

Stacey Cherny

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Deciphering the Causal Relationships Between Low Back Pain Complications, Metabolic Factors, and Comorbidities.. <i>Journal of Pain Research</i> , 2022 , 15, 215-227	2.9	0
178	Using common genetic variants to find drugs for common epilepsies.. <i>Brain Communications</i> , 2021 , 3, fcab287	4.5	0
177	Shared genetic basis between genetic generalized epilepsy and background electroencephalographic oscillations. <i>Epilepsia</i> , 2021 , 62, 1518-1527	6.4	1
176	Sub-genic intolerance, ClinVar, and the epilepsies: A whole-exome sequencing study of 29,165 individuals. <i>American Journal of Human Genetics</i> , 2021 , 108, 965-982	11	6
175	Revealing antibiotic cross-resistance patterns in hospitalized patients through Bayesian network modelling. <i>Journal of Antimicrobial Chemotherapy</i> , 2021 , 76, 239-248	5.1	7
174	Deviation from baseline mutation burden provides powerful and robust rare-variants association test for complex diseases.. <i>Nucleic Acids Research</i> , 2021 ,	20.1	1
173	Epilepsy subtype-specific copy number burden observed in a genome-wide study of 17 458 subjects. <i>Brain</i> , 2020 , 143, 2106-2118	11.2	14
172	Self-reported hearing loss questions provide a good measure for genetic studies: a polygenic risk score analysis from UK Biobank. <i>European Journal of Human Genetics</i> , 2020 , 28, 1056-1065	5.3	3
171	Statistical Power and the Classical Twin Design. <i>Twin Research and Human Genetics</i> , 2020 , 23, 87-89	2.2	0
170	A random forest-based framework for genotyping and accuracy assessment of copy number variations. <i>NAR Genomics and Bioinformatics</i> , 2020 , 2, lqaa071	3.7	4
169	The Genes We Inherit and Those We Don't: Maternal Genetic Nurture and Child BMI Trajectories. <i>Behavior Genetics</i> , 2020 , 50, 310-319	3.2	4
168	Ultra-Rare Genetic Variation in the Epilepsies: A Whole-Exome Sequencing Study of 17,606 Individuals. <i>American Journal of Human Genetics</i> , 2019 , 105, 267-282	11	104
167	Polygenic burden in focal and generalized epilepsies. <i>Brain</i> , 2019 , 142, 3473-3481	11.2	38
166	The analysis of causal relationships between blood lipid levels and BMD. <i>PLoS ONE</i> , 2019 , 14, e0212464	3.7	9
165	Polygenic risk score increases schizophrenia liability through cognition-relevant pathways. <i>Brain</i> , 2019 , 142, 471-485	11.2	42
164	Uncovering the genetic lesions underlying the most severe form of Hirschsprung disease by whole-genome sequencing. <i>European Journal of Human Genetics</i> , 2018 , 26, 818-826	5.3	14
163	Genetic variation in predicts phenytoin-induced maculopapular exanthema in European-descent patients. <i>Neurology</i> , 2018 , 90, e332-e341	6.5	33

162	De novo mutations in Caudal Type Homeo Box transcription Factor 2 (CDX2) in patients with persistent cloaca. <i>Human Molecular Genetics</i> , 2018 , 27, 351-358	5.6	4
161	SNP-based HLA allele tagging, imputation and association with antiepileptic drug-induced cutaneous reactions in Hong Kong Han Chinese. <i>Pharmacogenomics Journal</i> , 2018 , 18, 340-346	3.5	5
160	Rare variants and de novo variants in mesial temporal lobe epilepsy with hippocampal sclerosis. <i>Neurology: Genetics</i> , 2018 , 4, e245	3.8	10
159	Genetic overlap between epilepsy and schizophrenia: Evidence from cross phenotype analysis in Hong Kong Chinese population. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2018 , 177, 86-92	3.5	3
