **2017**, 9, 114	14.4	48
281	Mutation intolerant genes and targets of FMRP are enriched for nonsynonymous alleles in schizophrenia. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2017**, 174, 724-731	3.5	16
280	Genome-wide association analysis identifies common variants influencing infant brain volumes. *Translational Psychiatry*, **2017**, 7, e1188	8.6	17

279	Limited evidence of declining growth among moisture-limited black and white spruce in interior Alaska. *Scientific Reports*, **2017**, 7, 15344	4.9	24
278	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
277	Implication of LRRC4C and DPP6 in neurodevelopmental disorders. *American Journal of Medical Genetics, Part A*, **2017**, 173, 395-406	2.5	22
276	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
275	Genome-wide common and rare variant analysis provides novel insights into clozapine-associated neutropenia. *Molecular Psychiatry*, **2017**, 22, 1502-1508	15.1	45
274	Sequencing and de novo assembly of 150 genomes from Denmark as a population reference. *Nature*, **2017**, 548, 87-91	50.4	87
273	Exploration of large, rare copy number variants associated with psychiatric and neurodevelopmental disorders in individuals with anorexia nervosa. *Psychiatric Genetics*, **2017**, 27, 152-158	2.9	11
272	Deep Sequencing of Three Loci Implicated in Large-Scale Genome-Wide Association Study Smoking Meta-Analyses. *Nicotine and Tobacco Research*, **2016**, 18, 626-31	4.9	9
271	Heritability of Perinatal Depression and Genetic Overlap With Nonperinatal Depression. *American Journal of Psychiatry*, **2016**, 173, 158-65	11.9	62
270	Nationwide Genomic Study in Denmark Reveals Remarkable Population Homogeneity. *Genetics*, **2016**, 204, 711-722	4	40
269	Analysis of protein-coding genetic variation in 60,706 humans. *Nature*, **2016**, 536, 285-91	50.4	6940
268	Risk Overlap Between Clinical Disorders **2016**, 387-396		
267	Translating genome-wide association findings into new therapeutics for psychiatry. *Nature Neuroscience*, **2016**, 19, 1392-1396	25.5	86
266	Modeling psychiatric disorders: from genomic findings to cellular phenotypes. *Molecular Psychiatry*, **2016**, 21, 1167-79	15.1	49
265	Gene expression in major depressive disorder. *Molecular Psychiatry*, **2016**, 21, 339-47	15.1	133
264	Quantifying prion disease penetrance using large population control cohorts. *Science Translational Medicine*, **2016**, 8, 322ra9	17.5	205
263	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
262	What Next in Schizophrenia Genetics for the Psychiatric Genomics Consortium?. *Schizophrenia Bulletin*, **2016**, 42, 538-41	1.3	19

261	Comprehensive analysis of schizophrenia-associated loci highlights ion channel pathways and biologically plausible candidate causal genes. *Human Molecular Genetics*, **2016**, 25, 1247-54	5.6	42
260	Polygenic overlap between schizophrenia risk and antipsychotic response: a genomic medicine approach. *Lancet Psychiatry,the*, **2016**, 3, 350-7	23.3	77
259	Integrative approaches for large-scale transcriptome-wide association studies. *Nature Genetics*, **2016**, 48, 245-52	36.3	843
258	Genetic influences on schizophrenia and subcortical brain volumes: large-scale proof of concept. *Nature Neuroscience*, **2016**, 19, 420-431	25.5	163
257	Rare loss-of-function variants in SETD1A are associated with schizophrenia and developmental disorders. *Nature Neuroscience*, **2016**, 19, 571-7	25.5	284
256	A hidden Markov random field-based Bayesian method for the detection of long-range chromosomal interactions in Hi-C data. *Bioinformatics*, **2016**, 32, 650-6	7.2	32
255	No Reliable Association between Runs of Homozygosity and Schizophrenia in a Well-Powered Replication Study. *PLoS Genetics*, **2016**, 12, e1006343	6	15
254	One CNV Discordance in NRXN1 Observed Upon Genome-wide Screening in 38 Pairs of Adult Healthy Monozygotic Twins. *Twin Research and Human Genetics*, **2016**, 19, 97-103	2.2	2
253	Gene expression elucidates functional impact of polygenic risk for schizophrenia. *Nature Neuroscience*, **2016**, 19, 1442-1453	25.5	622
252	Increased burden of ultra-rare protein-altering variants among 4,877 individuals with schizophrenia. *Nature Neuroscience*, **2016**, 19, 1433-1441	25.5	291
251	Ultra-rare disruptive and damaging mutations influence educational attainment in the general population. *Nature Neuroscience*, **2016**, 19, 1563-1565	25.5	63
250	CNS-restricted Transduction and CRISPR/Cas9-mediated Gene Deletion with an Engineered AAV Vector. *Molecular Therapy - Nucleic Acids*, **2016**, 5, e338	10.7	48
249	A multi-megabase copy number gain causes maternal transmission ratio distortion on mouse chromosome 2. *PLoS Genetics*, **2015**, 11, e1004850	6	46
248	Functional characterization of the PCLO p.Ser4814Ala variant associated with major depressive disorder reveals cellular but not behavioral differences. *Neuroscience*, **2015**, 300, 518-38	3.9	9
247	CNV Concordance in 1,097 MZ Twin Pairs. *Twin Research and Human Genetics*, **2015**, 18, 1-12	2.2	31
246	No evidence for rare recessive and compound heterozygous disruptive variants in schizophrenia. *European Journal of Human Genetics*, **2015**, 23, 555-7	5.3	17
245	Genetics of disease: Associations with depression. *Nature*, **2015**, 523, 539-40	50.4	11
244	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

