Hakon H Hakonarson

List of Publications by Year
in descending order

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657	103,705	299 139	286 294
papers	citations	h-index	g-index

700	700	700	113779
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	ANNOVAR: functional annotation of genetic variants from high-throughput sequencing data. Nucleic Acids Research, 2010, 38, e164-e164.	14.5	10,960
2	Hostâ€“microbe interactions have shaped the genetic architecture of inflammatory bowel disease. Nature, 2012, 491, 119-124.	27.8	4,038
3	Meta-analysis of 74,046 individuals identifies 11 new susceptibility loci for Alzheimer's disease. Nature Genetics, 2013, 45, 1452-1458.	21.4	3,741
4	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. Nature, 2011, 476, 214-219.	27.8	2,400
5	Genome-wide meta-analysis increases to 71 the number of confirmed Crohn's disease susceptibility loci. Nature Genetics, 2010, 42, 1118-1125.	21.4	2,284
6	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. Nature Genetics, 2013, 45, 984-994.	21.4	2,067
7	Genetic meta-analysis of diagnosed Alzheimerâ€™s disease identifies new risk loci and implicates Aî², tau, immunity and lipid processing. Nature Genetics, 2019, 51, 414-430.	21.4	1,962
8	Functional impact of global rare copy number variation in autism spectrum disorders. Nature, 2010, 466, 368-372.	27.8	1,803
9	Common variants at MS4A4/MS4A6E, CD2AP, CD33 and EPHA1 are associated with late-onset Alzheimer's disease. Nature Genetics, 2011, 43, 436-441.	21.4	1,676
10	Discovery of the first genome-wide significant risk loci for attention deficit/hyperactivity disorder. Nature Genetics, 2019, 51, 63-75.	21.4	1,594
11	PennCNV: An integrated hidden Markov model designed for high-resolution copy number variation detection in whole-genome SNP genotyping data. Genome Research, 2007, 17, 1665-1674.	5.5	1,586
12	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, 240-256.	4.2	1,540
13	Autism genome-wide copy number variation reveals ubiquitin and neuronal genes. Nature, 2009, 459, 569-573.	27.8	1,270
14	Analysis of immune-related loci identifies 48 new susceptibility variants for multiple sclerosis. Nature Genetics, 2013, 45, 1353-1360.	21.4	1,213
15	Identification of ALK as a major familial neuroblastoma predisposition gene. Nature, 2008, 455, 930-935.	27.8	1,207
16	Meta-analysis identifies 29 additional ulcerative colitis risk loci, increasing the number of confirmed associations to 47. Nature Genetics, 2011, 43, 246-252.	21.4	1,201
17	Analysis of shared heritability in common disorders of the brain. Science, 2018, 360, .	12.6	1,085
18	Impact of in-scanner head motion on multiple measures of functional connectivity: Relevance for studies of neurodevelopment in youth. NeuroImage, 2012, 60, 623-632.	4.2	1,037

#	Article	IF	Citations
19	Genomic Relationships, Novel Loci, and Pleiotropic Mechanisms across Eight Psychiatric Disorders. Cell, 2019, 179, 1469-1482.e11.	28.9	935
20	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, 823-828.	7.1	925
21	Common genetic variants on 5p14.1 associate with autism spectrum disorders. Nature, 2009, 459, 528-533.	27.8	912
22	The interleukin-6 receptor as a target for prevention of coronary heart disease: a mendelian randomisation analysis. Lancet, The, 2012, 379, 1214-1224.	13.7	886
23	The gene encoding 5-lipoxygenase activating protein confers risk of myocardial infarction and stroke. Nature Genetics, 2004, 36, 233-239.	21.4	859
24	Convergence of Genes and Cellular Pathways Dysregulated in Autism Spectrum Disorders. American Journal of Human Genetics, 2014, 94, 677-694.	6.2	819
25	De novo mutations in histone-modifying genes in congenital heart disease. Nature, 2013, 498, 220-223.	27.8	798
26	Rare Variants Create Synthetic Genome-Wide Associations. PLoS Biology, 2010, 8, e1000294.	5.6	797
27	Rare coding variants in PLCG2, ABI3, and TREM2 implicate microglial-mediated innate immunity in Alzheimer's disease. Nature Genetics, 2017, 49, 1373-1384.	21.4	783
28	Analysing biological pathways in genome-wide association studies. Nature Reviews Genetics, 2010, 11, 843-854.	16.3	722
29	Multiple sclerosis genomic map implicates peripheral immune cells and microglia in susceptibility. Science, 2019, 365, .	12.6	710
30	Genome-wide association study identifies eight risk loci and implicates metabo-psychiatric origins for anorexia nervosa. Nature Genetics, 2019, 51, 1207-1214.	21.4	641
31	The Electronic Medical Records and Genomics (eMERGE) Network: past, present, and future. Genetics in Medicine, 2013, 15, 761-771.	2.4	611
32	Inherited determinants of Crohn's disease and ulcerative colitis phenotypes: a genetic association study. Lancet, The, 2016, 387, 156-167.	13.7	607
33	HMG-coenzyme A reductase inhibition, type 2 diabetes, and bodyweight: evidence from genetic analysis and randomised trials. Lancet, The, 2015, 385, 351-361.	13.7	562
34	A genome-wide scan for common alleles affecting risk for autism. Human Molecular Genetics, 2010, 19, 4072-4082.	2.9	538
35	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.	21.4	529
36	Association between alcohol and cardiovascular disease: Mendelian randomisation analysis based on individual participant data. BMJ, The, 2014, 349, g4164-g4164.	6.0	528