158	Actionable secondary findings from whole-genome sequencing of 954 East Asians. <i>Human Genetics</i> , 2018 , 137, 31-37	6.3	22
157	Genome-wide mega-analysis identifies 16 loci and highlights diverse biological mechanisms in the common epilepsies. <i>Nature Communications</i> , 2018 , 9, 5269	17.4	169
156	Whole exome sequencing coupled with unbiased functional analysis reveals new Hirschsprung disease genes. <i>Genome Biology</i> , 2017 , 18, 48	18.3	55
155	An Exome-Chip Association Analysis in Chinese Subjects Reveals a Functional Missense Variant of That Regulates FGF21 Levels. <i>Diabetes</i> , 2017 , 66, 1723-1728	0.9	8
154	Patient complexity and genotype-phenotype correlations in biliary atresia: a cross-sectional analysis. <i>BMC Medical Genomics</i> , 2017 , 10, 22	3.7	3
153	Sharing of Genes and Pathways Across Complex Phenotypes: A Multilevel Genome-Wide Analysis. <i>Genetics</i> , 2017 , 206, 1601-1609	4	7
152	Exome chip meta-analysis identifies novel loci and East Asian-specific coding variants that contribute to lipid levels and coronary artery disease. <i>Nature Genetics</i> , 2017 , 49, 1722-1730	36.3	83
151	Exome-chip association analysis reveals an Asian-specific missense variant in PAX4 associated with type 2 diabetes in Chinese individuals. <i>Diabetologia</i> , 2017 , 60, 107-115	10.3	11
150	Polygenic risk profile score increases schizophrenia liability mostly through cognition pathways: mathematical causation models with polygenic risk. <i>European Neuropsychopharmacology</i> , 2017 , 27, S885-S886 ¹²		
149	Contribution of GABRG2 Polymorphisms to Risk of Epilepsy and Febrile Seizure: a Multicenter Cohort Study and Meta-analysis. <i>Molecular Neurobiology</i> , 2016 , 53, 5457-67	6.2	19
148	Genome-wide search followed by replication reveals genetic interaction of CD80 and ALOX5AP associated with systemic lupus erythematosus in Asian populations. <i>Annals of the Rheumatic Diseases</i> , 2016 , 75, 891-8	2.4	19
147	Association of BDNF Polymorphisms with the Risk of Epilepsy: a Multicenter Study. <i>Molecular Neurobiology</i> , 2016 , 53, 2869-2877	6.2	11
146	Sacral agenesis: a pilot whole exome sequencing and copy number study. <i>BMC Medical Genetics</i> , 2016 , 17, 98	2.1	9
145	Novel pre-mRNA splicing of intronically integrated HBV generates oncogenic chimera in hepatocellular carcinoma. <i>Journal of Hepatology</i> , 2016 , 64, 1256-64	13.4	26

144	Interplay between Schizophrenia Polygenic Risk Score and Childhood Adversity in First-Presentation Psychotic Disorder: A Pilot Study. <i>PLoS ONE</i> , 2016 , 11, e0163319	3.7	38
143	Longitudinal heritability of childhood aggression. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2016 , 171, 697-707	3.5	68
142	A Mendelian randomization study of testosterone and cognition in men. <i>Scientific Reports</i> , 2016 , 6, 21304	4.9	11
141	Genetic study of congenital bile-duct dilatation identifies de novo and inherited variants in functionally related genes. <i>BMC Medical Genomics</i> , 2016 , 9, 75	3.7	8
140	Two subtypes of intervertebral disc degeneration distinguished by large-scale population-based study. <i>Spine Journal</i> , 2016 , 16, 1079-89	4	24
139	Trans-ethnic meta-analysis of genome-wide association studies for Hirschsprung disease. <i>Human Molecular Genetics</i> , 2016 , 25, 5265-5275	5.6	23
138	Cost effective assay choice for rare disease study designs. <i>Orphanet Journal of Rare Diseases</i> , 2015 , 10, 10	4.2	2
