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List of Publications by Citations

648 papers	75,835 citations	128 h-index	267 g-index
700 ext. papers	92,705 ext. citations	10.3 avg, IF	7.29 L-index

#	Paper	IF	Citations
648	ANNOVAR: functional annotation of genetic variants from high-throughput sequencing data. *Nucleic Acids Research*, **2010**, 38, e164	20.1	7273
647	Host-microbe interactions have shaped the genetic architecture of inflammatory bowel disease. *Nature*, **2012**, 491, 119-24	50.4	3239
646	Meta-analysis of 74,046 individuals identifies 11 new susceptibility loci for Alzheimer's disease. *Nature Genetics*, **2013**, 45, 1452-8	36.3	2714
645	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. *Nature*, **2011**, 476, 214-9	50.4	1948
644	Genome-wide meta-analysis increases to 71 the number of confirmed Crohn's disease susceptibility loci. *Nature Genetics*, **2010**, 42, 1118-25	36.3	1946
643	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. *Nature Genetics*, **2013**, 45, 984-94	36.3	1628
642	Functional impact of global rare copy number variation in autism spectrum disorders. *Nature*, **2010**, 466, 368-72	50.4	1499
641	Common variants at MS4A4/MS4A6E, CD2AP, CD33 and EPHA1 are associated with late-onset Alzheimer's disease. *Nature Genetics*, **2011**, 43, 436-41	36.3	1367
640	PennCNV: an integrated hidden Markov model designed for high-resolution copy number variation detection in whole-genome SNP genotyping data. *Genome Research*, **2007**, 17, 1665-74	9.7	1278
639	Autism genome-wide copy number variation reveals ubiquitin and neuronal genes. *Nature*, **2009**, 459, 569-73	50.4	1075
638	Meta-analysis identifies 29 additional ulcerative colitis risk loci, increasing the number of confirmed associations to 47. *Nature Genetics*, **2011**, 43, 246-52	36.3	1028
637	An improved framework for confound regression and filtering for control of motion artifact in the preprocessing of resting-state functional connectivity data. *NeuroImage*, **2013**, 64, 240-56	7.9	1024
636	Identification of ALK as a major familial neuroblastoma predisposition gene. *Nature*, **2008**, 455, 930-5	50.4	960
635	Analysis of immune-related loci identifies 48 new susceptibility variants for multiple sclerosis. *Nature Genetics*, **2013**, 45, 1353-60	36.3	934
634	Genetic meta-analysis of diagnosed Alzheimer's disease identifies new risk loci and implicates A tau, immunity and lipid processing. *Nature Genetics*, **2019**, 51, 414-430	36.3	917
633	Impact of in-scanner head motion on multiple measures of functional connectivity: relevance for studies of neurodevelopment in youth. *NeuroImage*, **2012**, 60, 623-32	7.9	837
632	Discovery of the first genome-wide significant risk loci for attention deficit/hyperactivity disorder. *Nature Genetics*, **2019**, 51, 63-75	36.3	826

631	The gene encoding 5-lipoxygenase activating protein confers risk of myocardial infarction and stroke. *Nature Genetics*, **2004**, 36, 233-9	36.3	770
630	Common genetic variants on 5p14.1 associate with autism spectrum disorders. *Nature*, **2009**, 459, 528-33	50.4	760
629	Rare variants create synthetic genome-wide associations. *PLoS Biology*, **2010**, 8, e1000294	9.7	693
628	Sex differences in the structural connectome of the human brain. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 823-8	11.5	692
627	Analysis of shared heritability in common disorders of the brain. *Science*, **2018**, 360,	33.3	666
626	The interleukin-6 receptor as a target for prevention of coronary heart disease: a mendelian randomisation analysis. *Lancet, The*, **2012**, 379, 1214-24	40	658
625	Convergence of genes and cellular pathways dysregulated in autism spectrum disorders. *American Journal of Human Genetics*, **2014**, 94, 677-94	11	635
624	Analysing biological pathways in genome-wide association studies. *Nature Reviews Genetics*, **2010**, 11, 843-54	30.1	629
623	De novo mutations in histone-modifying genes in congenital heart disease. *Nature*, **2013**, 498, 220-3	50.4	591
