Stacey Cherny

List of Publications by Citations

179 papers	13,789 citations	51 h-index	115 g-index
202 ext. papers	15,436 ext. citations	6.1 avg, IF	6.39 L-index

#	Paper	IF	Citations
179	Merlin--rapid analysis of dense genetic maps using sparse gene flow trees. *Nature Genetics*, **2002**, 30, 97-101	36.3	2878
178	Genetic Power Calculator: design of linkage and association genetic mapping studies of complex traits. *Bioinformatics*, **2003**, 19, 149-50	7.2	1845
177	Venezuelan kindreds reveal that genetic and environmental factors modulate Huntington's disease age of onset. *Proceedings of the National Academy of Sciences of the United States of America*, **2004**, 101, 3498-503	11.5	572
176	Evaluating the effective numbers of independent tests and significant p-value thresholds in commercial genotyping arrays and public imputation reference datasets. *Human Genetics*, **2012**, 131, 747-56	6.3	434
175	Combined linkage and association sib-pair analysis for quantitative traits. *American Journal of Human Genetics*, **1999**, 64, 259-67	11	387
174	GRR: graphical representation of relationship errors. *Bioinformatics*, **2001**, 17, 742-3	7.2	356
173	Diabetes prevalence and therapeutic target achievement in the United States, 1999 to 2006. *American Journal of Medicine*, **2009**, 122, 443-53	2.4	277
172	Powerful regression-based quantitative-trait linkage analysis of general pedigrees. *American Journal of Human Genetics*, **2002**, 71, 238-53	11	250
171	Evaluating the heritability explained by known susceptibility variants: a survey of ten complex diseases. *Genetic Epidemiology*, **2011**, 35, 310-7	2.6	222
170	Quantitative-trait locus for specific language and reading deficits on chromosome 6p. *American Journal of Human Genetics*, **1999**, 64, 157-64	11	217
169	Power of linkage versus association analysis of quantitative traits, by use of variance-components models, for sibship data. *American Journal of Human Genetics*, **2000**, 66, 1616-30	11	214
168	Linkage between sexual orientation and chromosome Xq28 in males but not in females. *Nature Genetics*, **1995**, 11, 248-56	36.3	208
167	High-resolution mapping of quantitative trait loci in outbred mice. *Nature Genetics*, **1999**, 21, 305-8	36.3	200
166	Genetic determinants of common epilepsies: a meta-analysis of genome-wide association studies. *Lancet Neurology, The*, **2014**, 13, 893-903	24.1	194
165	Identifying gene-environment interactions in schizophrenia: contemporary challenges for integrated, large-scale investigations. *Schizophrenia Bulletin*, **2014**, 40, 729-36	1.3	186
164	Genome-wide mega-analysis identifies 16 loci and highlights diverse biological mechanisms in the common epilepsies. *Nature Communications*, **2018**, 9, 5269	17.4	169
163	Association of JAG1 with bone mineral density and osteoporotic fractures: a genome-wide association study and follow-up replication studies. *American Journal of Human Genetics*, **2010**, 86, 229-39	11	156

162	Genome-wide association study identifies NRG1 as a susceptibility locus for Hirschsprung's disease. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 2694-9	11.5	146
161	Meta-analysis followed by replication identifies loci in or near CDKN1B, TET3, CD80, DRAM1, and ARID5B as associated with systemic lupus erythematosus in Asians. *American Journal of Human Genetics*, **2013**, 92, 41-51	11	144
160	An improved multipoint sib-pair analysis of quantitative traits. *Behavior Genetics*, **1996**, 26, 527-32	3.2	132
159	The impact of genotyping error on family-based analysis of quantitative traits. *European Journal of Human Genetics*, **2001**, 9, 130-4	5.3	112
158	Multipoint interval mapping of quantitative trait loci, using sib pairs. *American Journal of Human Genetics*, **1995**, 56, 1224-33	11	111
157	Use of multivariate linkage analysis for dissection of a complex cognitive trait. *American Journal of Human Genetics*, **2003**, 72, 561-70	11	110