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37	Identification of common variants influencing risk of the tauopathy progressive supranuclear palsy. Nature Genetics, 2011, 43, 699-705.	21.4	502
38	A genome-wide association study identifies KIAA0350 as a type 1 diabetes gene. Nature, 2007, 448, 591-594.	27.8	497
39	A genome-wide association study identifies CDHR3 as a susceptibility locus for early childhood asthma with severe exacerbations. Nature Genetics, 2014, 46, 51-55.	21.4	497
40	Common variants at 7p21 are associated with frontotemporal lobar degeneration with TDP-43 inclusions. Nature Genetics, 2010, 42, 234-239.	21.4	479
41	Common variants at five new loci associated with early-onset inflammatory bowel disease. Nature Genetics, 2009, 41, 1335-1340.	21.4	459
42	Neuroimaging of the Philadelphia Neurodevelopmental Cohort. NeuroImage, 2014, 86, 544-553.	4.2	452
43	Age group and sex differences in performance on a computerized neurocognitive battery in children age 8â˜21.. Neuropsychology, 2012, 26, 251-265.	1.3	432
44	Meta-Analysis of Genome-Wide Association Studies of Attention-Deficit/Hyperactivity Disorder. Journal of the American Academy of Child and Adolescent Psychiatry, 2010, 49, 884-897.	0.5	423
45	Significant Locus and Metabolic Genetic Correlations Revealed in Genome-Wide Association Study of Anorexia Nervosa. American Journal of Psychiatry, 2017, 174, 850-858.	7.2	410
46	Genome-wide associations for birth weight and correlations with adult disease. Nature, 2016, 538, 248-252.	27.8	406
47	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. Nature Genetics, 2019, 51, 804-814.	21.4	402
48	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, 302-316.	7.2	398
49	Common variants at 5q22 associate with pediatric eosinophilic esophagitis. Nature Genetics, 2010, 42, 289-291.	21.4	397
50	Low concordance of multiple variant-calling pipelines: practical implications for exome and genome sequencing. Genome Medicine, 2013, 5, 28.	8.2	381
51	Meta-analysis Confirms CR1, CLU, and PICALM as Alzheimer Disease Risk Loci and Reveals Interactions With APOE Genotypes. Archives of Neurology, 2010, 67, 1473.	4.5	376
52	Genome-Wide Analyses of Exonic Copy Number Variants in a Family-Based Study Point to Novel Autism Susceptibility Genes. PLoS Genetics, 2009, 5, e1000536.	3.5	374
53	Mechanisms of mosaicism, chimerism and uniparental disomy identified by single nucleotide polymorphism array analysis. Human Molecular Genetics, 2010, 19, 1263-1275.	2.9	373
54	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	27.8	353