622	Rare coding variants in PLCG2, ABI3, and TREM2 implicate microglial-mediated innate immunity in Alzheimer's disease. *Nature Genetics*, **2017**, 49, 1373-1384	36.3	508
621	The Electronic Medical Records and Genomics (eMERGE) Network: past, present, and future. *Genetics in Medicine*, **2013**, 15, 761-71	8.1	484
620	Inherited determinants of Crohn's disease and ulcerative colitis phenotypes: a genetic association study. *Lancet, The*, **2016**, 387, 156-67	40	449
619	A genome-wide scan for common alleles affecting risk for autism. *Human Molecular Genetics*, **2010**, 19, 4072-82	5.6	443
618	A genome-wide association study identifies KIAA0350 as a type 1 diabetes gene. *Nature*, **2007**, 448, 591-4	50.4	424
617	HMG-coenzyme A reductase inhibition, type 2 diabetes, and bodyweight: evidence from genetic analysis and randomised trials. *Lancet, The*, **2015**, 385, 351-61	40	409
616	Association between alcohol and cardiovascular disease: Mendelian randomisation analysis based on individual participant data. *BMJ, The*, **2014**, 349, g4164	5.9	406
615	Genomic Relationships, Novel Loci, and Pleiotropic Mechanisms across Eight Psychiatric Disorders. *Cell*, **2019**, 179, 1469-1482.e11	56.2	402
614	Common variants at five new loci associated with early-onset inflammatory bowel disease. *Nature Genetics*, **2009**, 41, 1335-40	36.3	389

613	Identification of common variants influencing risk of the tauopathy progressive supranuclear palsy. *Nature Genetics*, **2011**, 43, 699-705	36.3	386
612	A genome-wide association study identifies CDHR3 as a susceptibility locus for early childhood asthma with severe exacerbations. *Nature Genetics*, **2014**, 46, 51-5	36.3	376
611	Common variants at 7p21 are associated with frontotemporal lobar degeneration with TDP-43 inclusions. *Nature Genetics*, **2010**, 42, 234-9	36.3	361
610	Meta-analysis of genome-wide association studies of attention-deficit/hyperactivity disorder. *Journal of the American Academy of Child and Adolescent Psychiatry*, **2010**, 49, 884-97	7.2	357
609	Copy number variants in schizophrenia: confirmation of five previous findings and new evidence for 3q29 microdeletions and VIPR2 duplications. *American Journal of Psychiatry*, **2011**, 168, 302-16	11.9	344
608	Meta-analysis confirms CR1, CLU, and PICALM as alzheimer disease risk loci and reveals interactions with APOE genotypes. *Archives of Neurology*, **2010**, 67, 1473-84		330
607	Multi-ancestry genome-wide association study of 21,000 cases and 95,000 controls identifies new risk loci for atopic dermatitis. *Nature Genetics*, **2015**, 47, 1449-1456	36.3	329
606	Age group and sex differences in performance on a computerized neurocognitive battery in children age 8-21. *Neuropsychology*, **2012**, 26, 251-265	3.8	325
605	Common variants at 5q22 associate with pediatric eosinophilic esophagitis. *Nature Genetics*, **2010**, 42, 289-91	36.3	321
604	Concept, design and implementation of a cardiovascular gene-centric 50 k SNP array for large-scale genomic association studies. *PLoS ONE*, **2008**, 3, e3583	3.7	321
603	Systematic review and meta-analysis of the association between {beta}2-adrenoceptor polymorphisms and asthma: a HuGE review. *American Journal of Epidemiology*, **2005**, 162, 201-11	3.8	319
602	Low concordance of multiple variant-calling pipelines: practical implications for exome and genome sequencing. *Genome Medicine*, **2013**, 5, 28	14.4	315
601	Multiple sclerosis genomic map implicates peripheral immune cells and microglia in susceptibility. *Science*, **2019**, 365,	33.3	309
600	Neuroimaging of the Philadelphia neurodevelopmental cohort. *NeuroImage*, **2014**, 86, 544-53	7.9	307
599	Mechanisms of mosaicism, chimerism and uniparental disomy identified by single nucleotide polymorphism array analysis. *Human Molecular Genetics*, **2010**, 19, 1263-75	5.6	306
598	Genome-wide analyses of exonic copy number variants in a family-based study point to novel autism susceptibility genes. *PLoS Genetics*, **2009**, 5, e1000536	6	305
597	A variant of the gene encoding leukotriene A4 hydrolase confers ethnicity-specific risk of myocardial infarction. *Nature Genetics*, **2006**, 38, 68-74	36.3	304