243	Meta-analysis of the heritability of human traits based on fifty years of twin studies. *Nature Genetics*, **2015**, 47, 702-9	36.3	1184
242	Analyses of allele-specific gene expression in highly divergent mouse crosses identifies pervasive allelic imbalance. *Nature Genetics*, **2015**, 47, 353-60	36.3	136
241	Biological pathways and networks implicated in psychiatric disorders. *Current Opinion in Behavioral Sciences*, **2015**, 2, 58-68	4	17
240	Expression analysis in a rat psychosis model identifies novel candidate genes validated in a large case-control sample of schizophrenia. *Translational Psychiatry*, **2015**, 5, e656	8.6	25
239	New data and an old puzzle: the negative association between schizophrenia and rheumatoid arthritis. *International Journal of Epidemiology*, **2015**, 44, 1706-21	7.8	43
238	The PsychENCODE project. *Nature Neuroscience*, **2015**, 18, 1707-12	25.5	226
237	Disruption of the microRNA 137 primary transcript results in early embryonic lethality in mice. *Biological Psychiatry*, **2015**, 77, e5-7	7.9	18
236	Genome-Wide Meta-Analysis of Longitudinal Alcohol Consumption Across Youth and Early Adulthood. *Twin Research and Human Genetics*, **2015**, 18, 335-47	2.2	20
235	Multiple SNP Set Analysis for Genome-Wide Association Studies Through Bayesian Latent Variable Selection. *Genetic Epidemiology*, **2015**, 39, 664-77	2.6	11
234	Fast eQTL Analysis for Twin Studies. *Genetic Epidemiology*, **2015**, 39, 357-65	2.6	3
233	Combined Whole Methylome and Genomewide Association Study Implicates CNTN4 in Alcohol Use. *Alcoholism: Clinical and Experimental Research*, **2015**, 39, 1396-405	3.7	13
232	A New Method for Detecting Associations with Rare Copy-Number Variants. *PLoS Genetics*, **2015**, 11, e1005403	6	10
231	Evaluating historical candidate genes for schizophrenia. *Molecular Psychiatry*, **2015**, 20, 555-62	15.1	219
230	IsoDOT Detects Differential RNA-isoform Expression/Usage with respect to a Categorical or Continuous Covariate with High Sensitivity and Specificity. *Journal of the American Statistical Association*, **2015**, 110, 975-986	2.8	7
229	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
228	Refinement of schizophrenia GWAS loci using methylome-wide association data. *Human Genetics*, **2015**, 134, 77-87	6.3	16
227	Educational attainment influences levels of homozygosity through migration and assortative mating. *PLoS ONE*, **2015**, 10, e0118935	3.7	28
226	The Mouse Universal Genotyping Array: From Substrains to Subspecies. *G3: Genes, Genomes, Genetics*, **2015**, 6, 263-79	3.2	109