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55	A genome-wide association meta-analysis identifies new childhood obesity loci. Nature Genetics, 2012, 44, 526-531.	21.4	352
56	Thymic stromal lymphopoietinâ€“elicited basophil responses promote eosinophilic esophagitis. Nature Medicine, 2013, 19, 1005-1013.	30.7	351
57	Systematic Review and Meta-Analysis of the Association between Î²2-Adrenoceptor Polymorphisms and Asthma: A HuGE Review. American Journal of Epidemiology, 2005, 162, 201-211.	3.4	344
58	A variant of the gene encoding leukotriene A4 hydrolase confers ethnicity-specific risk of myocardial infarction. Nature Genetics, 2006, 38, 68-74.	21.4	339
59	Concept, Design and Implementation of a Cardiovascular Gene-Centric 50 K SNP Array for Large-Scale Genomic Association Studies. PLoS ONE, 2008, 3, e3583.	2.5	339
60	Individual common variants exert weak effects on the risk for autism spectrum disorders. Human Molecular Genetics, 2012, 21, 4781-4792.	2.9	334
61	Genome-wide copy number variation study associates metabotropic glutamate receptor gene networks with attention deficit hyperactivity disorder. Nature Genetics, 2012, 44, 78-84.	21.4	334
62	Copy number variation at 1q21.1 associated with neuroblastoma. Nature, 2009, 459, 987-991.	27.8	329
63	Common variation in KITLG and at 5q31.3 predisposes to testicular germ cell cancer. Nature Genetics, 2009, 41, 811-815.	21.4	319
64	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, 1682-1690.	5.5	313
65	Meta-analysis of genome-wide association studies identifies three new risk loci for atopic dermatitis. Nature Genetics, 2012, 44, 187-192.	21.4	311
66	Loci on 20q13 and 21q22 are associated with pediatric-onset inflammatory bowel disease. Nature Genetics, 2008, 40, 1211-1215.	21.4	310
67	Variants ofDENND1BAssociated with Asthma in Children. New England Journal of Medicine, 2010, 362, 36-44.	27.0	306
68	Linked Sex Differences in Cognition and Functional Connectivity in Youth. Cerebral Cortex, 2015, 25, 2383-2394.	2.9	302
69	PCSK9 genetic variants and risk of type 2 diabetes: a mendelian randomisation study. Lancet Diabetes and Endocrinology,the, 2017, 5, 97-105.	11.4	298
70	Adjustment of genomic waves in signal intensities from whole-genome SNP genotyping platforms. Nucleic Acids Research, 2008, 36, e126-e126.	14.5	297
71	A Genome-Wide Meta-Analysis of Six Type 1 Diabetes Cohorts Identifies Multiple Associated Loci. PLoS Genetics, 2011, 7, e1002293.	3.5	297
72	Genome-wide Association Analysis Identifies PDE4D as an Asthma-Susceptibility Gene. American Journal of Human Genetics, 2009, 84, 581-593.	6.2	296

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73	New loci associated with birth weight identify genetic links between intrauterine growth and adult height and metabolism. Nature Genetics, 2013, 45, 76-82.	21.4	293
74	Distinct features of SARS-CoV-2-specific IgA response in COVID-19 patients. European Respiratory Journal, 2020, 56, 2001526.	6.7	292
75	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	21.4	286
76	Integrative genomics identifies LMO1 as a neuroblastoma oncogene. Nature, 2011, 469, 216-220.	27.8	276
77	Genome-wide association analysis identifies three new susceptibility loci for childhood body mass index. Human Molecular Genetics, 2016, 25, 389-403.	2.9	275
78	Familial aggregation of atrial fibrillation in Iceland. European Heart Journal, 2006, 27, 708-712.	2.2	272
79	Psychometric properties of the Penn Computerized Neurocognitive Battery.. Neuropsychology, 2015, 29, 235-246.	1.3	272
80	Chromosome 6p22 Locus Associated with Clinically Aggressive Neuroblastoma. New England Journal of Medicine, 2008, 358, 2585-2593.	27.0	271
81	The Philadelphia Neurodevelopmental Cohort: A publicly available resource for the study of normal and abnormal brain development in youth. NeuroImage, 2016, 124, 1115-1119.	4.2	268
82	Common variations in BARD1 influence susceptibility to high-risk neuroblastoma. Nature Genetics, 2009, 41, 718-723.	21.4	266
83	Genetic predisposition to neuroblastoma mediated by a LMO1 super-enhancer polymorphism. Nature, 2015, 528, 418-421.	27.8	263
84	A novel Alzheimer disease locus located near the gene encoding tau protein. Molecular Psychiatry, 2016, 21, 108-117.	7.9	260
85	A Genome-Wide Association Study Identifies a Locus for Nonsyndromic Cleft Lip with or without Cleft Palate on 8q24. Journal of Pediatrics, 2009, 155, 909-913.	1.8	252
86	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.	7.1	251
87	Diverse Genome-wide Association Studies Associate the IL12/IL23 Pathway with Crohn Disease. American Journal of Human Genetics, 2009, 84, 399-405.	6.2	246
88	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.	7.2	242
89	Large-Scale Gene-Centric Meta-Analysis across 39 Studies Identifies Type 2 Diabetes Loci. American Journal of Human Genetics, 2012, 90, 410-425.	6.2	239
90	Genome-wide association study implicates novel loci and reveals candidate effector genes for longitudinal pediatric bone accrual. Genome Biology, 2021, 22, 1.	8.8	239