596	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

595	Common variation in KITLG and at 5q31.3 predisposes to testicular germ cell cancer. *Nature Genetics*, **2009**, 41, 811-5	36.3	294
594	High-resolution mapping and analysis of copy number variations in the human genome: a data resource for clinical and research applications. *Genome Research*, **2009**, 19, 1682-90	9.7	293
593	A genome-wide association meta-analysis identifies new childhood obesity loci. *Nature Genetics*, **2012**, 44, 526-31	36.3	292
592	Copy number variation at 1q21.1 associated with neuroblastoma. *Nature*, **2009**, 459, 987-91	50.4	285
591	Genome-wide copy number variation study associates metabotropic glutamate receptor gene networks with attention deficit hyperactivity disorder. *Nature Genetics*, **2011**, 44, 78-84	36.3	279
590	Individual common variants exert weak effects on the risk for autism spectrum disorders. *Human Molecular Genetics*, **2012**, 21, 4781-92	5.6	279
589	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
588	Thymic stromal lymphopoietin-elicited basophil responses promote eosinophilic esophagitis. *Nature Medicine*, **2013**, 19, 1005-13	50.5	271
587	Genome-wide associations for birth weight and correlations with adult disease. *Nature*, **2016**, 538, 248-252	50.4	266
586	Genome-wide association analysis identifies PDE4D as an asthma-susceptibility gene. *American Journal of Human Genetics*, **2009**, 84, 581-93	11	264
585	Variants of DENND1B associated with asthma in children. *New England Journal of Medicine*, **2010**, 362, 36-44	59.2	261
584	Loci on 20q13 and 21q22 are associated with pediatric-onset inflammatory bowel disease. *Nature Genetics*, **2008**, 40, 1211-5	36.3	256
583	Adjustment of genomic waves in signal intensities from whole-genome SNP genotyping platforms. *Nucleic Acids Research*, **2008**, 36, e126	20.1	255
582	Meta-analysis of genome-wide association studies identifies three new risk loci for atopic dermatitis. *Nature Genetics*, **2011**, 44, 187-92	36.3	244
581	A genome-wide meta-analysis of six type 1 diabetes cohorts identifies multiple associated loci. *PLoS Genetics*, **2011**, 7, e1002293	6	237
580	Familial aggregation of atrial fibrillation in Iceland. *European Heart Journal*, **2006**, 27, 708-12	9.5	237
579	New loci associated with birth weight identify genetic links between intrauterine growth and adult height and metabolism. *Nature Genetics*, **2013**, 45, 76-82	36.3	232
578	Integrative genomics identifies LMO1 as a neuroblastoma oncogene. *Nature*, **2011**, 469, 216-20	50.4	231

577	Common variations in BARD1 influence susceptibility to high-risk neuroblastoma. *Nature Genetics*, **2009**, 41, 718-23	36.3	226
576	PCSK9 genetic variants and risk of type 2 diabetes: a mendelian randomisation study. *Lancet Diabetes and Endocrinology,the*, **2017**, 5, 97-105	18.1	225
575	Chromosome 6p22 locus associated with clinically aggressive neuroblastoma. *New England Journal of Medicine*, **2008**, 358, 2585-93	59.2	224
574	Diverse genome-wide association studies associate the IL12/IL23 pathway with Crohn Disease. *American Journal of Human Genetics*, **2009**, 84, 399-405	11	219
573	Large-scale gene-centric meta-analysis across 39 studies identifies type 2 diabetes loci. *American Journal of Human Genetics*, **2012**, 90, 410-25	11	214
572	A genome-wide association study identifies a locus for nonsyndromic cleft lip with or without cleft palate on 8q24. *Journal of Pediatrics*, **2009**, 155, 909-13	3.6	214
571	Linked Sex Differences in Cognition and Functional Connectivity in Youth. *Cerebral Cortex*, **2015**, 25, 2383-94	5.1	209
570	Genome-wide association analysis identifies three new susceptibility loci for childhood body mass index. *Human Molecular Genetics*, **2016**, 25, 389-403	5.6	202
569	Genetic predisposition to neuroblastoma mediated by a LMO1 super-enhancer polymorphism. *Nature*, **2015**, 528, 418-21	50.4	201
568	Common variation at 6q16 within HACE1 and LIN28B influences susceptibility to neuroblastoma. *Nature Genetics*, **2012**, 44, 1126-30	36.3	198