225	Heritability and genomics of gene expression in peripheral blood. *Nature Genetics*, **2014**, 46, 430-7	36.3	258
224	Genetic variation associated with euphorigenic effects of d-amphetamine is associated with diminished risk for schizophrenia and attention deficit hyperactivity disorder. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 5968-73	11.5	15
223	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
222	Evidence that duplications of 22q11.2 protect against schizophrenia. *Molecular Psychiatry*, **2014**, 19, 37-40	15.1	130
221	A polygenic burden of rare disruptive mutations in schizophrenia. *Nature*, **2014**, 506, 185-90	50.4	1059
220	Partitioning heritability of regulatory and cell-type-specific variants across 11 common diseases. *American Journal of Human Genetics*, **2014**, 95, 535-52	11	411
219	Copy number variation in schizophrenia in Sweden. *Molecular Psychiatry*, **2014**, 19, 762-73	15.1	191
218	A meta-analysis of gene expression quantitative trait loci in brain. *Translational Psychiatry*, **2014**, 4, e459	8.6	56
217	Polygenic dissection of diagnosis and clinical dimensions of bipolar disorder and schizophrenia. *Molecular Psychiatry*, **2014**, 19, 1017-1024	15.1	258
216	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
215	A genome-wide association study of anorexia nervosa. *Molecular Psychiatry*, **2014**, 19, 1085-94	15.1	224
214	A novel statistical approach for jointly analyzing RNA-Seq data from F1 reciprocal crosses and inbred lines. *Genetics*, **2014**, 197, 389-99	4	17
213	Effect of polygenic risk scores on depression in childhood trauma. *British Journal of Psychiatry*, **2014** , 205, 113-9	5.4	133
212	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
211	The antipsychotic olanzapine interacts with the gut microbiome to cause weight gain in mouse. *PLoS ONE*, **2014**, 9, e115225	3.7	97
210	Clozapine-induced agranulocytosis is associated with rare HLA-DQB1 and HLA-B alleles. *Nature Communications*, **2014**, 5, 4757	17.4	118
209	Using ancestry-informative markers to identify fine structure across 15 populations of European origin. *European Journal of Human Genetics*, **2014**, 22, 1190-200	5.3	30
208	Specific glial functions contribute to schizophrenia susceptibility. *Schizophrenia Bulletin*, **2014**, 40, 925-35	1.3	82

207	Genetics of adverse reactions to haloperidol in a mouse diallel: a drug-placebo experiment and Bayesian causal analysis. *Genetics*, **2014**, 196, 321-47	4	18
206	Transcriptional targets of the schizophrenia risk gene MIR137. *Translational Psychiatry*, **2014**, 4, e404	8.6	42
205	Applying polygenic risk scores to postpartum depression. *Archives of Womens Mental Health*, **2014**, 17, 519-28	5	49
204	A recessive genetic model and runs of homozygosity in major depressive disorder. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2014**, 165B, 157-66	3.5	19
203	Clonal hematopoiesis and blood-cancer risk inferred from blood DNA sequence. *New England Journal of Medicine*, **2014**, 371, 2477-87	59.2	1855
202	An inherited duplication at the gene p21 Protein-Activated Kinase 7 (PAK7) is a risk factor for psychosis. *Human Molecular Genetics*, **2014**, 23, 3316-26	5.6	32
201	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
200	Methylome-wide association study of schizophrenia: identifying blood biomarker signatures of environmental insults. *JAMA Psychiatry*, **2014**, 71, 255-64	14.5	172
199	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
198	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
197	Genome-wide association analysis identifies 13 new risk loci for schizophrenia. *Nature Genetics*, **2013**, 45, 1150-9	36.3	1153
196	Detecting large copy number variants using exome genotyping arrays in a large Swedish schizophrenia sample. *Molecular Psychiatry*, **2013**, 18, 1178-84	15.1	27
195	Deletion of TOP3β, a component of FMRP-containing mRNPs, contributes to neurodevelopmental disorders. *Nature Neuroscience*, **2013**, 16, 1228-1237	25.5	110
194	Brain levels of the neurotoxic pyridinium metabolite HPP+ and extrapyramidal symptoms in haloperidol-treated mice. *NeuroToxicology*, **2013**, 39, 153-7	4.4	3
193	Genetic predictors of risk and resilience in psychiatric disorders: a cross-disorder genome-wide association study of functional impairment in major depressive disorder, bipolar disorder, and schizophrenia. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2013**, 162B, 779-88	3.5	32
192	Association between autozygosity and major depression: stratification due to religious assortment. *Behavior Genetics*, **2013**, 43, 455-67	3.2	20
191	Non-random mating, parent-of-origin, and maternal-fetal incompatibility effects in schizophrenia. *Schizophrenia Research*, **2013**, 143, 11-7	3.6	1
190	Estimation of SNP heritability from dense genotype data. *American Journal of Human Genetics*, **2013**, 93, 1151-5	11	85