156	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
155	Impaired intellect and memory: a missing link between genetic risk and schizophrenia?. *Archives of General Psychiatry*, **2010**, 67, 905-13		94
154	Genome-wide association study identifies a susceptibility locus for biliary atresia on 10q24.2. *Human Molecular Genetics*, **2010**, 19, 2917-25	5.6	90
153	Genome-wide linkage analysis of a composite index of neuroticism and mood-related scales in extreme selected sibships. *Human Molecular Genetics*, **2004**, 13, 2173-82	5.6	90
152	The relationship between CAG repeat length and age of onset differs for Huntington's disease patients with juvenile onset or adult onset. *Annals of Human Genetics*, **2007**, 71, 295-301	2.2	89
151	A germline mutation (A339V) in thyroid transcription factor-1 (TITF-1/NKX2.1) in patients with multinodular goiter and papillary thyroid carcinoma. *Journal of the National Cancer Institute*, **2009**, 101, 162-75	9.7	88
150	Genome-wide association study in a Chinese population identifies a susceptibility locus for type 2 diabetes at 7q32 near PAX4. *Diabetologia*, **2013**, 56, 1291-305	10.3	85
149	Genetic and environmental contributions to general cognitive ability through the first 16 years of life. *Developmental Psychology*, **2004**, 40, 805-12	3.7	85
148	Exome chip meta-analysis identifies novel loci and East Asian-specific coding variants that contribute to lipid levels and coronary artery disease. *Nature Genetics*, **2017**, 49, 1722-1730	36.3	83
147	Increase in power through multivariate analyses. *Behavior Genetics*, **1998**, 28, 357-63	3.2	81
146	Lumbar disc degeneration is linked to a carbohydrate sulfotransferase 3 variant. *Journal of Clinical Investigation*, **2013**, 123, 4909-17	15.9	81
145	Utility of the trnH-psbA intergenic spacer region and its combinations as plant DNA barcodes: a meta-analysis. *PLoS ONE*, **2012**, 7, e48833	3.7	79

144	Longitudinal heritability of childhood aggression. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2016**, 171, 697-707	3.5	68
143	Significant linkage to migraine with aura on chromosome 11q24. *Human Molecular Genetics*, **2003**, 12, 2511-7	5.6	67
142	European bone mineral density loci are also associated with BMD in East-Asian populations. *PLoS ONE*, **2010**, 5, e13217	3.7	67
141	Replication of twelve association studies for Huntington's disease residual age of onset in large Venezuelan kindreds. *Journal of Medical Genetics*, **2007**, 44, 44-50	5.8	65
140	Association of genetic variants in the adiponectin gene with adiponectin level and hypertension in Hong Kong Chinese. *European Journal of Endocrinology*, **2010**, 163, 251-7	6.5	62
139	Exome-wide association analysis reveals novel coding sequence variants associated with lipid traits in Chinese. *Nature Communications*, **2015**, 6, 10206	17.4	60
138	Hedgehog/Notch-induced premature gliogenesis represents a new disease mechanism for Hirschsprung disease in mice and humans. *Journal of Clinical Investigation*, **2011**, 121, 3467-78	15.9	60
137	ELF1 is associated with systemic lupus erythematosus in Asian populations. *Human Molecular Genetics*, **2011**, 20, 601-7	5.6	58
136	Differential heritability across levels of cognitive ability. *Behavior Genetics*, **1992**, 22, 153-62	3.2	58
135	Heritability of longitudinal measures of body mass index and lipid and lipoprotein levels in aging twins. *Twin Research and Human Genetics*, **2007**, 10, 703-11	2.2	56
134	Whole exome sequencing coupled with unbiased functional analysis reveals new Hirschsprung disease genes. *Genome Biology*, **2017**, 18, 48	18.3	55
133	Multiple regression analysis of twin data: a model-fitting approach. *Behavior Genetics*, **1992**, 22, 489-97	3.2	55
132	Common genetic variants regulating ADD3 gene expression alter biliary atresia risk. *Journal of Hepatology*, **2013**, 59, 1285-91	13.4	53