567	RAD21 mutations cause a human cohesinopathy. *American Journal of Human Genetics*, **2012**, 90, 1014-27	11	197
566	Genome-wide analysis of copy number variants in attention deficit hyperactivity disorder: the role of rare variants and duplications at 15q13.3. *American Journal of Psychiatry*, **2012**, 169, 195-204	11.9	195
565	Duplication of 7q34 in pediatric low-grade astrocytomas detected by high-density single-nucleotide polymorphism-based genotype arrays results in a novel BRAF fusion gene. *Brain Pathology*, **2009**, 19, 449-58	6	194
564	SNVer: a statistical tool for variant calling in analysis of pooled or individual next-generation sequencing data. *Nucleic Acids Research*, **2011**, 39, e132	20.1	193
563	Distinct features of SARS-CoV-2-specific IgA response in COVID-19 patients. *European Respiratory Journal*, **2020**, 56,	13.6	192
562	A meta-analysis identifies new loci associated with body mass index in individuals of African ancestry. *Nature Genetics*, **2013**, 45, 690-6	36.3	192
561	Large-scale gene-centric meta-analysis across 32 studies identifies multiple lipid loci. *American Journal of Human Genetics*, **2012**, 91, 823-38	11	189
560	Effects of a 5-lipoxygenase-activating protein inhibitor on biomarkers associated with risk of myocardial infarction: a randomized trial. *JAMA - Journal of the American Medical Association*, **2005**, 293, 2245-56	27.4	187

559	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. *Nature Genetics*, **2018**, 50, 26-41	36.3	186
558	Variants in ADCY5 and near CCNL1 are associated with fetal growth and birth weight. *Nature Genetics*, **2010**, 42, 430-5	36.3	184
557	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. *Nature Genetics*, **2019**, 51, 804-814	36.3	181
556	Progressive increase in mtDNA 3243A>G heteroplasmy causes abrupt transcriptional reprogramming. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, E4033-42	11.5	180
555	A genome-wide association study on African-ancestry populations for asthma. *Journal of Allergy and Clinical Immunology*, **2010**, 125, 336-346.e4	11.5	179
554	A novel Alzheimer disease locus located near the gene encoding tau protein. *Molecular Psychiatry*, **2016**, 21, 108-17	15.1	175
553	The Philadelphia Neurodevelopmental Cohort: A publicly available resource for the study of normal and abnormal brain development in youth. *NeuroImage*, **2016**, 124, 1115-1119	7.9	173
552	Psychometric properties of the Penn Computerized Neurocognitive Battery. *Neuropsychology*, **2015**, 29, 235-46	3.8	169
551	Functional maturation of the executive system during adolescence. *Journal of Neuroscience*, **2013**, 33, 16249-61	6.6	168
550	Heterogeneous impact of motion on fundamental patterns of developmental changes in functional connectivity during youth. *NeuroImage*, **2013**, 83, 45-57	7.9	167
549	Using VAAST to identify an X-linked disorder resulting in lethality in male infants due to N-terminal acetyltransferase deficiency. *American Journal of Human Genetics*, **2011**, 89, 28-43	11	166
548	Strong synaptic transmission impact by copy number variations in schizophrenia. *Proceedings of the National Academy of Sciences of the United States of America*, **2010**, 107, 10584-9	11.5	165
547	Joint analysis of psychiatric disorders increases accuracy of risk prediction for schizophrenia, bipolar disorder, and major depressive disorder. *American Journal of Human Genetics*, **2015**, 96, 283-94	11	161
546	Copy-number disorders are a common cause of congenital kidney malformations. *American Journal of Human Genetics*, **2012**, 91, 987-97	11	161
545	Association analysis of the FTO gene with obesity in children of Caucasian and African ancestry reveals a common tagging SNP. *PLoS ONE*, **2008**, 3, e1746	3.7	161
544	Neurocognitive growth charting in psychosis spectrum youths. *JAMA Psychiatry*, **2014**, 71, 366-74	14.5	160
543	A genome-wide association study on obesity and obesity-related traits. *PLoS ONE*, **2011**, 6, e18939	3.7	160