189	Assessment of gene expression in peripheral blood using RNAseq before and after weight restoration in anorexia nervosa. *Psychiatry Research*, **2013**, 210, 287-93	9.9	9
188	Comprehensive analysis of copy number variation in monozygotic twins discordant for bipolar disorder or schizophrenia. *Schizophrenia Research*, **2013**, 146, 289-90	3.6	16
187	A mega-analysis of genome-wide association studies for major depressive disorder. *Molecular Psychiatry*, **2013**, 18, 497-511	15.1	853
186	Deep resequencing and association analysis of schizophrenia candidate genes. *Molecular Psychiatry*, **2013**, 18, 138-40	15.1	13
185	A comprehensive family-based replication study of schizophrenia genes. *JAMA Psychiatry*, **2013**, 70, 573-81	14.5	115
184	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
183	Identifying bipolar disorder susceptibility loci in a densely affected pedigree. *Molecular Psychiatry*, **2013**, 18, 1245-6	15.1	21
182	Genome-wide association study of patient-rated and clinician-rated global impression of severity during antipsychotic treatment. *Pharmacogenetics and Genomics*, **2013**, 23, 69-77	1.9	33
181	The genomics of schizophrenia: update and implications. *Journal of Clinical Investigation*, **2013**, 123, 4557-63	13.9	73
180	Genotype-based ancestral background consistently predicts efficacy and side effects across treatments in CATIE and STAR*D. *PLoS ONE*, **2013**, 8, e55239	3.7	6
179	Utilizing twins as controls for non-twin case-materials in genome wide association studies. *PLoS ONE*, **2013**, 8, e83101	3.7	5
178	Estimating the proportion of variation in susceptibility to schizophrenia captured by common SNPs. *Nature Genetics*, **2012**, 44, 247-50	36.3	471
177	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
176	Multivariate phenotype association analysis by marker-set kernel machine regression. *Genetic Epidemiology*, **2012**, 36, 686-95	2.6	59
175	Discovery and statistical genotyping of copy-number variation from whole-exome sequencing depth. *American Journal of Human Genetics*, **2012**, 91, 597-607	11	391
174	SNP-based analysis of neuroactive ligand-receptor interaction pathways implicates PGE2 as a novel mediator of antipsychotic treatment response: data from the CATIE study. *Schizophrenia Research*, **2012**, 135, 200-1	3.6	28
173	Hypothesis-driven candidate genes for schizophrenia compared to genome-wide association results. *Psychological Medicine*, **2012**, 42, 607-16	6.9	69
172	Puzzling over schizophrenia: schizophrenia as a pathway disease. *Nature Medicine*, **2012**, 18, 210-1	50.5	61

171	Genetic architectures of psychiatric disorders: the emerging picture and its implications. *Nature Reviews Genetics*, **2012**, 13, 537-51	30.1	866
170	Extremely low-coverage sequencing and imputation increases power for genome-wide association studies. *Nature Genetics*, **2012**, 44, 631-5	36.3	184
169	Exome sequencing and the genetic basis of complex traits. *Nature Genetics*, **2012**, 44, 623-30	36.3	303
168	Genome-wide association mapping of loci for antipsychotic-induced extrapyramidal symptoms in mice. *Mammalian Genome*, **2012**, 23, 322-35	3.2	30
167	Genome-wide association study of major depressive disorder: new results, meta-analysis, and lessons learned. *Molecular Psychiatry*, **2012**, 17, 36-48	15.1	335
166	Runs of homozygosity implicate autozygosity as a schizophrenia risk factor. *PLoS Genetics*, **2012**, 8, e1002656		91
165	Family history of schizophrenia and bipolar disorder as risk factors for autism. *Archives of General Psychiatry*, **2012**, 69, 1099-1103		167
164	Transcriptome atlases of mouse brain reveals differential expression across brain regions and genetic backgrounds. *G3: Genes, Genomes, Genetics*, **2012**, 2, 203-11	3.2	13
163	Familial aggregation of schizophrenia: the moderating effect of age at onset, parental immigration, paternal age and season of birth. *Scandinavian Journal of Public Health*, **2012**, 40, 43-50	3	23
162	seeQTL: a searchable database for human eQTLs. *Bioinformatics*, **2012**, 28, 451-2	7.2	256
161	zCall: a rare variant caller for array-based genotyping: genetics and population analysis. *Bioinformatics*, **2012**, 28, 2543-5	7.2	154
160	Functional gene group analysis identifies synaptic gene groups as risk factor for schizophrenia. *Molecular Psychiatry*, **2012**, 17, 996-1006	15.1	123
159	Genome-wide association study of antipsychotic-induced QTc interval prolongation. *Pharmacogenomics Journal*, **2012**, 12, 165-72	3.5	61
158	Antipsychotic-induced vacuous chewing movements and extrapyramidal side effects are highly heritable in mice. *Pharmacogenomics Journal*, **2012**, 12, 147-55	3.5	26
157	The genetic structure of the Swedish population. *PLoS ONE*, **2011**, 6, e22547	3.7	53
156	Replication of association of 3p21.1 with susceptibility to bipolar disorder but not major depression. *Nature Genetics*, **2011**, 43, 3-5; author reply 5	36.3	23
155	Meta-analysis of genome-wide association data of bipolar disorder and major depressive disorder. *Molecular Psychiatry*, **2011**, 16, 2-4	15.1	130
154	Genome-wide pharmacogenomic analysis of response to treatment with antipsychotics. *Molecular Psychiatry*, **2011**, 16, 76-85	15.1	124

