

Transmission test for linkage disequilibrium: the insulin
diabetes mellitus (IDDM)

American Journal of Human Genetics

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Citation Report

#	ARTICLE	IF	CITATIONS
1	The status of genetic investigations of schizophrenia. , 0, , 288-308.		0
2	Associations of disease with genetic markers: DÃ©jÃ© vu all over again. American Journal of Medical Genetics Part A, 1993, 48, 71-73.	2.4	160
3	Homozygous parent affected sib pair method for detecting disease predisposing variants: Application to insulin dependent diabetes mellitus. Genetic Epidemiology, 1993, 10, 273-288.	0.6	53
4	Involvement of human muscle acetylcholine receptor alpha-subunit gene (CHRNA) in susceptibility to myasthenia gravis.. Proceedings of the National Academy of Sciences of the United States of America, 1994, 91, 4668-4672.	3.3	81
5	Gene for familial psoriasis susceptibility mapped to the distal end of human chromosome 17q. Science, 1994, 264, 1141-1145.	6.0	403
6	Linkage analyses of chromosome 6 loci, including HLA, in familial aggregations of Crohn disease. American Journal of Medical Genetics Part A, 1994, 52, 207-213.	2.4	42
7	What association analysis can and cannot tell us about the genetics of complex disease. American Journal of Medical Genetics Part A, 1994, 54, 318-323.	2.4	75
8	Genetic susceptibility to multiple sclerosis. Annals of Neurology, 1994, 36, S204-S210.	2.8	28
9	A genome-wide search for human type 1 diabetes susceptibility genes. Nature, 1994, 371, 130-136.	13.7	1,326
10	Effect of genetic architecture on the power of human linkage studies to resolve the contribution of quantitative trait loci. Heredity, 1994, 72, 175-192.	1.2	48
11	Angiotensin II type 1 receptor gene polymorphisms in human essential hypertension.. Hypertension, 1994, 24, 63-69.	1.3	660
12	Genetic dissection of complex traits. Science, 1994, 265, 2037-2048.	6.0	3,158
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15	Genetic analysis of type 1 diabetes using whole genome approaches.. Proceedings of the National Academy of Sciences of the United States of America, 1995, 92, 8560-8565.	3.3	249
16	Multifactorial inheritance in type 1 diabetes. Trends in Genetics, 1995, 11, 499-504.	2.9	93
17	Polygenic disease: methods for mapping complex disease traits. Trends in Genetics, 1995, 11, 513-519.	2.9	221
18	Potential linkage disequilibrium between schizophrenia and locus D22S278 on the long arm of chromosome 22. American Journal of Medical Genetics Part A, 1995, 60, 465-467.	2.4	57

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20	Variation in HLA-associated risks of childhood insulin-dependent diabetes in the finnish population: I. Allele effects at A, B, and DR Loci. <i>Genetic Epidemiology</i> , 1995, 12, 441-453.	0.6	31
21	Variation in HLA-associated risks of childhood insulin-dependent diabetes in the finnish population: II. Haplotype effects. <i>Genetic Epidemiology</i> , 1995, 12, 455-466.	0.6	20
22	An oligogenic disease displaying weak marker associations: A summary of contributions to problem 1 of GAW9. <i>Genetic Epidemiology</i> , 1995, 12, 545-554.	0.6	13
23	Use of sibling risk ratios and components of genetic variance in the characterization of a simulated oligogenic disease. <i>Genetic Epidemiology</i> , 1995, 12, 565-570.	0.6	5
24	Model-free association analysis of a rare Disease. <i>Genetic Epidemiology</i> , 1995, 12, 571-575.	0.6	7
25	Systematic search of susceptibility loci with methods using gametic disequilibrium. <i>Genetic Epidemiology</i> , 1995, 12, 577-582.	0.6	5
26	Comparing the power of linkage detection by the transmission disequilibrium test and the identity-by-descent test. <i>Genetic Epidemiology</i> , 1995, 12, 583-588.	0.6	22
27	Screening a 2 cM genetic map for allelic association: A simulated oligogenic trait. <i>Genetic Epidemiology</i> , 1995, 12, 595-600.	0.6	13
28	Logistic transmission modeling of simulated data. <i>Genetic Epidemiology</i> , 1995, 12, 607-612.	0.6	23