542	Increased frequency of de novo copy number variants in congenital heart disease by integrative analysis of single nucleotide polymorphism array and exome sequence data. *Circulation Research*, **2014**, 115, 884-896	15.7	158

541	Causal effects of body mass index on cardiometabolic traits and events: a Mendelian randomization analysis. *American Journal of Human Genetics*, **2014**, 94, 198-208	11	156
540	Age-Related Effects and Sex Differences in Gray Matter Density, Volume, Mass, and Cortical Thickness from Childhood to Young Adulthood. *Journal of Neuroscience*, **2017**, 37, 5065-5073	6.6	152
539	A novel approach of homozygous haplotype sharing identifies candidate genes in autism spectrum disorder. *Human Genetics*, **2012**, 131, 565-79	6.3	150
538	From disease association to risk assessment: an optimistic view from genome-wide association studies on type 1 diabetes. *PLoS Genetics*, **2009**, 5, e1000678	6	150
537	Genetic Evidence for Causal Relationships Between Maternal Obesity-Related Traits and Birth Weight. *JAMA - Journal of the American Medical Association*, **2016**, 315, 1129-40	27.4	149
536	Convergent genetic and expression data implicate immunity in Alzheimer's disease. *Alzheimer's and Dementia*, **2015**, 11, 658-71	1.2	146
535	Epilepsy, hippocampal sclerosis and febrile seizures linked by common genetic variation around SCN1A. *Brain*, **2013**, 136, 3140-50	11.2	144
534	Meta-analysis of shared genetic architecture across ten pediatric autoimmune diseases. *Nature Medicine*, **2015**, 21, 1018-27	50.5	143
533	Genome-wide association identifies diverse causes of common variable immunodeficiency. *Journal of Allergy and Clinical Immunology*, **2011**, 127, 1360-7.e6	11.5	143
532	Mutations in PDGFRB cause autosomal-dominant infantile myofibromatosis. *American Journal of Human Genetics*, **2013**, 92, 1001-7	11	142
531	Rare copy number variants in tourette syndrome disrupt genes in histaminergic pathways and overlap with autism. *Biological Psychiatry*, **2012**, 71, 392-402	7.9	142
530	The role of obesity-associated loci identified in genome-wide association studies in the determination of pediatric BMI. *Obesity*, **2009**, 17, 2254-7	8	141
529	Genome-wide association and longitudinal analyses reveal genetic loci linking pubertal height growth, pubertal timing and childhood adiposity. *Human Molecular Genetics*, **2013**, 22, 2735-47	5.6	138
528	The Philadelphia Neurodevelopmental Cohort: constructing a deep phenotyping collaborative. *Journal of Child Psychology and Psychiatry and Allied Disciplines*, **2015**, 56, 1356-1369	7.9	136
527	Comparative genetic analysis of inflammatory bowel disease and type 1 diabetes implicates multiple loci with opposite effects. *Human Molecular Genetics*, **2010**, 19, 2059-67	5.6	136
526	GWAS identifies four novel eosinophilic esophagitis loci. *Nature Communications*, **2014**, 5, 5593	17.4	135
525	Imaging patterns of brain development and their relationship to cognition. *Cerebral Cortex*, **2015**, 25, 1676-84	5.1	133
524	Profiling of genes expressed in peripheral blood mononuclear cells predicts glucocorticoid sensitivity in asthma patients. *Proceedings of the National Academy of Sciences of the United States of America*, **2005**, 102, 14789-94	11.5	133

523	Network-based multiple sclerosis pathway analysis with GWAS data from 15,000 cases and 30,000 controls. *American Journal of Human Genetics*, **2013**, 92, 854-65	11	132
522	Gene-centric meta-analysis in 87,736 individuals of European ancestry identifies multiple blood-pressure-related loci. *American Journal of Human Genetics*, **2014**, 94, 349-60	11	131
521	Effects of multiple genetic loci on age at onset in late-onset Alzheimer disease: a genome-wide association study. *JAMA Neurology*, **2014**, 71, 1394-404	17.2	129
520	The impact of quality assurance assessment on diffusion tensor imaging outcomes in a large-scale population-based cohort. *NeuroImage*, **2016**, 125, 903-919	7.9	128
519	The role of TREM2 R47H as a risk factor for Alzheimer's disease, frontotemporal lobar degeneration, amyotrophic lateral sclerosis, and Parkinson's disease. *Alzheimerfs and Dementia*, **2015**, 11, 1407-1416	1.2	126