153	Genomewide pharmacogenomic study of metabolic side effects to antipsychotic drugs. *Molecular Psychiatry*, **2011**, 16, 321-32	15.1	123
152	Poor replication of candidate genes for major depressive disorder using genome-wide association data. *Molecular Psychiatry*, **2011**, 16, 516-32	15.1	219
151	Genetic risk profiles for depression and anxiety in adult and elderly cohorts. *Molecular Psychiatry*, **2011**, 16, 773-83	15.1	116
150	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
149	LifeGene--a large prospective population-based study of global relevance. *European Journal of Epidemiology*, **2011**, 26, 67-77	12.1	77
148	An unbiased metagenomic search for infectious agents using monozygotic twins discordant for chronic fatigue. *BMC Microbiology*, **2011**, 11, 2	4.5	17
147	Schizophrenia genetics: where next?. *Schizophrenia Bulletin*, **2011**, 37, 456-63	1.3	84
146	Genome-wide pharmacogenomic study of neurocognition as an indicator of antipsychotic treatment response in schizophrenia. *Neuropsychopharmacology*, **2011**, 36, 616-26	8.7	87
145	Modifiers and subtype-specific analyses in whole-genome association studies: a likelihood framework. *Human Heredity*, **2011**, 72, 10-20	1.1	19
144	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
143	Response to Mitchell and Porteus. *Molecular Psychiatry*, **2010**, 15, 450-2	15.1	3
142	Haplotype-based pharmacogenetic analysis for longitudinal quantitative traits in the presence of dropout. *Journal of Biopharmaceutical Statistics*, **2010**, 20, 334-50	1.3	3
141	A quality control algorithm for filtering SNPs in genome-wide association studies. *Bioinformatics*, **2010**, 26, 1731-7	7.2	15
140	Cross-disorder genomewide analysis of schizophrenia, bipolar disorder, and depression. *American Journal of Psychiatry*, **2010**, 167, 1254-63	11.9	157
139	Genome-wide association study of suicide attempts in mood disorder patients. *American Journal of Psychiatry*, **2010**, 167, 1499-507	11.9	113
138	Genomewide association study of movement-related adverse antipsychotic effects. *Biological Psychiatry*, **2010**, 67, 279-82	7.9	107
137	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
136	The psychiatric GWAS consortium: big science comes to psychiatry. *Neuron*, **2010**, 68, 182-6	13.9	185

135	Genome-wide association studies: a primer. *Psychological Medicine*, **2010**, 40, 1063-77	6.9	73
134	A candidate gene study of Tardive dyskinesia in the CATIE schizophrenia trial. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2010**, 153B, 336-40	3.5	21
133	No association of the serotonin transporter polymorphisms 5-HTTLPR and RS25531 with schizophrenia or neurocognition. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2010**, 153B, 1115-7	3.5	7
132	Association study of 182 candidate genes in anorexia nervosa. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2010**, 153B, 1070-80	3.5	45
131	Fine-mapping reveals novel alternative splicing of the dopamine transporter. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2010**, 153B, 1434-47	3.5	16
130	A population-based twin study of functional somatic syndromes. *Psychological Medicine*, **2009**, 39, 497-505	6.9	150
129	Genome-wide association study of alcohol dependence. *Archives of General Psychiatry*, **2009**, 66, 773-84		318
128	Genomewide association studies: history, rationale, and prospects for psychiatric disorders. *American Journal of Psychiatry*, **2009**, 166, 540-56	11.9	355
127	Suggestive linkage on chromosome 2, 8, and 17 for lifetime major depression. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2009**, 150B, 352-8	3.5	17
126	Genome-wide association for major depressive disorder: a possible role for the presynaptic protein piccolo. *Molecular Psychiatry*, **2009**, 14, 359-75	15.1	322
125	Common polygenic variation contributes to risk of schizophrenia and bipolar disorder. *Nature*, **2009** , 460, 748-52	50.4	3568
124	Microduplications of 16p11.2 are associated with schizophrenia. *Nature Genetics*, **2009**, 41, 1223-7	36.3	550
123	Genome-wide association study of smoking initiation and current smoking. *American Journal of Human Genetics*, **2009**, 84, 367-79	11	116
122	Meta-analysis of genome-wide association studies with overlapping subjects. *American Journal of Human Genetics*, **2009**, 85, 862-72	11	101
121	A systematic method for estimating individual responses to treatment with antipsychotics in CATIE. *Schizophrenia Research*, **2009**, 107, 13-21	3.6	34
120	Common genetic determinants of schizophrenia and bipolar disorder in Swedish families: a population-based study. *Lancet, The*, **2009**, 373, 234-9	40	1467
119	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
118	Gene expression in peripheral blood leukocytes in monozygotic twins discordant for chronic fatigue: no evidence of a biomarker. *PLoS ONE*, **2009**, 4, e5805	3.7	19