131	Risk prediction of complex diseases from family history and known susceptibility loci, with applications for cancer screening. *American Journal of Human Genetics*, **2011**, 88, 548-65	11	53
130	Two-stage genome-wide association study identifies variants in CAMSAP1L1 as susceptibility loci for epilepsy in Chinese. *Human Molecular Genetics*, **2012**, 21, 1184-9	5.6	52
129	Life events and depression in a community sample of siblings. *Psychological Medicine*, **2001**, 31, 401-10	6.9	52
128	Genomewide linkage scan reveals novel loci modifying age of onset of Huntington's disease in the Venezuelan HD kindreds. *Genetic Epidemiology*, **2008**, 32, 445-53	2.6	50
127	Parent ratings of temperament in twins: explaining the 'too low' DZ correlations. *Twin Research and Human Genetics*, **2000**, 3, 224-33		48

126	Genetic influences on the difference in variability of height, weight and body mass index between Caucasian and East Asian adolescent twins. *International Journal of Obesity*, **2008**, 32, 1455-67	5.5	47
125	Genome-wide copy number analysis uncovers a new HSCR gene: NRG3. *PLoS Genetics*, **2012**, 8, e1002687	6	46
124	Continuity and change in infant shyness from 14 to 20 months. *Behavior Genetics*, **1994**, 24, 365-79	3.2	46
123	Mutations in the NRG1 gene are associated with Hirschsprung disease. *Human Genetics*, **2012**, 131, 67-76	6.3	45
122	Comparisons of seven algorithms for pathway analysis using the WTCCC Crohn's Disease dataset. *BMC Research Notes*, **2011**, 4, 386	2.3	45
121	Replication study of SNP associations for colorectal cancer in Hong Kong Chinese. *British Journal of Cancer*, **2011**, 104, 369-75	8.7	43
120	Polygenic risk score increases schizophrenia liability through cognition-relevant pathways. *Brain*, **2019**, 142, 471-485	11.2	42
119	Development genetic analysis of general cognitive ability from 1 to 12 years in a sample of adoptees, biological siblings, and twins. *Intelligence*, **2003**, 31, 31-49	3	41
118	Common variants on Xq28 conferring risk of schizophrenia in Han Chinese. *Schizophrenia Bulletin*, **2014**, 40, 777-86	1.3	40
117	A knowledge-based weighting framework to boost the power of genome-wide association studies. *PLoS ONE*, **2010**, 5, e14480	3.7	39
116	A genome-wide scan for loci influencing adolescent cannabis dependence symptoms: evidence for linkage on chromosomes 3 and 9. *Drug and Alcohol Dependence*, **2007**, 89, 34-41	4.9	39
115	Genetic and environmental influences on early childhood behavior. *Behavior Genetics*, **1994**, 24, 25-34	3.2	39
114	Polygenic burden in focal and generalized epilepsies. *Brain*, **2019**, 142, 3473-3481	11.2	38
113	RET and NRG1 interplay in Hirschsprung disease. *Human Genetics*, **2013**, 132, 591-600	6.3	38
112	Identification of IGF1, SLC4A4, WWOX, and SFMBT1 as hypertension susceptibility genes in Han Chinese with a genome-wide gene-based association study. *PLoS ONE*, **2012**, 7, e32907	3.7	38
111	Interplay between Schizophrenia Polygenic Risk Score and Childhood Adversity in First-Presentation Psychotic Disorder: A Pilot Study. *PLoS ONE*, **2016**, 11, e0163319	3.7	38
110	Association analysis in a variance components framework. *Genetic Epidemiology*, **2001**, 21 Suppl 1, S341-6	2.6	37
109	Optimal selection strategies for QTL mapping using pooled DNA samples. *European Journal of Human Genetics*, **2002**, 10, 125-32	5.3	36

108	Sleep duration and memory in the elderly Chinese: longitudinal analysis of the Guangzhou Biobank Cohort Study. *Sleep*, **2014**, 37, 1737-44	1.1	35
107	GENESiS: creating a composite index of the vulnerability to anxiety and depression in a community-based sample of siblings. *Twin Research and Human Genetics*, **2000**, 3, 316-22		34
106	Genetic variation in predicts phenytoin-induced maculopapular exanthema in European-descent patients. *Neurology*, **2018**, 90, e332-e341	6.5	33
105	Variance-Components QTL linkage analysis of selected and non-normal samples: conditioning on trait values. *Genetic Epidemiology*, **2000**, 19 Suppl 1, S22-8	2.6	30