518	Common and Dissociable Mechanisms of Executive System Dysfunction Across Psychiatric Disorders in Youth. *American Journal of Psychiatry*, **2016**, 173, 517-26	11.9	125
517	The diabetes susceptibility gene Clec16a regulates mitophagy. *Cell*, **2014**, 157, 1577-90	56.2	125
516	Interpretation of association signals and identification of causal variants from genome-wide association studies. *American Journal of Human Genetics*, **2010**, 86, 730-42	11	125
515	Novel late-onset Alzheimer disease loci variants associate with brain gene expression. *Neurology*, **2012**, 79, 221-8	6.5	124
514	Phenotype restricted genome-wide association study using a gene-centric approach identifies three low-risk neuroblastoma susceptibility Loci. *PLoS Genetics*, **2011**, 7, e1002026	6	123
513	Impact of puberty on the evolution of cerebral perfusion during adolescence. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 8643-8	11.5	122
512	The psychosis spectrum in a young U.S. community sample: findings from the Philadelphia Neurodevelopmental Cohort. *World Psychiatry*, **2014**, 13, 296-305	14.4	120
511	Directional dominance on stature and cognition in diverse human populations. *Nature*, **2015**, 523, 459-462	30.4	119
510	Loci influencing blood pressure identified using a cardiovascular gene-centric array. *Human Molecular Genetics*, **2013**, 22, 1663-78	5.6	119
509	Assessment of the genetic variance of late-onset Alzheimer's disease. *Neurobiology of Aging*, **2016**, 41, 200.e13-200.e20	5.6	119
508	A novel susceptibility locus for type 1 diabetes on Chr12q13 identified by a genome-wide association study. *Diabetes*, **2008**, 57, 1143-6	0.9	118
507	A genome-wide scan of Ashkenazi Jewish Crohn's disease suggests novel susceptibility loci. *PLoS Genetics*, **2012**, 8, e1002559	6	117
506	Association of Arrhythmia-Related Genetic Variants With Phenotypes Documented in Electronic Medical Records. *JAMA - Journal of the American Medical Association*, **2016**, 315, 47-57	27.4	115

505	Large sample size, wide variant spectrum, and advanced machine-learning technique boost risk prediction for inflammatory bowel disease. *American Journal of Human Genetics*, **2013**, 92, 1008-12	11	114
504	A second independent locus within DMRT1 is associated with testicular germ cell tumor susceptibility. *Human Molecular Genetics*, **2011**, 20, 3109-17	5.6	114
503	Leprosy and the adaptation of human toll-like receptor 1. *PLoS Pathogens*, **2010**, 6, e1000979	7.6	112
502	Follow-up analysis of genome-wide association data identifies novel loci for type 1 diabetes. *Diabetes*, **2009**, 58, 290-5	0.9	112
501	High loading of polygenic risk for ADHD in children with comorbid aggression. *American Journal of Psychiatry*, **2013**, 170, 909-16	11.9	110
500	Being right is its own reward: load and performance related ventral striatum activation to correct responses during a working memory task in youth. *NeuroImage*, **2012**, 61, 723-9	7.9	109
499	Transethnic genome-wide scan identifies novel Alzheimer's disease loci. *Alzheimer's and Dementia*, **2017**, 13, 727-738	1.2	106
498	GRIN2D Recurrent De Novo Dominant Mutation Causes a Severe Epileptic Encephalopathy Treatable with NMDA Receptor Channel Blockers. *American Journal of Human Genetics*, **2016**, 99, 802-816	11	106
497	Genome wide association (GWA) predictors of anti-TNFalpha therapeutic responsiveness in pediatric inflammatory bowel disease. *Inflammatory Bowel Diseases*, **2010**, 16, 1357-66	4.5	105
496	Ultra-Rare Genetic Variation in the Epilepsies: A Whole-Exome Sequencing Study of 17,606 Individuals. *American Journal of Human Genetics*, **2019**, 105, 267-282	11	104
495	The Congenital Heart Disease Genetic Network Study: rationale, design, and early results. *Circulation Research*, **2013**, 112, 698-706	15.7	104
494	Common variants at 6q22 and 17q21 are associated with intracranial volume. *Nature Genetics*, **2012** , 44, 539-44	36.3	104
493	A major susceptibility gene for asthma maps to chromosome 14q24. *American Journal of Human Genetics*, **2002**, 71, 483-91	11	104