117	Genomewide association for schizophrenia in the CATIE study: results of stage 1. *Molecular Psychiatry*, **2008**, 13, 570-84	15.1	308
116	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
115	Association of RGS2 and RGS5 variants with schizophrenia symptom severity. *Schizophrenia Research*, **2008**, 101, 67-75	3.6	31
114	The dice are rolling for schizophrenia genetics. *Psychological Medicine*, **2008**, 38, 1693-6; discussion 1818-20	6.9	13
113	Ethnic stratification of the association of RGS4 variants with antipsychotic treatment response in schizophrenia. *Biological Psychiatry*, **2008**, 63, 32-41	7.9	54
112	Genomewide linkage survey of nicotine dependence phenotypes. *Drug and Alcohol Dependence*, **2008**, 93, 210-6	4.9	8
111	The STAGE cohort: a prospective study of tobacco use among Swedish twins. *Nicotine and Tobacco Research*, **2008**, 10, 1727-35	4.9	43
110	Genetic determinants of variable metabolism have little impact on the clinical use of leading antipsychotics in the CATIE study. *Genetics in Medicine*, **2008**, 10, 720-9	8.1	40
109	Snus use and other correlates of smoking cessation in the Swedish Twin Registry. *Psychological Medicine*, **2008**, 38, 1299-308	6.9	17
108	Schizophrenia genetics: the search for a hard lead. *Current Opinion in Psychiatry*, **2008**, 21, 157-60	4.9	21
107	Model-based gene selection shows engrailed 1 is associated with antipsychotic response. *Pharmacogenetics and Genomics*, **2008**, 18, 751-9	1.9	11
106	Genome-wide linkage analysis of multiple measures of neuroticism of 2 large cohorts from Australia and the Netherlands. *Archives of General Psychiatry*, **2008**, 65, 649-58		31
105	The neuregulin 1 promoter polymorphism rs6994992 is not associated with chronic schizophrenia or neurocognition. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2008**, 147B, 1298-300	3.5	24
104	A searchable database of genetic evidence for psychiatric disorders. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2008**, 147B, 671-5	3.5	30
103	Comment on a simple and improved correction for population stratification. *American Journal of Human Genetics*, **2008**, 82, 524-6; author reply 526-8	11	13
102	NCAM1 and neurocognition in schizophrenia. *Biological Psychiatry*, **2007**, 61, 902-10	7.9	70
101	Spurious genetic associations. *Biological Psychiatry*, **2007**, 61, 1121-6	7.9	268
100	Comparison of full-text searching to metadata searching for genes in two biomedical literature cohorts. *Journal of the Association for Information Science and Technology*, **2007**, 58, 2341-2352		13

99	New models of collaboration in genome-wide association studies: the Genetic Association Information Network. *Nature Genetics*, **2007**, 39, 1045-51	36.3	258
98	Irritable bowel syndrome: a co-twin control analysis. *American Journal of Gastroenterology*, **2007**, 102, 2220-9	0.7	30
97	Twin analyses of fatigue. *Twin Research and Human Genetics*, **2007**, 10, 729-33	2.2	23
96	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
95	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
94	TAMAL: an integrated approach to choosing SNPs for genetic studies of human complex traits. *Bioinformatics*, **2006**, 22, 626-7	7.2	64
93	Author's Response to Dr. Leo. *PLoS Medicine*, **2006**, 3, e376	11.6	78
92	The Swedish Twin Registry in the Third Millennium: An Update. *Twin Research and Human Genetics*, **2006**, 9, 875-882	2.2	290
91	Empirical Evaluation of the Genetic Similarity of Samples From Twin Registries in Australia and the Netherlands Using 359 STRP Markers. *Twin Research and Human Genetics*, **2006**, 9, 600-602	2.2	10
90	Recurrence risks for schizophrenia in a Swedish national cohort. *Psychological Medicine*, **2006**, 36, 1417-26	6.9	127
89	Neuropsychological function in bulimia with comorbid borderline personality disorder and depression. *Acta Neuropsychiatrica*, **2006**, 18, 162-7	3.9	5
88	Cigarettes and oral snuff use in Sweden: Prevalence and transitions. *Addiction*, **2006**, 101, 1509-15	4.6	65
87	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
86	The Swedish Twin Registry in the third millennium: an update. *Twin Research and Human Genetics*, **2006**, 9, 875-82	2.2	145
85	Empirical evaluation of the genetic similarity of samples from twin registries in Australia and the Netherlands using 359 STRP markers. *Twin Research and Human Genetics*, **2006**, 9, 600-2	2.2	6
84	The prevalence of self-reported chronic fatigue in a U.S. twin registry. *Journal of Psychosomatic Research*, **2005**, 59, 283-90	4.1	20
83	Chronic fatigue in a population sample: definitions and heterogeneity. *Psychological Medicine*, **2005** , 35, 1337-48	6.9	56
82	Twin analyses of chronic fatigue in a Swedish national sample. *Psychological Medicine*, **2005**, 35, 1327-36	6.9	45