137	Chinese family with diffuse oesophageal leiomyomatosis: a new COL4A5/COL4A6 deletion and a case of gonosomal mosaicism. <i>BMC Medical Genetics</i> , 2015 , 16, 49	2.1	9
136	Reciprocal causation models of cognitive vs volumetric cerebral intermediate phenotypes for schizophrenia in a pan-European twin cohort. <i>Molecular Psychiatry</i> , 2015 , 20, 1386-96	15.1	26
135	Meta-analysis of GWAS on two Chinese populations followed by replication identifies novel genetic variants on the X chromosome associated with systemic lupus erythematosus. <i>Human Molecular Genetics</i> , 2015 , 24, 274-84	5.6	28
134	Exome sequencing reveals a high genetic heterogeneity on familial Hirschsprung disease. <i>Scientific Reports</i> , 2015 , 5, 16473	4.9	22
133	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. <i>Arthritis and Rheumatology</i> , 2015 , 67, 2966-77	9.5	11
132	Meta-analysis of two Chinese populations identifies an autoimmune disease risk allele in 22q11.21 as associated with systemic lupus erythematosus. <i>Arthritis Research and Therapy</i> , 2015 , 17, 67	5.7	5
131	Exome-wide association analysis reveals novel coding sequence variants associated with lipid traits in Chinese. <i>Nature Communications</i> , 2015 , 6, 10206	17.4	60
130	Common variants on Xq28 conferring risk of schizophrenia in Han Chinese. <i>Schizophrenia Bulletin</i> , 2014 , 40, 777-86	1.3	40
129	Genetic determinants of common epilepsies: a meta-analysis of genome-wide association studies. <i>Lancet Neurology, The</i> , 2014 , 13, 893-903	24.1	194
128	Influence of Alzheimer's disease genes on cognitive decline: the Guangzhou Biobank Cohort Study. <i>Neurobiology of Aging</i> , 2014 , 35, 2422.e3-8	5.6	11
127	Sleep duration and memory in the elderly Chinese: longitudinal analysis of the Guangzhou Biobank Cohort Study. <i>Sleep</i> , 2014 , 37, 1737-44	1.1	35

126	Identifying gene-environment interactions in schizophrenia: contemporary challenges for integrated, large-scale investigations. <i>Schizophrenia Bulletin</i> , 2014 , 40, 729-36	1.3	186
125	Three SNPs in chromosome 11q23.3 are independently associated with systemic lupus erythematosus in Asians. <i>Human Molecular Genetics</i> , 2014 , 23, 524-33	5.6	24
124	Targeted next-generation sequencing on Hirschsprung disease: a pilot study exploits DNA pooling. <i>Annals of Human Genetics</i> , 2014 , 78, 381-7	2.2	8
123	Genome-wide association study in a Chinese population identifies a susceptibility locus for type 2 diabetes at 7q32 near PAX4. <i>Diabetologia</i> , 2013 , 56, 1291-305	10.3	85
122	RET and NRG1 interplay in Hirschsprung disease. <i>Human Genetics</i> , 2013 , 132, 591-600	6.3	38
121	Common genetic variants regulating ADD3 gene expression alter biliary atresia risk. <i>Journal of Hepatology</i> , 2013 , 59, 1285-91	13.4	53
120	Genome-wide copy number variation study in anorectal malformations. <i>Human Molecular Genetics</i> , 2013 , 22, 621-31	5.6	19
119	Meta-analysis followed by replication identifies loci in or near CDKN1B, TET3, CD80, DRAM1, and ARID5B as associated with systemic lupus erythematosus in Asians. <i>American Journal of Human Genetics</i> , 2013 , 92, 41-51	11	144
118	Genetic Analyses of a Three Generation Family Segregating Hirschsprung Disease and Iris Heterochromia. <i>PLoS ONE</i> , 2013 , 8, e66631	3.7	11
117	Lumbar disc degeneration is linked to a carbohydrate sulfotransferase 3 variant. <i>Journal of Clinical Investigation</i> , 2013 , 123, 4909-17	15.9	81
116	Gene network analysis of candidate loci for human anorectal malformations. <i>PLoS ONE</i> , 2013 , 8, e69142	3.7	13