492	HLA-DRB1*11 and variants of the MHC class II locus are strong risk factors for systemic juvenile idiopathic arthritis. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, 15970-5	11.5	103
491	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. *American Journal of Human Genetics*, **2011**, 88, 6-18	11	103
490	Common variants in HSPB7 and FRMD4B associated with advanced heart failure. *Circulation: Cardiovascular Genetics*, **2010**, 3, 147-54		103
489	Hyaluronan synthase 3 variant and anthracycline-related cardiomyopathy: a report from the children's oncology group. *Journal of Clinical Oncology*, **2014**, 32, 647-53	2.2	101
488	Investigating the Causal Relationship of C-Reactive Protein with 32 Complex Somatic and Psychiatric Outcomes: A Large-Scale Cross-Consortium Mendelian Randomization Study. *PLoS Medicine*, **2016**, 13, e1001976	11.6	100

487	Loss-of-function HDAC8 mutations cause a phenotypic spectrum of Cornelia de Lange syndrome-like features, ocular hypertelorism, large fontanelle and X-linked inheritance. *Human Molecular Genetics*, **2014**, 23, 2888-900	5.6	99
486	Regulation of TH1- and TH2-type cytokine expression and action in atopic asthmatic sensitized airway smooth muscle. *Journal of Clinical Investigation*, **1999**, 103, 1077-87	15.9	99
485	Genome-wide association study of offspring birth weight in 86 577 women identifies five novel loci and highlights maternal genetic effects that are independent of fetal genetics. *Human Molecular Genetics*, **2018**, 27, 742-756	5.6	98
484	Hotspots of missense mutation identify neurodevelopmental disorder genes and functional domains. *Nature Neuroscience*, **2017**, 20, 1043-1051	25.5	94
483	Common variants at 12q15 and 12q24 are associated with infant head circumference. *Nature Genetics*, **2012**, 44, 532-538	36.3	94
482	A Genetic Investigation of Sex Bias in the Prevalence of Attention-Deficit/Hyperactivity Disorder. *Biological Psychiatry*, **2018**, 83, 1044-1053	7.9	93
481	Autocrine interaction between IL-5 and IL-1beta mediates altered responsiveness of atopic asthmatic sensitized airway smooth muscle. *Journal of Clinical Investigation*, **1999**, 104, 657-67	15.9	92
480	ANGPT2 genetic variant is associated with trauma-associated acute lung injury and altered plasma angiopoietin-2 isoform ratio. *American Journal of Respiratory and Critical Care Medicine*, **2011**, 183, 1344-53	19.2	90
479	Gene-wide analysis detects two new susceptibility genes for Alzheimer's disease. *PLoS ONE*, **2014**, 9, e94661	3.7	90
478	Evidence from human and zebrafish that GPC1 is a biliary atresia susceptibility gene. *Gastroenterology*, **2013**, 144, 1107-1115.e3	13.3	87
477	Phasing of many thousands of genotyped samples. *American Journal of Human Genetics*, **2012**, 91, 238-51	11	87
476	Genome-Wide Association Study Identifies African-Specific Susceptibility Loci in African Americans With Inflammatory Bowel Disease. *Gastroenterology*, **2017**, 152, 206-217.e2	13.3	85
475	Genetic Drivers of Kidney Defects in the DiGeorge Syndrome. *New England Journal of Medicine*, **2017**, 376, 742-754	59.2	83
474	Rare variants in TP53 and susceptibility to neuroblastoma. *Journal of the National Cancer Institute*, **2014**, 106, dju047	9.7	83
473	Replication of GWAS-identified neuroblastoma risk loci strengthens the role of BARD1 and affirms the cumulative effect of genetic variations on disease susceptibility. *Carcinogenesis*, **2013**, 34, 605-11	4.6	82
472	Role of BMI-associated loci identified in GWAS meta-analyses in the context of common childhood obesity in European Americans. *Obesity*, **2011**, 19, 2436-9	8	82
471	ORMDL3 variants associated with asthma susceptibility in North Americans of European ancestry. *Journal of Allergy and Clinical Immunology*, **2008**, 122, 1225-7	11.5	82
470	Allelic frequencies and patterns of single-nucleotide polymorphisms in candidate genes for asthma and atopy in Iceland. *American Journal of Respiratory and Critical Care Medicine*, **2001**, 164, 2036-44	10.2	82

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