104	Gamma-glutamyl transferase level predicts the development of hypertension in Hong Kong Chinese. *Clinica Chimica Acta*, **2011**, 412, 1326-31	6.2	29
103	C-reactive protein as a predictor of hypertension in the Hong Kong Cardiovascular Risk Factor Prevalence Study (CRISPS) cohort. *Journal of Human Hypertension*, **2012**, 26, 108-16	2.6	29
102	Meta-analysis of GWAS on two Chinese populations followed by replication identifies novel genetic variants on the X chromosome associated with systemic lupus erythematosus. *Human Molecular Genetics*, **2015**, 24, 274-84	5.6	28
101	Using glycosylated hemoglobin to define the metabolic syndrome in United States adults. *Diabetes Care*, **2010**, 33, 1856-8	14.6	28
100	A genome-wide scan in forty large pedigrees with multiple sclerosis. *Journal of Human Genetics*, **2007**, 52, 955-962	4.3	28
99	The familial aggregation of depressive symptoms, antisocial behavior, and alcohol abuse. *American Journal of Medical Genetics Part A*, **1997**, 74, 183-91		27
98	Rapid assessment of infant predictors of adult IQ: Midtwin^midparent analyses.. *Developmental Psychology*, **1993**, 29, 434-447	3.7	27
97	Fine mapping of the NRG1 Hirschsprung's disease locus. *PLoS ONE*, **2011**, 6, e16181	3.7	27
96	Reciprocal causation models of cognitive vs volumetric cerebral intermediate phenotypes for schizophrenia in a pan-European twin cohort. *Molecular Psychiatry*, **2015**, 20, 1386-96	15.1	26
95	Novel pre-mRNA splicing of intronically integrated HBV generates oncogenic chimera in hepatocellular carcinoma. *Journal of Hepatology*, **2016**, 64, 1256-64	13.4	26
94	Association of a polymorphism in the lipin 1 gene with systolic blood pressure in men. *American Journal of Hypertension*, **2008**, 21, 539-45	2.3	26
93	A Developmental-Genetic Analysis of Continuity and Change in the Bayley Mental Development Index from 14 to 24 Months: The MacArthur Longitudinal Twin Study. *Psychological Science*, **1994**, 5, 354-360	7.8	26
92	Repeat instability in the 27-39 CAG range of the HD gene in the Venezuelan kindreds: Counseling implications. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2009**, 150B, 425-9	3.5	25
91	Optimal sibship selection for genotyping in quantitative trait locus linkage analysis. *Human Heredity* , **2001**, 52, 1-13	1.1	25

90	Three SNPs in chromosome 11q23.3 are independently associated with systemic lupus erythematosus in Asians. *Human Molecular Genetics*, **2014**, 23, 524-33	5.6	24
89	Elevated plasma level of soluble F11 receptor/junctional adhesion molecule-A (F11R/JAM-A) in hypertension. *American Journal of Hypertension*, **2009**, 22, 500-5	2.3	24
88	Association of CD247 with systemic lupus erythematosus in Asian populations. *Lupus*, **2012**, 21, 75-83	2.6	24
87	Two subtypes of intervertebral disc degeneration distinguished by large-scale population-based study. *Spine Journal*, **2016**, 16, 1079-89	4	24
86	Heritability of hallucinations in adolescent twins. *Psychiatry Research*, **2012**, 199, 98-101	9.9	23
85	Distinguishing Population Stratification from Genuine Allelic Effects with Mx: Association of ADH2 with Alcohol Consumption. *Behavior Genetics*, **1999**, 29, 233-243	3.2	23
84	Trans-ethnic meta-analysis of genome-wide association studies for Hirschsprung disease. *Human Molecular Genetics*, **2016**, 25, 5265-5275	5.6	23
83	Exome sequencing reveals a high genetic heterogeneity on familial Hirschsprung disease. *Scientific Reports*, **2015**, 5, 16473	4.9	22
82	Two missense variants in UHRF1BP1 are independently associated with systemic lupus erythematosus in Hong Kong Chinese. *Genes and Immunity*, **2011**, 12, 231-4	4.4	22
81	Exploring the genetic etiology of low general cognitive ability from 14 to 36 months.. *Developmental Psychology*, **1997**, 33, 544-548	3.7	22
80	Actionable secondary findings from whole-genome sequencing of 954 East Asians. *Human Genetics*, **2018**, 137, 31-37	6.3	22