115	Mutations in the NRG1 gene are associated with Hirschsprung disease. <i>Human Genetics</i> , 2012 , 131, 67-76	6.3	45
114	Screening of the RET gene of Vietnamese Hirschsprung patients identifies 2 novel missense mutations. <i>Journal of Pediatric Surgery</i> , 2012 , 47, 1859-64	2.6	3
113	Heritability of hallucinations in adolescent twins. <i>Psychiatry Research</i> , 2012 , 199, 98-101	9.9	23
112	Utility of the trnH-psbA intergenic spacer region and its combinations as plant DNA barcodes: a meta-analysis. <i>PLoS ONE</i> , 2012 , 7, e48833	3.7	79
111	Evaluating the effective numbers of independent tests and significant p-value thresholds in commercial genotyping arrays and public imputation reference datasets. <i>Human Genetics</i> , 2012 , 131, 747-56	6.3	434
110	Genome-wide copy number analysis uncovers a new HSCR gene: NRG3. <i>PLoS Genetics</i> , 2012 , 8, e1002687	46	46
109	Association of CD247 with systemic lupus erythematosus in Asian populations. <i>Lupus</i> , 2012 , 21, 75-83	2.6	24

108	Two-stage genome-wide association study identifies variants in CAMSAP1L1 as susceptibility loci for epilepsy in Chinese. <i>Human Molecular Genetics</i> , 2012 , 21, 1184-9	5.6	52
107	C-reactive protein as a predictor of hypertension in the Hong Kong Cardiovascular Risk Factor Prevalence Study (CRISPS) cohort. <i>Journal of Human Hypertension</i> , 2012 , 26, 108-16	2.6	29
106	A genome-wide linkage and association scan reveals novel loci for hypertension and blood pressure traits. <i>PLoS ONE</i> , 2012 , 7, e31489	3.7	21
105	Identification of IGF1, SLC4A4, WWOX, and SFMBT1 as hypertension susceptibility genes in Han Chinese with a genome-wide gene-based association study. <i>PLoS ONE</i> , 2012 , 7, e32907	3.7	38
104	A genetic variant in the gene encoding adrenomedullin predicts the development of dysglycemia over 6.4 years in Chinese. <i>Clinica Chimica Acta</i> , 2011 , 412, 353-7	6.2	14
103	Gamma-glutamyl transferase level predicts the development of hypertension in Hong Kong Chinese. <i>Clinica Chimica Acta</i> , 2011 , 412, 1326-31	6.2	29
102	Genetic Architecture of Complex Diseases 2011 , 1-13		2
101	RET mutational spectrum in Hirschsprung disease: evaluation of 601 Chinese patients. <i>PLoS ONE</i> , 2011 , 6, e28986	3.7	21
100	No NRG1 V266L in Chinese patients with schizophrenia. <i>Psychiatric Genetics</i> , 2011 , 21, 47-9	2.9	2
99	Replication study of SNP associations for colorectal cancer in Hong Kong Chinese. <i>British Journal of Cancer</i> , 2011 , 104, 369-75	8.7	43
98	Two missense variants in UHRF1BP1 are independently associated with systemic lupus erythematosus in Hong Kong Chinese. <i>Genes and Immunity</i> , 2011 , 12, 231-4	4.4	22
97	Comparisons of seven algorithms for pathway analysis using the WTCCC Crohn's Disease dataset. <i>BMC Research Notes</i> , 2011 , 4, 386	2.3	45
96	Risk prediction of complex diseases from family history and known susceptibility loci, with applications for cancer screening. <i>American Journal of Human Genetics</i> , 2011 , 88, 548-65	11	53
95	Statistical issues and approaches in endophenotype research. <i>Science Bulletin</i> , 2011 , 56, 3403-3408	0	
94	Evaluating the heritability explained by known susceptibility variants: a survey of ten complex diseases. <i>Genetic Epidemiology</i> , 2011 , 35, 310-7	2.6	222
93	Homozygosity mapping on a single patient: identification of homozygous regions of recent common ancestry by using population data. <i>Human Mutation</i> , 2011 , 32, 345-53	4.7	13