29	Detection of vulnerability loci by association and sib-pair methods. <i>Genetic Epidemiology</i> , 1995, 12, 631-635.	0.6	1
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31	Genome scanning for complex disease genes using the transmission/disequilibrium test and haplotype-based haplotype relative risk. <i>Genetic Epidemiology</i> , 1995, 12, 641-645.	0.6	4
32	Sequential analysis of marker data for a rare oligogenic disease. <i>Genetic Epidemiology</i> , 1995, 12, 647-651.	0.6	1
33	Integration of linkage analyses and disease association studies. <i>Genetic Epidemiology</i> , 1995, 12, 653-658.	0.6	2
34	TDT with covariates and genomic screens with mod scores: Their behavior on simulated data. <i>Genetic Epidemiology</i> , 1995, 12, 659-664.	0.6	36
35	Evaluation of screening strategies to detect an oligogenic disease. <i>Genetic Epidemiology</i> , 1995, 12, 665-669.	0.6	1
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40	The genetic dissection of multifactorial traits. <i>Clinical and Experimental Allergy</i> , 1995, 25, 103-106.	1.4	29
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42	Linkage disequilibrium mapping of a type 1 diabetes susceptibility gene (IDDM7) to chromosome 2q31-q33. <i>Nature Genetics</i> , 1995, 9, 80-85.	9.4	226
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44	Susceptibility to human type 1 diabetes at IDDM2 is determined by tandem repeat variation at the insulin gene minisatellite locus. <i>Nature Genetics</i> , 1995, 9, 284-292.	9.4	712
45	A missense mutation in the glucagon receptor gene is associated with non-insulin-dependent diabetes mellitus. <i>Nature Genetics</i> , 1995, 9, 299-304.	9.4	177
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53	An extended transmission/disequilibrium test (TDT) for multi-allele marker loci. <i>Annals of Human Genetics</i> , 1995, 59, 323-336.	0.3	625
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57	Génétique du diabète insulino-dépendant. Annales De L'Institut Pasteur / Actualités, 1996, 7, 13-19.	0.1	0
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1483	Evaluation of AGR2 and AGR3 as candidate genes for inflammatory bowel disease. <i>Genes and Immunity</i> , 2006, 7, 11-18.	2.2	113
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1940	A thymic stromal lymphopoietin gene variant is associated with asthma and airway hyperresponsiveness. <i>Journal of Allergy and Clinical Immunology</i> , 2009, 124, 222-229.	1.5	95
1941	Season of birth and not vitamin D receptor promoter polymorphisms is a risk factor for multiple sclerosis. <i>Multiple Sclerosis Journal</i> , 2009, 15, 1146-1152.	1.4	44
1942	The T Allele of the 677C>T Polymorphism of <i>Methylenetetrahydrofolate Reductase</i> Gene is Associated With an Increased Risk of Ischemic Stroke in Polish Children. <i>Journal of Child Neurology</i> , 2009, 24, 1262-1267.	0.7	23
1943	TLR9 polymorphisms in African populations: no association with severe malaria, but evidence of cis-variants acting on gene expression. <i>Malaria Journal</i> , 2009, 8, 44.	0.8	30
1944	Sex chromosomes and genetic association studies. <i>Genome Medicine</i> , 2009, 1, 110.	3.6	52
1945	Association of MICA with rheumatoid arthritis independent of known HLA-DRB1 risk alleles in a family-based and a case control study. <i>Arthritis Research and Therapy</i> , 2009, 11, R60.	1.6	40
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1947	Applications of Linkage Disequilibrium and Association Mapping in Maize. <i>Biotechnology in Agriculture and Forestry</i> , 2009, , 173-195.	0.2	41
1948	An extensive screen of the HLA region reveals an independent association of HLA class I and class II with susceptibility for systemic lupus erythematosus. <i>Scandinavian Journal of Rheumatology</i> , 2009, 38, 256-262.	0.6	15