79	RET mutational spectrum in Hirschsprung disease: evaluation of 601 Chinese patients. *PLoS ONE*, **2011**, 6, e28986	3.7	21
78	Plasma adrenomedullin level is related to a single nucleotide polymorphism in the adrenomedullin gene. *European Journal of Endocrinology*, **2011**, 165, 571-7	6.5	21
77	A genome-wide linkage and association scan reveals novel loci for hypertension and blood pressure traits. *PLoS ONE*, **2012**, 7, e31489	3.7	21
76	Contribution of GABRG2 Polymorphisms to Risk of Epilepsy and Febrile Seizure: a Multicenter Cohort Study and Meta-analysis. *Molecular Neurobiology*, **2016**, 53, 5457-67	6.2	19
75	Genome-wide search followed by replication reveals genetic interaction of CD80 and ALOX5AP associated with systemic lupus erythematosus in Asian populations. *Annals of the Rheumatic Diseases*, **2016**, 75, 891-8	2.4	19
74	Genome-wide copy number variation study in anorectal malformations. *Human Molecular Genetics*, **2013**, 22, 621-31	5.6	19
73	Haplotype analysis reveals a possible founder effect of RET mutation R114H for Hirschsprung's disease in the Chinese population. *PLoS ONE*, **2010**, 5, e10918	3.7	18

72	Relationship of plasma interleukin-6 and its genetic variants with hypertension in Hong Kong Chinese. *American Journal of Hypertension*, **2011**, 24, 1331-7	2.3	18
71	Exploring the Genetic and Environmental Etiology of High General Cognitive Ability in Fourteen- to Thirty-Six-Month-Old Twins. *Child Development*, **1998**, 69, 68-74	4.9	18
70	Application of genome-wide SNP data for uncovering pairwise relationships and quantitative trait loci. *Genetica*, **2009**, 136, 237-43	1.5	17
69	Fine mapping of the 9q31 Hirschsprung's disease locus. *Human Genetics*, **2010**, 127, 675-83	6.3	17
68	Association of F11 receptor gene polymorphisms with central obesity and blood pressure. *Journal of Internal Medicine*, **2008**, 263, 322-32	10.8	17
67	The effect of genotype and pedigree error on linkage analysis: analysis of three asthma genome scans. *Genetic Epidemiology*, **2001**, 21 Suppl 1, S117-22	2.6	17
66	Identification of neuroglycan C and interacting partners as potential susceptibility genes for schizophrenia in a Southern Chinese population. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2010**, 153B, 103-13	3.5	16
65	Mapping of a Hirschsprung's disease locus in 3p21. *European Journal of Human Genetics*, **2008**, 16, 833-40	5.3	15
64	Mutational analysis of SHH and GLI3 in anorectal malformations. *Birth Defects Research Part A: Clinical and Molecular Teratology*, **2008**, 82, 644-8		15
63	DeFries-Fulker multiple regression analysis of sibship QTL data: a SAS macro. *Bioinformatics*, **2001**, 17, 371-2	7.2	15
62	Epilepsy subtype-specific copy number burden observed in a genome-wide study of 17 458 subjects. *Brain*, **2020**, 143, 2106-2118	11.2	14
61	Uncovering the genetic lesions underlying the most severe form of Hirschsprung disease by whole-genome sequencing. *European Journal of Human Genetics*, **2018**, 26, 818-826	5.3	14
60	A genetic variant in the gene encoding adrenomedullin predicts the development of dysglycemia over 6.4 years in Chinese. *Clinica Chimica Acta*, **2011**, 412, 353-7	6.2	14
59	Homozygosity mapping on a single patient: identification of homozygous regions of recent common ancestry by using population data. *Human Mutation*, **2011**, 32, 345-53	4.7	13
58	Gene network analysis of candidate loci for human anorectal malformations. *PLoS ONE*, **2013**, 8, e69142	3.7	13
57	Gender-controlled measures of socially desirable responding. *Journal of Clinical Psychology*, **1994**, 50, 746-52	2.8	12
56	Association of BDNF Polymorphisms with the Risk of Epilepsy: a Multicenter Study. *Molecular Neurobiology*, **2016**, 53, 2869-2877	6.2	11
55	Influence of Alzheimer's disease genes on cognitive decline: the Guangzhou Biobank Cohort Study. *Neurobiology of Aging*, **2014**, 35, 2422.e3-8	5.6	11