92	Relationship of plasma interleukin-6 and its genetic variants with hypertension in Hong Kong Chinese. <i>American Journal of Hypertension</i> , 2011 , 24, 1331-7	2.3	18
91	Role of genetic variants in the gene encoding lipocalin-2 in the development of elevated blood pressure. <i>Clinical and Experimental Hypertension</i> , 2011 , 33, 484-91	2.2	7

90	Plasma adrenomedullin level is related to a single nucleotide polymorphism in the adrenomedullin gene. <i>European Journal of Endocrinology</i> , 2011 , 165, 571-7	6.5	21
89	ELF1 is associated with systemic lupus erythematosus in Asian populations. <i>Human Molecular Genetics</i> , 2011 , 20, 601-7	5.6	58
88	Hedgehog/Notch-induced premature gliogenesis represents a new disease mechanism for Hirschsprung disease in mice and humans. <i>Journal of Clinical Investigation</i> , 2011 , 121, 3467-78	15.9	60
87	Fine mapping of the NRG1 Hirschsprung's disease locus. <i>PLoS ONE</i> , 2011 , 6, e16181	3.7	27
86	Haplotype analysis reveals a possible founder effect of RET mutation R114H for Hirschsprung's disease in the Chinese population. <i>PLoS ONE</i> , 2010 , 5, e10918	3.7	18
85	A knowledge-based weighting framework to boost the power of genome-wide association studies. <i>PLoS ONE</i> , 2010 , 5, e14480	3.7	39
84	A genetic variant in the gene encoding fibrinogen beta chain predicted development of hypertension in Chinese men. <i>Thrombosis and Haemostasis</i> , 2010 , 103, 728-35	7	5
83	Association of genetic variants in the adiponectin gene with adiponectin level and hypertension in Hong Kong Chinese. <i>European Journal of Endocrinology</i> , 2010 , 163, 251-7	6.5	62
82	Using glycosylated hemoglobin to define the metabolic syndrome in United States adults. <i>Diabetes Care</i> , 2010 , 33, 1856-8	14.6	28
81	Genome-wide association study identifies a susceptibility locus for biliary atresia on 10q24.2. <i>Human Molecular Genetics</i> , 2010 , 19, 2917-25	5.6	90
80	Identification of neuroglycan C and interacting partners as potential susceptibility genes for schizophrenia in a Southern Chinese population. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2010 , 153B, 103-13	3.5	16
79	Impaired intellect and memory: a missing link between genetic risk and schizophrenia?. <i>Archives of General Psychiatry</i> , 2010 , 67, 905-13		94
78	Association of JAG1 with bone mineral density and osteoporotic fractures: a genome-wide association study and follow-up replication studies. <i>American Journal of Human Genetics</i> , 2010 , 86, 229-39 ¹¹		156
77	Fine mapping of the 9q31 Hirschsprung's disease locus. <i>Human Genetics</i> , 2010 , 127, 675-83	6.3	17
76	European bone mineral density loci are also associated with BMD in East-Asian populations. <i>PLoS ONE</i> , 2010 , 5, e13217	3.7	67
75	Genome-wide association study identifies NRG1 as a susceptibility locus for Hirschsprung's disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 2694-9	11.5	146
74	Elevated plasma level of soluble F11 receptor/junctional adhesion molecule-A (F11R/JAM-A) in hypertension. <i>American Journal of Hypertension</i> , 2009 , 22, 500-5	2.3	24
73	A germline mutation (A339V) in thyroid transcription factor-1 (TTF-1/NKX2.1) in patients with multinodular goiter and papillary thyroid carcinoma. <i>Journal of the National Cancer Institute</i> , 2009 , 101, 162-75	9.7	88