81	The Irish Affected Sib Pair Study of Alcohol Dependence: study methodology and validation of diagnosis by interview and family history. *Alcoholism: Clinical and Experimental Research*, **2005**, 29, 417-29	3.7	40
80	Epidemiology of cancer-related fatigue in the Swedish twin registry. *Cancer*, **2005**, 104, 2022-31	6.4	35
79	The genetics of schizophrenia. *PLoS Medicine*, **2005**, 2, e212	11.6	182
78	Is Swedish snus associated with smoking initiation or smoking cessation?. *Tobacco Control*, **2005**, 14, 422-4	5.3	64
77	The epidemiology of chronic fatigue in the Swedish Twin Registry. *Psychological Medicine*, **2005**, 35, 1317-26	6.9	56
76	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
75	Candidate genes for nicotine dependence via linkage, epistasis, and bioinformatics. *American Journal of Medical Genetics Part A*, **2004**, 126B, 23-36		69
74	Evaluation of genetic substructure in the Irish Study of High-Density Schizophrenia Families. *Psychiatric Genetics*, **2004**, 14, 187-9	2.9	
73	Genotyping accuracy for whole-genome amplification of DNA from buccal epithelial cells. *Twin Research and Human Genetics*, **2004**, 7, 482-4		6
72	Fatigue in a community sample of twins. *Psychological Medicine*, **2003**, 33, 263-81	6.9	34
71	A framework for controlling false discovery rates and minimizing the amount of genotyping in the search for disease mutations. *Human Heredity*, **2003**, 56, 188-99	1.1	40
70	False discoveries and models for gene discovery. *Trends in Genetics*, **2003**, 19, 537-42	8.5	114
69	Multipoint and single point non-parametric linkage analysis with imperfect data. *American Journal of Medical Genetics Part A*, **2003**, 121B, 89-94		13
68	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
67	Single nucleotide polymorphism genotyping: biochemistry, protocol, cost and throughput. *Pharmacogenomics Journal*, **2003**, 3, 77-96	3.5	196
66	Discrepant results regarding long-term survival of patients with anorexia nervosa?. *Mayo Clinic Proceedings*, **2003**, 78, 273-4	6.4	16
65	Schizophrenia as a complex trait: evidence from a meta-analysis of twin studies. *Archives of General Psychiatry*, **2003**, 60, 1187-92		1593
64	The subtypes of major depression in a twin registry. *Journal of Affective Disorders*, **2002**, 68, 273-84	6.6	103

63	Evaluation of analyses of univariate discrete twin data. *Behavior Genetics*, **2002**, 32, 221-7	3.2	75
62	Latent class analysis of symptoms associated with chronic fatigue syndrome and fibromyalgia. *Psychological Medicine*, **2002**, 32, 881-8	6.9	55
61	An association study of DRD5 with smoking initiation and progression to nicotine dependence. *American Journal of Medical Genetics Part A*, **2001**, 105, 259-65		39
60	Analysis of epistasis in linked regions in the Irish study of high-density schizophrenia families. *American Journal of Medical Genetics Part A*, **2001**, 105, 266-70		8
59	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
58	Genetic case-control association studies in neuropsychiatry. *Archives of General Psychiatry*, **2001**, 58, 1015-24		87
57	Twin studies of eating disorders: a review. *International Journal of Eating Disorders*, **2000**, 27, 1-20	6.3	205
56	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
55	Outcome of anorexia nervosa: eating attitudes, personality, and parental bonding. *International Journal of Eating Disorders*, **2000**, 28, 139-47	6.3	147
54	Genetic epidemiology of major depression: review and meta-analysis. *American Journal of Psychiatry*, **2000**, 157, 1552-62	11.9	2142
53	Optimal treatment for Maori with alcohol and drug-use-related problems: an investigation of cultural factors in treatment. *Substance Use and Misuse*, **2000**, 35, 281-300	2.2	22
52	Twin studies of eating disorders: A review **2000**, 27, 1		1
51	Twin studies of eating disorders: A review **2000**, 27, 1		1
50	The genetic epidemiology of smoking. *Nicotine and Tobacco Research*, **1999**, 1 Suppl 2, S51-7; discussion S69-70	4.9	309
49	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
48	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
47	Food cravers: characteristics of those who binge. *International Journal of Eating Disorders*, **1998**, 23, 353-60	6.3	68
46	Elevated total cholesterol in bulimia nervosa. *International Journal of Eating Disorders*, **1998**, 23, 425-32	6.3	12