1949	Combining Case-Control and Case-Trio Data From the Same Population in Genetic Association Analyses: Overview of Approaches and Illustration With a Candidate Gene Study. <i>American Journal of Epidemiology</i> , 2009, 170, 657-664.	1.6	28
1950	Linkage Analysis of Qualitative Traits. , 2009, , 81-118.		0
1951	Population-Based Association Studies. , 2009, , 171-190.		1
1952	A Genome-Wide Association Study Primer for Clinicians. <i>Taiwanese Journal of Obstetrics and Gynecology</i> , 2009, 48, 89-95.	0.5	16
1953	Analytical Approaches and Population Types for Finding and Utilizing QTL in Complex Plant Populations. <i>Crop Science</i> , 2009, 49, 363-380.	0.8	53
1954	Association of the protein Z ATG haplotype with symptomatic nonvascular stroke or thromboembolism in white children: a family-based cohort study. <i>Blood</i> , 2009, 113, 2336-2341.	0.6	16
1955	Fibrinogen β and β genes and factor VLeiden in children with thromboembolism: results from 2 family-based association studies. <i>Blood</i> , 2009, 114, 1947-1953.	0.6	29
1956	Characterisation of psoriasis susceptibility locus 6 (PSORS6) in patients with early onset psoriasis and evidence for interaction with PSORS1. <i>Journal of Medical Genetics</i> , 2009, 46, 736-744.	1.5	34
1957	Genetic association tests: a method for the joint analysis of family and case-control data. <i>Human Genomics</i> , 2009, 4, 2.	1.4	14
1958	Association between <i>TGFB3</i> and Nonsyndromic Cleft Lip with or Without Cleft Palate in a Chilean Population. <i>Cleft Palate-Craniofacial Journal</i> , 2010, 47, 513-517.	0.5	17
1959	Genetic Variation in the Vascular Endothelial Growth Factor Gene is Associated With Biliary Atresia. <i>Journal of Clinical Gastroenterology</i> , 2010, 44, 135-139.	1.1	47
1960	Linkage of angiotensinogen gene polymorphisms with hypertension in a sibling study of Hong Kong Chinese. <i>Journal of Hypertension</i> , 2010, 28, 1203-1209.	0.3	32
1961	Gene-environment interaction tests for family studies with quantitative phenotypes: A review and extension to longitudinal measures. <i>Human Genomics</i> , 2010, 4, 302.	1.4	5
1962	ROADTRIPS: Case-Control Association Testing with Partially or Completely Unknown Population and Pedigree Structure. <i>American Journal of Human Genetics</i> , 2010, 86, 172-184.	2.6	153
1963	On Genome-wide Association Studies for Family-Based Designs: An Integrative Analysis Approach Combining Ascertained Family Samples with Unselected Controls. <i>American Journal of Human Genetics</i> , 2010, 86, 573-580.	2.6	30
1964	Differential Contributions of Rare and Common, Coding and Noncoding Ret Mutations to Multifactorial Hirschsprung Disease Liability. <i>American Journal of Human Genetics</i> , 2010, 87, 60-74.	2.6	230

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1966	Genome-wide association filtering using a highly locus-specific transmission/disequilibrium test. <i>Human Genetics</i> , 2010, 128, 325-344.	1.8	5
1967	Evidence of gene-environment interaction for the IRF6 gene and maternal multivitamin supplementation in controlling the risk of cleft lip with/without cleft palate. <i>Human Genetics</i> , 2010, 128, 401-410.	1.8	65
1968	A Genome-Wide Association Study of Social and Non-Social Autistic-Like Traits in the General Population Using Pooled DNA, 500K SNP Microarrays and Both Community and Diagnosed Autism Replication Samples. <i>Behavior Genetics</i> , 2010, 40, 31-45.	1.4	49
1969	Chromosome region 2p25 is linked and associated with type 1 diabetes in Colombia. <i>Journal of Genetics</i> , 2010, 89, 457-461.	0.4	3
1970	Study on DBH Genetic Polymorphisms and Plasma Activity in Attention Deficit Hyperactivity Disorder Patients from Eastern India. <i>Cellular and Molecular Neurobiology</i> , 2010, 30, 265-274.	1.7	19
1971	Quantitative genetics: past and present. <i>Molecular Breeding</i> , 2010, 26, 135-143.	1.0	10
1972	Current findings, challenges and novel approaches in human genetic susceptibility to tuberculosis. <i>Tuberculosis</i> , 2010, 90, 71-83.	0.8	201