72	Repeat instability in the 27-39 CAG range of the HD gene in the Venezuelan kindreds: Counseling implications. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2009 , 150B, 425-9	3.5	25
71	Novel sib pair selection strategy increases power in quantitative association analysis. <i>Behavior Genetics</i> , 2009 , 39, 571-9	3.2	4
70	Application of genome-wide SNP data for uncovering pairwise relationships and quantitative trait loci. <i>Genetica</i> , 2009 , 136, 237-43	1.5	17
69	Diabetes prevalence and therapeutic target achievement in the United States, 1999 to 2006. <i>American Journal of Medicine</i> , 2009 , 122, 443-53	2.4	277
68	QTL Methodology in Behavior Genetics 2009 , 35-45	0	
67	Mapping of a Hirschsprung's disease locus in 3p21. <i>European Journal of Human Genetics</i> , 2008 , 16, 833-40	3.3	15
66	Genetic influences on the difference in variability of height, weight and body mass index between Caucasian and East Asian adolescent twins. <i>International Journal of Obesity</i> , 2008 , 32, 1455-67	5.5	47
65	Association of F11 receptor gene polymorphisms with central obesity and blood pressure. <i>Journal of Internal Medicine</i> , 2008 , 263, 322-32	10.8	17
64	OpenADAM: an open source genome-wide association data management system for Affymetrix SNP arrays. <i>BMC Genomics</i> , 2008 , 9, 636	4.5	8
63	Association of a polymorphism in the lipin 1 gene with systolic blood pressure in men. <i>American Journal of Hypertension</i> , 2008 , 21, 539-45	2.3	26
62	Variance Components and Related Methods for Mapping Quantitative Trait Loci. <i>Sociological Methods and Research</i> , 2008 , 37, 227-250	2.9	3
61	(iii) Whole-genome association studies of complex diseases. <i>Orthopaedics and Trauma</i> , 2008 , 22, 251-258	2	
60	Genomewide linkage scan reveals novel loci modifying age of onset of Huntington's disease in the Venezuelan HD kindreds. <i>Genetic Epidemiology</i> , 2008 , 32, 445-53	2.6	50
59	Mutational analysis of SHH and GLI3 in anorectal malformations. <i>Birth Defects Research Part A: Clinical and Molecular Teratology</i> , 2008 , 82, 644-8	15	
58	A first stage genome-wide screen for regions shared identical-by-descent in Hutterite families with multiple sclerosis. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2008 , 147B, 467-72	3.5	4
57	The relationship between CAG repeat length and age of onset differs for Huntington's disease patients with juvenile onset or adult onset. <i>Annals of Human Genetics</i> , 2007 , 71, 295-301	2.2	89
56	A genome-wide scan in forty large pedigrees with multiple sclerosis. <i>Journal of Human Genetics</i> , 2007 , 52, 955-962	4.3	28
55	Replication of twelve association studies for Huntington's disease residual age of onset in large Venezuelan kindreds. <i>Journal of Medical Genetics</i> , 2007 , 44, 44-50	5.8	65

54	Heritability of longitudinal measures of body mass index and lipid and lipoprotein levels in aging twins. <i>Twin Research and Human Genetics</i> , 2007 , 10, 703-11	2.2	56
53	A genome-wide scan for loci influencing adolescent cannabis dependence symptoms: evidence for linkage on chromosomes 3 and 9. <i>Drug and Alcohol Dependence</i> , 2007 , 89, 34-41	4.9	39
52	Introduction to the special issue: human linkage studies for behavioral traits. <i>Behavior Genetics</i> , 2006 , 36, 1-3	3.2	5
51	Cholesky Decomposition 2005 ,		2
50	Genome-wide linkage analysis of a composite index of neuroticism and mood-related scales in extreme selected sibships. <i>Human Molecular Genetics</i> , 2004 , 13, 2173-82	5.6	90