45	Personality and dimensions of dietary restraint. *International Journal of Eating Disorders*, **1998**, 24, 371-96	3	46
44	Typology of common psychiatric syndromes. An empirical study. *British Journal of Psychiatry*, **1998**, 173, 312-9	5.4	53
43	Genetic epidemiology of binging and vomiting. *British Journal of Psychiatry*, **1998**, 173, 75-9	5.4	112
42	Family history of depression in clinic and community samples. *Journal of Affective Disorders*, **1996**, 40, 159-68	6.6	24
41	Effects of exclusion criteria in depression treatment studies. *Journal of Affective Disorders*, **1994**, 32, 21-6	6.6	16
40	Genetic investigations in the CATIE sample237-254		
39	Rare schizophrenia risk variant burden is conserved in diverse human populations		1
38	Bipolar II Disorder: Personality and Outcome in two Clinical Samples		3
37	Mania in the Swedish Twin Registry: Criterion Validity and Prevalence		2
36	Genetic variation in the Major Histocompatibility Complex and association with depression		1
35	Characterization of single gene copy number variants in schizophrenia		1
34	Epigenetic age is accelerated in schizophrenia with age- and sex-specific effects and associated with polygenic disease risk		2
33	Antipsychotic behavioral phenotypes in the mouse Collaborative Cross recombinant inbred inter-crosses (RIX)		1
32	Analysis of protein-coding genetic variation in 60,706 humans		81
31	Gene Expression Elucidates Functional Impact of Polygenic Risk for Schizophrenia		3
30	Transcriptome-wide association study of schizophrenia and chromatin activity yields mechanistic disease insights		15
29	Genome-Wide Association Study Reveals First Locus for Anorexia Nervosa and Metabolic Correlations		4
28	Psychiatric Genomics: An Update and an Agenda		3

27	Proof of concept: Molecular prediction of schizophrenia risk	1
26	Genetic stratification of depression in UK Biobank suggests a subgroup linked to age of natural menopause	6
25	Evaluation of Chromatin Accessibility in Prefrontal Cortex of Schizophrenia Cases and Controls	5
24	Genetic identification Of brain cell types underlying schizophrenia	7
23	Discovery of the first genome-wide significant risk loci for ADHD	62
22	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depressive disorder	21
21	Genome-wide association study of depression phenotypes in UK Biobank (n = 322,580) identifies the enrichment of variants in excitatory synaptic pathways	8
20	GWAS meta-analysis (N=279,930) identifies new genes and functional links to intelligence	9
19	Large-scale analysis of DNA methylation identifies cellular alterations in blood from psychosis patients and molecular biomarkers of treatment-resistant schizophrenia	1
18	Gene expression imputation across multiple brain regions reveals schizophrenia risk throughout development	6
17	Common risk variants identified in autism spectrum disorder	32
16	Identifying tissues implicated in Anorexia Nervosa using Transcriptomic Imputation	1
15	Using three-dimensional regulatory chromatin interactions from adult and fetal cortex to interpret genetic results for psychiatric disorders and cognitive traits	26
14	Evidence of causal effect of major depression on alcohol dependence: Findings from the Psychiatric Genomics Consortium	4
13	Genome-wide meta-analysis of depression identifies 102 independent variants and highlights the importance of the prefrontal brain regions	8
12	Comparative genetic architectures of schizophrenia in East Asian and European populations	8
11	Genome wide meta-analysis identifies genomic relationships, novel loci, and pleiotropic mechanisms across eight psychiatric disorders	10
10	Genetic Identification of Cell Types Underlying Brain Complex Traits Yields Novel Insights Into the Etiology of Parkinson□ Disease	9

9	Reproducible Risk Loci and Psychiatric Comorbidities in Anxiety: Results from ~200,000 Million Veteran Program Participants		2
8	Human loss-of-function variants suggest that partial LRRK2 inhibition is a safe therapeutic strategy for Parkinson disease		7
7	Conditional GWAS analysis identifies putative disorder-specific SNPs for psychiatric disorders		6
6	Robust Hi-C chromatin loop maps in human neurogenesis and brain tissues at high-resolution		1
5	Functional partitioning of local and distal gene expression regulation in multiple human tissues		2
4	Quantifying the impact of rare and ultra-rare coding variation across the phenotypic spectrum		1
3	Functional consequences of genetic loci associated with intelligence in a meta-analysis of 87,740 individuals		3
2	Genetic heterogeneity and subtypes of major depression		2
1	Delusions, Hallucinations, and Cognitive Decline in Middle Age: A Case of Dementia, GIGYF2 Gene Mutation, and 22q11 Duplication. *Indian Journal of Psychological Medicine*,025371762210848	1.8	1