54	Exome-chip association analysis reveals an Asian-specific missense variant in PAX4 associated with type 2 diabetes in Chinese individuals. *Diabetologia*, **2017**, 60, 107-115	10.3	11
53	Gene-based meta-analysis of genome-wide association study data identifies independent single-nucleotide polymorphisms in ANXA6 as being associated with systemic lupus erythematosus in Asian populations. *Arthritis and Rheumatology*, **2015**, 67, 2966-77	9.5	11
52	Genetic Analyses of a Three Generation Family Segregating Hirschsprung Disease and Iris Heterochromia. *PLoS ONE*, **2013**, 8, e66631	3.7	11
51	A powerful and rapid approach to human genome scanning using small quantities of genomic DNA. *Genetical Research*, **2001**, 77, 129-34	1.1	11
50	A Mendelian randomization study of testosterone and cognition in men. *Scientific Reports*, **2016**, 6, 21306	4.9	11
49	Rare variants and de novo variants in mesial temporal lobe epilepsy with hippocampal sclerosis. *Neurology: Genetics*, **2018**, 4, e245	3.8	10
48	Chinese family with diffuse oesophageal leiomyomatosis: a new COL4A5/COL4A6 deletion and a case of gonosomal mosaicism. *BMC Medical Genetics*, **2015**, 16, 49	2.1	9
47	Sacral agenesis: a pilot whole exome sequencing and copy number study. *BMC Medical Genetics*, **2016**, 17, 98	2.1	9
46	A FIVE-FACTOR NUCLEAR MODEL OF SOCIALLY DESIRABLE RESPONDING. *Social Behavior and Personality*, **1992**, 20, 163-191	1.2	9
45	The analysis of causal relationships between blood lipid levels and BMD. *PLoS ONE*, **2019**, 14, e0212464	3.7	9
44	Exploring the genetic and environmental etiology of high general cognitive ability in fourteen- to thirty-six-month-old twins. *Child Development*, **1998**, 69, 68-74	4.9	9
43	An Exome-Chip Association Analysis in Chinese Subjects Reveals a Functional Missense Variant of That Regulates FGF21 Levels. *Diabetes*, **2017**, 66, 1723-1728	0.9	8
42	Targeted next-generation sequencing on Hirschsprung disease: a pilot study exploits DNA pooling. *Annals of Human Genetics*, **2014**, 78, 381-7	2.2	8
41	OpenADAM: an open source genome-wide association data management system for Affymetrix SNP arrays. *BMC Genomics*, **2008**, 9, 636	4.5	8
40	Genetic study of congenital bile-duct dilatation identifies de novo and inherited variants in functionally related genes. *BMC Medical Genomics*, **2016**, 9, 75	3.7	8
39	Sharing of Genes and Pathways Across Complex Phenotypes: A Multilevel Genome-Wide Analysis. *Genetics*, **2017**, 206, 1601-1609	4	7
38	Role of genetic variants in the gene encoding lipocalin-2 in the development of elevated blood pressure. *Clinical and Experimental Hypertension*, **2011**, 33, 484-91	2.2	7
37	Revealing antibiotic cross-resistance patterns in hospitalized patients through Bayesian network modelling. *Journal of Antimicrobial Chemotherapy*, **2021**, 76, 239-248	5.1	7

36	Introduction to the Special Issue on Variance Components Methods for Mapping Quantitative Trait Loci. *Behavior Genetics*, **2004**, 34, 125-126	3.2	6
35	Parent ratings of temperament in twins: explaining the Eoo lowDZ correlations		6
34	Sub-genic intolerance, ClinVar, and the epilepsies: A whole-exome sequencing study of 29,165 individuals. *American Journal of Human Genetics*, **2021**, 108, 965-982	11	6
33	SNP-based HLA allele tagging, imputation and association with antiepileptic drug-induced cutaneous reactions in Hong Kong Han Chinese. *Pharmacogenomics Journal*, **2018**, 18, 340-346	3.5	5
32	Meta-analysis of two Chinese populations identifies an autoimmune disease risk allele in 22q11.21 as associated with systemic lupus erythematosus. *Arthritis Research and Therapy*, **2015**, 17, 67	5.7	5
31	A genetic variant in the gene encoding fibrinogen beta chain predicted development of hypertension in Chinese men. *Thrombosis and Haemostasis*, **2010**, 103, 728-35	7	5
30	Introduction to the special issue: human linkage studies for behavioral traits. *Behavior Genetics*, **2006**, 36, 1-3	3.2	5