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91	RAD21 Mutations Cause a Human Cohesinopathy. American Journal of Human Genetics, 2012, 90, 1014-1027.	6.2	238
92	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.	6.2	237
93	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.	3.6	235
94	A meta-analysis identifies new loci associated with body mass index in individuals of African ancestry. Nature Genetics, 2013, 45, 690-696.	21.4	232
95	Common variation at 6q16 within HACE1 and LIN28B influences susceptibility to neuroblastoma. Nature Genetics, 2012, 44, 1126-1130.	21.4	231
96	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.	4.5	229
97	Duplication of 7q34 in Pediatric Lowâ€Grade Astrocytomas Detected by Highâ€Density Singleâ€Nucleotide Polymorphismâ€Based Genotype Arrays Results in a Novel BRAF Fusion Gene. Brain Pathology, 2009, 19, 449-458.	4.1	227
98	Large-Scale Gene-Centric Meta-analysis across 32 Studies Identifies Multiple Lipid Loci. American Journal of Human Genetics, 2012, 91, 823-838.	6.2	227
99	SNVer: a statistical tool for variant calling in analysis of pooled or individual next-generation sequencing data. Nucleic Acids Research, 2011, 39, e132-e132.	14.5	225
100	Functional Maturation of the Executive System during Adolescence. Journal of Neuroscience, 2013, 33, 16249-16261.	3.6	225
101	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, 283-294.	6.2	225
102	Variants in ADCY5 and near CCNL1 are associated with fetal growth and birth weight. Nature Genetics, 2010, 42, 430-435.	21.4	223
103	Heterogeneous impact of motion on fundamental patterns of developmental changes in functional connectivity during youth. NeuroImage, 2013, 83, 45-57.	4.2	223
104	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.	6.2	222
105	Genetic Evidence for Causal Relationships Between Maternal Obesity-Related Traits and Birth Weight. JAMA - Journal of the American Medical Association, 2016, 315, 1129.	7.4	220
106	A genome-wide association study on African-ancestry populations for asthma. Journal of Allergy and Clinical Immunology, 2010, 125, 336-346.e4.	2.9	213
107	Effects of a 5-Lipoxygenaseâ€“Activating Protein Inhibitor on Biomarkers Associated With Risk of Myocardial Infarction. JAMA - Journal of the American Medical Association, 2005, 293, 2245.	7.4	212
108	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, 10584-10589.	7.1	212

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109	Meta-analysis of shared genetic architecture across ten pediatric autoimmune diseases. Nature Medicine, 2015, 21, 1018-1027.	30.7	212
110	The Philadelphia Neurodevelopmental Cohort: constructing a deep phenotyping collaborative. Journal of Child Psychology and Psychiatry and Allied Disciplines, 2015, 56, 1356-1369.	5.2	208
111	Neurocognitive Growth Charting in Psychosis Spectrum Youths. JAMA Psychiatry, 2014, 71, 366.	11.0	206
112	The impact of quality assurance assessment on diffusion tensor imaging outcomes in a large-scale population-based cohort. NeuroImage, 2016, 125, 903-919.	4.2	202
113	A Genome-Wide Association Study on Obesity and Obesity-Related Traits. PLoS ONE, 2011, 6, e18939.	2.5	201
114	Copy-Number Disorders Are a Common Cause of Congenital Kidney Malformations. American Journal of Human Genetics, 2012, 91, 987-997.	6.2	201
115	Causal Effects of Body Mass Index on Cardiometabolic Traits and Events: A Mendelian Randomization Analysis. American Journal of Human Genetics, 2014, 94, 198-208.	6.2	199
116	Imaging Patterns of Brain Development and their Relationship to Cognition. Cerebral Cortex, 2015, 25, 1676-1684.	2.9	196
117	Common and Dissociable Mechanisms of Executive System Dysfunction Across Psychiatric Disorders in Youth. American Journal of Psychiatry, 2016, 173, 517-526.	7.2	191
118	Genome-wide association and longitudinal analyses reveal genetic loci linking pubertal height growth, pubertal timing and childhood adiposity. Human Molecular Genetics, 2013, 22, 2735-2747.	2.9	188
119	From Disease Association to Risk Assessment: An Optimistic View from Genome-Wide Association Studies on Type 1 Diabetes. PLoS Genetics, 2009, 5, e1000678.	3.5	186
120	GWAS identifies four novel eosinophilic esophagitis loci. Nature Communications, 2014, 5, 5593.	12.8	181
121	A novel approach of homozygous haplotype sharing identifies candidate genes in autism spectrum disorder. Human Genetics, 2012, 131, 565-579.	3.8	180
122	Genome-wide association identifies diverse causes of common variable immunodeficiency. Journal of Allergy and Clinical Immunology, 2011, 127, 1360-1367.e6.	2.9	179
123	The psychosis spectrum in a young U.S. community sample: findings from the Philadelphia Neurodevelopmental Cohort. World Psychiatry, 2014, 13, 296-305.	10.4	178
124	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.	2.5	176
125	Mutations in PDGFRB Cause Autosomal-Dominant Infantile Myofibromatosis. American Journal of Human Genetics, 2013, 92, 1001-1007.	6.2	174
126	Assessment of the genetic variance of late-onset Alzheimer's disease. Neurobiology of Aging, 2016, 41, 200.e13-200.e20.	3.1	174