1973	Haplotype association analyses in resources of mixed structure using Monte Carlo testing. <i>BMC Bioinformatics</i> , 2010, 11, 592.	1.2	3
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1975	Variation in folate pathway genes contributes to risk of congenital heart defects among individuals with Down syndrome. <i>Genetic Epidemiology</i> , 2010, 34, 613-623.	0.6	66
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1981	A functional polymorphism in the reduced folate carrier gene and DNA hypomethylation in mothers of children with autism. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2010, 153B, 1209-1220.	1.1	76
1982	Association analysis of the E-selectin 98C>>T polymorphism and the risk of childhood ischemic stroke. <i>Cell Biochemistry and Function</i> , 2010, 28, 591-596.	1.4	3
1983	A three-stage approach for genome-wide association studies with family data for quantitative traits. <i>BMC Genetics</i> , 2010, 11, 40.	2.7	8

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1985	Polymorphisms in leucine-rich repeat genes are associated with autism spectrum disorder susceptibility in populations of European ancestry. <i>Molecular Autism</i> , 2010, 1, 7.	2.6	51
1986	Efficiency robust statistics for genetic linkage and association studies under genetic model uncertainty. <i>Statistics in Medicine</i> , 2010, 29, 158-180.	0.8	27
1987	Using ancestry matching to combine family-based and unrelated samples for genome-wide association studies. <i>Statistics in Medicine</i> , 2010, 29, 2932-2945.	0.8	15
1988	Inferring Haplotype/Disease Association by Joint Use of Case-Parents Trios and Case-Parent Pairs. <i>Annals of Human Genetics</i> , 2010, 74, 263-274.	0.3	2
1989	Influence of population stratification on population-based marker-disease association analysis. <i>Annals of Human Genetics</i> , 2010, 74, 351-360.	0.3	2
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1991	Correction for Multiplicity in Genetic Association Studies of Triads: The Permutational TDT. <i>Annals of Human Genetics</i> , 2010, 75, no-no.	0.3	5
1992	Perspectives on the use of landscape genetics to detect genetic adaptive variation in the field. <i>Molecular Ecology</i> , 2010, 19, 3760-3772.	2.0	237
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1995	An omnibus test for family-based association studies with multiple SNPs and multiple phenotypes. <i>European Journal of Human Genetics</i> , 2010, 18, 720-725.	1.4	7
1996	Differential decay of parent-of-origin-specific genomic sharing in cystic fibrosis-affected sib pairs maps a paternally imprinted locus to 7q34. <i>European Journal of Human Genetics</i> , 2010, 18, 553-559.	1.4	2
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1998	The power of the Transmission Disequilibrium Test in the presence of population stratification. <i>European Journal of Human Genetics</i> , 2010, 18, 1032-1038.	1.4	10
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2000	A common variant of the latrophilin 3 gene, LPHN3, confers susceptibility to ADHD and predicts effectiveness of stimulant medication. <i>Molecular Psychiatry</i> , 2010, 15, 1053-1066.	4.1	245
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2003	AHL1 is required for photoreceptor outer segment development and is a modifier for retinal degeneration in nephronophthisis. <i>Nature Genetics</i> , 2010, 42, 175-180.	9.4	171
2004	New approaches to population stratification in genome-wide association studies. <i>Nature Reviews Genetics</i> , 2010, 11, 459-463.	7.7	1,047
2005	DRD4 and DAT1 in ADHD: Functional neurobiology to pharmacogenetics. <i>Pharmacogenomics and Personalized Medicine</i> , 2010, 3, 61.	0.4	16
2006	Allelic Selection of Amplicons in Glioblastoma Revealed by Combining Somatic and Germline Analysis. <i>PLoS Genetics</i> , 2010, 6, e1001086.	1.5	27
2007	The Type 1 Diabetes - HLA Susceptibility Interactome - Identification of HLA Genotype-Specific Disease Genes for Type 1 Diabetes. <i>PLoS ONE</i> , 2010, 5, e9576.	1.1	21