29	De novo mutations in Caudal Type Homeo Box transcription Factor 2 (CDX2) in patients with persistent cloaca. *Human Molecular Genetics*, **2018**, 27, 351-358	5.6	4
28	Novel sib pair selection strategy increases power in quantitative association analysis. *Behavior Genetics*, **2009**, 39, 571-9	3.2	4
27	A first stage genome-wide screen for regions shared identical-by-descent in Hutterite families with multiple sclerosis. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2008**, 147B, 467-72	3.5	4
26	Genetic and environmental influences on cognition during childhood. *Population Research and Policy Review*, **1995**, 14, 283-300	1.6	4
25	Genetic Influences on Temperament in Early Adolescence **2003**, 166-184		4
24	A random forest-based framework for genotyping and accuracy assessment of copy number variations. *NAR Genomics and Bioinformatics*, **2020**, 2, lqaa071	3.7	4
23	The Genes We Inherit and Those We Don't: Maternal Genetic Nurture and Child BMI Trajectories. *Behavior Genetics*, **2020**, 50, 310-319	3.2	4
22	Patient complexity and genotype-phenotype correlations in biliary atresia: a cross-sectional analysis. *BMC Medical Genomics*, **2017**, 10, 22	3.7	3
21	Self-reported hearing loss questions provide a good measure for genetic studies: a polygenic risk score analysis from UK Biobank. *European Journal of Human Genetics*, **2020**, 28, 1056-1065	5.3	3
20	Screening of the RET gene of Vietnamese Hirschsprung patients identifies 2 novel missense mutations. *Journal of Pediatric Surgery*, **2012**, 47, 1859-64	2.6	3
19	Variance Components and Related Methods for Mapping Quantitative Trait Loci. *Sociological Methods and Research*, **2008**, 37, 227-250	2.9	3

18	Genetic overlap between epilepsy and schizophrenia: Evidence from cross phenotype analysis in Hong Kong Chinese population. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2018**, 177, 86-92	3.5	3
17	Cost effective assay choice for rare disease study designs. *Orphanet Journal of Rare Diseases*, **2015**, 10, 10	4.2	2
16	Genetic Architecture of Complex Diseases **2011**, 1-13		2
15	No NRG1 V266L in Chinese patients with schizophrenia. *Psychiatric Genetics*, **2011**, 21, 47-9	2.9	2
14	(iii) Whole-genome association studies of complex diseases. *Orthopaedics and Trauma*, **2008**, 22, 251-258		2
13	Cholesky Decomposition **2005**,		2
12	Linkage analysis of a common oligogenic disease using selected sib pairs. *Genetic Epidemiology*, **1995**, 12, 741-6	2.6	2
11	A maximum-likelihood model-fitting approach to conducting a Hayman analysis of diallel tables with complete or missing data. *Behavior Genetics*, **1993**, 23, 69-76	3.2	2
10	Developmental Analysis of IQ **2003**, 13-27		2
9	Shared genetic basis between genetic generalized epilepsy and background electroencephalographic oscillations. *Epilepsia*, **2021**, 62, 1518-1527	6.4	1
8	Deviation from baseline mutation burden provides powerful and robust rare-variants association test for complex diseases.. *Nucleic Acids Research*, **2021**,	20.1	1
7	Exploring the genetic etiology of low general cognitive ability from 14 to 36 months. *Developmental Psychology*, **1997**, 33, 544-8	3.7	1
6	Statistical Power and the Classical Twin Design. *Twin Research and Human Genetics*, **2020**, 23, 87-89	2.2	0
5	Statistical issues and approaches in endophenotype research. *Science Bulletin*, **2011**, 56, 3403-3408		0
4	QTL Methodology in Behavior Genetics **2009**, 35-45		0
3	Deciphering the Causal Relationships Between Low Back Pain Complications, Metabolic Factors, and Comorbidities.. *Journal of Pain Research*, **2022**, 15, 215-227	2.9	0
2	Using common genetic variants to find drugs for common epilepsies.. *Brain Communications*, **2021**, 3, fcab287	4.5	0
1	Polygenic risk profile score increases schizophrenia liability mostly through cognition pathways: mathematical causation models with polygenic risk. *European Neuropsychopharmacology*, **2017**, 27, S885-S886	1.3	