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127	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	27.8	173
128	Convergent genetic and expression data implicate immunity in Alzheimer's disease. Alzheimer's and Dementia, 2015, 11, 658-671.	0.8	173
129	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, 8643-8648.	7.1	169
130	Epilepsy, hippocampal sclerosis and febrile seizures linked by common genetic variation around SCN1A. Brain, 2013, 136, 3140-3150.	7.6	168
131	Rare Copy Number Variants in Tourette Syndrome Disrupt Genes in Histaminergic Pathways and Overlap with Autism. Biological Psychiatry, 2012, 71, 392-402.	1.3	167
132	Effects of Multiple Genetic Loci on Age at Onset in Late-Onset Alzheimer Disease. JAMA Neurology, 2014, 71, 1394.	9.0	166
133	The Diabetes Susceptibility Gene Clec16a Regulates Mitophagy. Cell, 2014, 157, 1577-1590.	28.9	166
134	Transethnic genomeâ€wide scan identifies novel Alzheimer's disease loci. Alzheimer's and Dementia, 2017, 13, 727-738.	0.8	166
135	Network-Based Multiple Sclerosis Pathway Analysis with GWAS Data from 15,000 Cases and 30,000 Controls. American Journal of Human Genetics, 2013, 92, 854-865.	6.2	164
136	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, 1008-1012.	6.2	162
137	The Role of Obesityâ€associated Loci Identified in Genomeâ€wide Association Studies in the Determination of Pediatric BMI. Obesity, 2009, 17, 2254-2257.	3.0	159
138	Gene-centric Meta-analysis in 87,736 Individuals of European Ancestry Identifies Multiple Blood-Pressure-Related Loci. American Journal of Human Genetics, 2014, 94, 349-360.	6.2	158
139	Genetic correlations among psychiatric and immuneâ€related phenotypes based on genomeâ€wide association data. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2018, 177, 641-657.	1.7	158
140	Comparative genetic analysis of inflammatory bowel disease and type 1 diabetes implicates multiple loci with opposite effects. Human Molecular Genetics, 2010, 19, 2059-2067.	2.9	157
141	Genome-wide association study of offspring birth weight in 86â€‰577 women identifies five novel loci and highlights maternal genetic effects that are independent of fetal genetics. Human Molecular Genetics, 2018, 27, 742-756.	2.9	156
142	Gene-Wide Analysis Detects Two New Susceptibility Genes for Alzheimer's Disease. PLoS ONE, 2014, 9, e94661.	2.5	155
143	The role of TREM2 R47H as a risk factor for Alzheimer's disease, frontotemporal lobar degeneration, amyotrophic lateral sclerosis, and Parkinson's disease. Alzheimer's and Dementia, 2015, 11, 1407-1416.	0.8	152
144	Hotspots of missense mutation identify neurodevelopmental disorder genes and functional domains. Nature Neuroscience, 2017, 20, 1043-1051.	14.8	152