49	Genetic and environmental contributions to general cognitive ability through the first 16 years of life. <i>Developmental Psychology</i> , 2004 , 40, 805-12	3.7	85
48	Venezuelan kindreds reveal that genetic and environmental factors modulate Huntington's disease age of onset. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 3498-503	11.5	572
47	Introduction to the Special Issue on Variance Components Methods for Mapping Quantitative Trait Loci. <i>Behavior Genetics</i> , 2004 , 34, 125-126	3.2	6
46	Development genetic analysis of general cognitive ability from 1 to 12 years in a sample of adoptees, biological siblings, and twins. <i>Intelligence</i> , 2003 , 31, 31-49	3	41
45	Use of multivariate linkage analysis for dissection of a complex cognitive trait. <i>American Journal of Human Genetics</i> , 2003 , 72, 561-70	11	110
44	Genetic Power Calculator: design of linkage and association genetic mapping studies of complex traits. <i>Bioinformatics</i> , 2003 , 19, 149-50	7.2	1845
43	Significant linkage to migraine with aura on chromosome 11q24. <i>Human Molecular Genetics</i> , 2003 , 12, 2511-7	5.6	67
42	Developmental Analysis of IQ 2003 , 13-27		2
41	Genetic Influences on Temperament in Early Adolescence 2003 , 166-184		4
40	Merlin--rapid analysis of dense genetic maps using sparse gene flow trees. <i>Nature Genetics</i> , 2002 , 30, 97-101	36.3	2878
39	Optimal selection strategies for QTL mapping using pooled DNA samples. <i>European Journal of Human Genetics</i> , 2002 , 10, 125-32	5.3	36
38	Powerful regression-based quantitative-trait linkage analysis of general pedigrees. <i>American Journal of Human Genetics</i> , 2002 , 71, 238-53	11	250
37	Association analysis in a variance components framework. <i>Genetic Epidemiology</i> , 2001 , 21 Suppl 1, S341-6.6		37

36	The effect of genotype and pedigree error on linkage analysis: analysis of three asthma genome scans. <i>Genetic Epidemiology</i> , 2001 , 21 Suppl 1, S117-22	2.6	17
35	The impact of genotyping error on family-based analysis of quantitative traits. <i>European Journal of Human Genetics</i> , 2001 , 9, 130-4	5.3	112
34	Life events and depression in a community sample of siblings. <i>Psychological Medicine</i> , 2001 , 31, 401-10	6.9	52
33	GRR: graphical representation of relationship errors. <i>Bioinformatics</i> , 2001 , 17, 742-3	7.2	356
32	DeFries-Fulker multiple regression analysis of sibship QTL data: a SAS macro. <i>Bioinformatics</i> , 2001 , 17, 371-2	7.2	15
31	Optimal sibship selection for genotyping in quantitative trait locus linkage analysis. <i>Human Heredity</i> , 2001 , 52, 1-13	1.1	25
30	A powerful and rapid approach to human genome scanning using small quantities of genomic DNA. <i>Genetical Research</i> , 2001 , 77, 129-34	1.1	11
29	GENESiS: creating a composite index of the vulnerability to anxiety and depression in a community-based sample of siblings. <i>Twin Research and Human Genetics</i> , 2000 , 3, 316-22		34
28	Variance-Components QTL linkage analysis of selected and non-normal samples: conditioning on trait values. <i>Genetic Epidemiology</i> , 2000 , 19 Suppl 1, S22-8	2.6	30
27	Power of linkage versus association analysis of quantitative traits, by use of variance-components models, for sibship data. <i>American Journal of Human Genetics</i> , 2000 , 66, 1616-30	11	214
26	Parent ratings of temperament in twins: explaining the 'too low' DZ correlations. <i>Twin Research and Human Genetics</i> , 2000 , 3, 224-33		48