2008	Genome Wide Linkage Study, Using a 250K SNP Map, of Plasmodium falciparum Infection and Mild Malaria Attack in a Senegalese Population. <i>PLoS ONE</i> , 2010, 5, e11616.	1.1	36
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2011	Mendelian Randomization in the Era of Genomewide Association Studies. <i>Clinical Chemistry</i> , 2010, 56, 723-728.	1.5	66
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2013	Visualizing Chromosome Mosaicism and Detecting Ethnic Outliers by the Method of "Rare" Heterozygotes and Homozygotes (RHH). <i>Human Molecular Genetics</i> , 2010, 19, 2539-2553.	1.4	1
2014	Family-Based Analysis of Candidate Genes for Polycystic Ovary Syndrome. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2010, 95, 2306-2315.	1.8	113
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2016	MDM2 as a Modifier Gene in Retinoblastoma. <i>Journal of the National Cancer Institute</i> , 2010, 102, 1805-1808.	3.0	51
2017	Efficient Genome-Wide Association Testing of Gene-Environment Interaction in Case-Parent Trios. <i>American Journal of Epidemiology</i> , 2010, 172, 116-122.	1.6	35
2018	A doubly robust test for gene-environment interaction in family-based studies of affected offspring. <i>Biostatistics</i> , 2010, 11, 213-225.	0.9	13
2019	Transcobalamin II receptor polymorphisms are associated with increased risk for neural tube defects. <i>Journal of Medical Genetics</i> , 2010, 47, 677-685.	1.5	40
2020	Genetic Findings in Anorexia and Bulimia Nervosa. <i>Progress in Molecular Biology and Translational Science</i> , 2010, 94, 241-270.	0.9	23

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2021	Power to detect selective allelic amplification in genome-wide scans of tumor data. <i>Bioinformatics</i> , 2010, 26, 518-528.	1.8	9
2022	Allelic Heterogeneity in Genetic Association Meta-Analysis: An Application to <i>DTNBP1</i> and Schizophrenia. <i>Human Heredity</i> , 2010, 69, 71-79.	0.4	26
2023	A remark on rare variants. <i>Journal of Human Genetics</i> , 2010, 55, 219-226.	1.1	9
2024	ITPKC gene SNP rs28493229 and Kawasaki disease in Taiwanese children. <i>Human Molecular Genetics</i> , 2010, 19, 1147-1151.	1.4	40
2025	Methods for Investigating Gene-Environment Interactions in Candidate Pathway and Genome-Wide Association Studies. <i>Annual Review of Public Health</i> , 2010, 31, 21-36.	7.6	138
2026	Variation in IGHMBP2 is not associated with IgA nephropathy in independent studies of UK Caucasian and Chinese Han patients. <i>Nephrology Dialysis Transplantation</i> , 2010, 25, 1547-1554.	0.4	5
2027	Whole-Genome Linkage and Association Scan in Primary, Nonsyndromic Vesicoureteric Reflux. <i>Journal of the American Society of Nephrology: JASN</i> , 2010, 21, 113-123.	3.0	58
2028	CIITA variation in the presence of HLA-DRB1*1501 increases risk for multiple sclerosis. <i>Human Molecular Genetics</i> , 2010, 19, 2331-2340.	1.4	49
2029	Association Analysis under Population Stratification: A Two-Stage Procedure Utilizing Population- and Family-Based Analyses. <i>Human Heredity</i> , 2010, 69, 160-170.	0.4	6
2030	Familial Meniere's disease restricted to 1.48 Mb on chromosome 12p12.3 by allelic and haplotype association. <i>Journal of Human Genetics</i> , 2010, 55, 834-837.	1.1	26
2031	Is There a Genetic Basis for Polycystic Ovary Syndrome?. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2010, 95, 2058-2060.	1.8	13
2032	No association between LRP5 gene polymorphisms and bone and obesity phenotypes in Chinese male-offspring nuclear families. <i>Acta Pharmacologica Sinica</i> , 2010, 31, 1464-1469.	2.8	8
2033	Linkage to 20p13 including the ANGPT4 gene in families with mixed Alzheimer's disease and vascular dementia. <i>Journal of Human Genetics</i> , 2010, 55, 649-655.	1.1	9
2034	Mexican-American Admixture Mapping Analyses for Diabetic Nephropathy in Type 2 Diabetes Mellitus. <i>Seminars in Nephrology</i> , 2010, 30, 141-149.	0.6	8