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145	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, 14789-14794.	7.1	150
146	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.	8.4	150
147	Association of Arrhythmia-Related Genetic Variants With Phenotypes Documented in Electronic Medical Records. JAMA - Journal of the American Medical Association, 2016, 315, 47.	7.4	148
148	Interpretation of Association Signals and Identification of Causal Variants from Genome-wide Association Studies. American Journal of Human Genetics, 2010, 86, 730-742.	6.2	146
149	A Genetic Investigation of Sex Bias in the Prevalence of Attention-Deficit/Hyperactivity Disorder. Biological Psychiatry, 2018, 83, 1044-1053.	1.3	146
150	A Genome-Wide Scan of Ashkenazi Jewish Crohn's Disease Suggests Novel Susceptibility Loci. PLoS Genetics, 2012, 8, e1002559.	3.5	144
151	Novel late-onset Alzheimer disease loci variants associate with brain gene expression. Neurology, 2012, 79, 221-228.	1.1	144
152	The copy number variation landscape of congenital anomalies of the kidney and urinary tract. Nature Genetics, 2019, 51, 117-127.	21.4	144
153	Novel Alzheimer Disease Risk Loci and Pathways in African American Individuals Using the African Genome Resources Panel. JAMA Neurology, 2021, 78, 102.	9.0	144
154	The Congenital Heart Disease Genetic Network Study. Circulation Research, 2013, 112, 698-706.	4.5	142
155	Phenotype Restricted Genome-Wide Association Study Using a Gene-Centric Approach Identifies Three Low-Risk Neuroblastoma Susceptibility Loci. PLoS Genetics, 2011, 7, e1002026.	3.5	141
156	Loci influencing blood pressure identified using a cardiovascular gene-centric array. Human Molecular Genetics, 2013, 22, 1663-1678.	2.9	141
157	Leprosy and the Adaptation of Human Toll-Like Receptor 1. PLoS Pathogens, 2010, 6, e1000979.	4.7	139
158	HLA-DRB1*11and 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, 15970-15975.	7.1	139
159	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.	6.2	138
160	A Novel Susceptibility Locus for Type 1 Diabetes on Chr12q13 Identified by a Genome-Wide Association Study. Diabetes, 2008, 57, 1143-1146.	0.6	137
161	Follow-Up Analysis of Genome-Wide Association Data Identifies Novel Loci for Type 1 Diabetes. Diabetes, 2009, 58, 290-295.	0.6	136
162	ARAF recurrent mutation causes central conducting lymphatic anomaly treatable with a MEK inhibitor. Nature Medicine, 2019, 25, 1116-1122.	30.7	136

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163	Phenome-wide association studies across large population cohorts support drug target validation. Nature Communications, 2018, 9, 4285.	12.8	134
164	Common variants at 12q15 and 12q24 are associated with infant head circumference. Nature Genetics, 2012, 44, 532-538.	21.4	130
165	High Loading of Polygenic Risk for ADHD in Children With Comorbid Aggression. American Journal of Psychiatry, 2013, 170, 909-916.	7.2	127
166	Common variants at 6q22 and 17q21 are associated with intracranial volume. Nature Genetics, 2012, 44, 539-544.	21.4	126
167	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, 723-729.	4.2	126
168	Evidence From Human and Zebrafish That GPC1 Is a Biliary Atresia Susceptibility Gene. Gastroenterology, 2013, 144, 1107-1115.e3.	1.3	125
169	Genome wide association (GWA) predictors of anti-TNFÎ± therapeutic responsiveness in pediatric inflammatory bowel disease. Inflammatory Bowel Diseases, 2010, 16, 1357-1366.	1.9	124
170	A second independent locus within DMRT1 is associated with testicular germ cell tumor susceptibility. Human Molecular Genetics, 2011, 20, 3109-3117.	2.9	124
171	Genome-wide Modeling of Polygenic Risk Score in Colorectal Cancer Risk. American Journal of Human Genetics, 2020, 107, 432-444.	6.2	124
172	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. American Journal of Human Genetics, 2011, 88, 6-18.	6.2	122
173	Hyaluronan Synthase 3 Variant and Anthracycline-Related Cardiomyopathy: A Report From the Children's Oncology Group. Journal of Clinical Oncology, 2014, 32, 647-653.	1.6	122
174	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, 2888-2900.	2.9	120
175	Genetic Drivers of Kidney Defects in the DiGeorge Syndrome. New England Journal of Medicine, 2017, 376, 742-754.	27.0	120
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