25	High-resolution mapping of quantitative trait loci in outbred mice. <i>Nature Genetics</i> , 1999 , 21, 305-8	36.3	200
24	Distinguishing Population Stratification from Genuine Allelic Effects with Mx: Association of ADH2 with Alcohol Consumption. <i>Behavior Genetics</i> , 1999 , 29, 233-243	3.2	23
23	Quantitative-trait locus for specific language and reading deficits on chromosome 6p. <i>American Journal of Human Genetics</i> , 1999 , 64, 157-64	11	217
22	Combined linkage and association sib-pair analysis for quantitative traits. <i>American Journal of Human Genetics</i> , 1999 , 64, 259-67	11	387
21	Increase in power through multivariate analyses. <i>Behavior Genetics</i> , 1998 , 28, 357-63	3.2	81
20	Exploring the Genetic and Environmental Etiology of High General Cognitive Ability in Fourteen- to Thirty-Six-Month-Old Twins. <i>Child Development</i> , 1998 , 69, 68-74	4.9	18
19	Exploring the genetic and environmental etiology of high general cognitive ability in fourteen- to thirty-six-month-old twins. <i>Child Development</i> , 1998 , 69, 68-74	4.9	9

18	Exploring the genetic etiology of low general cognitive ability from 14 to 36 months.. <i>Developmental Psychology</i> , 1997, 33, 544-548	3.7	22
17	The familial aggregation of depressive symptoms, antisocial behavior, and alcohol abuse. <i>American Journal of Medical Genetics Part A</i> , 1997, 74, 183-91		27
16	Exploring the genetic etiology of low general cognitive ability from 14 to 36 months. <i>Developmental Psychology</i> , 1997, 33, 544-8	3.7	1
15	An improved multipoint sib-pair analysis of quantitative traits. <i>Behavior Genetics</i> , 1996, 26, 527-32	3.2	132
14	Genetic and environmental influences on cognition during childhood. <i>Population Research and Policy Review</i> , 1995, 14, 283-300	1.6	4
13	Linkage between sexual orientation and chromosome Xq28 in males but not in females. <i>Nature Genetics</i> , 1995, 11, 248-56	36.3	208
12	Linkage analysis of a common oligogenic disease using selected sib pairs. <i>Genetic Epidemiology</i> , 1995, 12, 741-6	2.6	2
11	Multipoint interval mapping of quantitative trait loci, using sib pairs. <i>American Journal of Human Genetics</i> , 1995, 56, 1224-33	11	111
10	A Developmental-Genetic Analysis of Continuity and Change in the Bayley Mental Development Index from 14 to 24 Months: The MacArthur Longitudinal Twin Study. <i>Psychological Science</i> , 1994, 5, 354-360	7.9	26
9	Continuity and change in infant shyness from 14 to 20 months. <i>Behavior Genetics</i> , 1994, 24, 365-79	3.2	46
8	Genetic and environmental influences on early childhood behavior. <i>Behavior Genetics</i> , 1994, 24, 25-34	3.2	39
7	Gender-controlled measures of socially desirable responding. <i>Journal of Clinical Psychology</i> , 1994, 50, 746-52	2.8	12
6	Rapid assessment of infant predictors of adult IQ: Midtwin^midparent analyses.. <i>Developmental Psychology</i> , 1993, 29, 434-447	3.7	27
5	A maximum-likelihood model-fitting approach to conducting a Hayman analysis of diallel tables with complete or missing data. <i>Behavior Genetics</i> , 1993, 23, 69-76	3.2	2
4	A FIVE-FACTOR NUCLEAR MODEL OF SOCIALLY DESIRABLE RESPONDING. <i>Social Behavior and Personality</i> , 1992, 20, 163-191	1.2	9
3	Multiple regression analysis of twin data: a model-fitting approach. <i>Behavior Genetics</i> , 1992, 22, 489-97	3.2	55
2	Differential heritability across levels of cognitive ability. <i>Behavior Genetics</i> , 1992, 22, 153-62	3.2	58
1	Parent ratings of temperament in twins: explaining the low DZ correlations		6