2035	Methods: Genetic Epidemiology. <i>Clinics in Laboratory Medicine</i> , 2010, 30, 795-814.	0.7	0
2036	Genetics of Osteoporosis. <i>Endocrine Reviews</i> , 2010, 31, 629-662.	8.9	316
2037	Designs for Linkage Analysis and Association Studies of Complex Diseases. <i>Methods in Molecular Biology</i> , 2010, 620, 219-242.	0.4	16
2038	Nonparametric Methods for Molecular Biology. <i>Methods in Molecular Biology</i> , 2010, 620, 105-153.	0.4	13

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2041	Formal Genetics of Humans: Multifactorial Inheritance and Common Diseases. , 2010, , 263-286.		1
2042	APOE Gene ϵ Polymorphism Does Not Determine Predisposition to Ischemic Stroke in Children. <i>Pediatric Neurology</i> , 2010, 43, 25-28.	1.0	14
2043	Genetics of Susceptibility and Resistance to Infection. <i>Methods in Microbiology</i> , 2010, 37, 67-99.	0.4	2
2044	Statistical challenges for genome-wide association studies of suicidality using family data. <i>European Psychiatry</i> , 2010, 25, 307-309.	0.1	3
2045	Deliberative assessment of surrogate consent in dementia research. <i>Alzheimer's and Dementia</i> , 2010, 6, 342-350.	0.4	30
2046	An Association Test for Multiple Traits Based on the Generalized Kendall's Tau. <i>Journal of the American Statistical Association</i> , 2010, 105, 473-481.	1.8	54
2047	The Genetics of Allergic Disease and Asthma. , 2010, , 22-39.		0
2048	Methods: Genetic Epidemiology. <i>Psychiatric Clinics of North America</i> , 2010, 33, 15-34.	0.7	0
2050	Multiple Sclerosis in the Elderly Patient. <i>Drugs and Aging</i> , 2010, 27, 283-294.	1.3	55
2051	Variable effects of maternal and paternal fetal contribution to the risk for preeclampsia combining GSTP1, eNOS, and LPL gene polymorphisms. <i>Journal of Maternal-Fetal and Neonatal Medicine</i> , 2011, 24, 628-635.	0.7	15
2052	A comprehensive analysis of the COL29A1 gene does not support a role in eczema. <i>Journal of Allergy and Clinical Immunology</i> , 2011, 127, 1187-1194.e7.	1.5	15
2053	FTO and MC4R Gene Variants Are Associated with Obesity in Polycystic Ovary Syndrome. <i>PLoS ONE</i> , 2011, 6, e16390.	1.1	92
2054	Type 2 diabetes susceptibility single-nucleotide polymorphisms are not associated with polycystic ovary syndrome. <i>Fertility and Sterility</i> , 2011, 95, 2538-2541.e6.	0.5	31
2055	Family-Based Genetic Association Tests. <i>Cold Spring Harbor Protocols</i> , 2011, 2011, pdb.top96.	0.2	1
2056	Human leukocyte antigen class II and type 1 diabetes in Latin America: A combined meta-analysis of association and family-based studies. <i>Human Immunology</i> , 2011, 72, 581-586.	1.2	14
2057	The APOC3 T-455C and C-482T promoter region polymorphisms are not associated with the severity of liver damage independently of PNPLA3 I148M genotype in patients with nonalcoholic fatty liver. <i>Journal of Hepatology</i> , 2011, 55, 1409-1414.	1.8	74
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2060	Family-based Association Methods. , 2011, , 231-250.		0
2061	Current Gene Discovery Strategies for Ocular Conditions. , 2011, 52, 7761.		4
2062	INTEGRATIVE GENOMICS. , 2011, , 60-70.		0
2063	Family-based Gene-by-environment Interaction Studies. <i>Epidemiology</i> , 2011, 22, 400-407.	1.2	27
2064	Statistical Analysis in Genetic Studies of Mental Illnesses. <i>Statistical Science</i> , 2011, 26, 116-129.	1.6	6
2065	Power and robustness of three whole genome association mapping approaches in selected populations. <i>Journal of Animal Breeding and Genetics</i> , 2011, 128, 3-14.	0.8	4
2066	Susceptibility variants on chromosome 7p21.1 suggest HDAC9 as a new candidate gene for male-pattern baldness. <i>British Journal of Dermatology</i> , 2011, 165, 1293-1302.	1.4	50
2067	8q24.3 and 11q25 chromosomal loci association with low HDL-C in metabolic syndrome. <i>European Journal of Clinical Investigation</i> , 2011, 41, 1105-1112.	1.7	4
2068	Plasma glutathione peroxidase in pediatric stroke families. <i>Journal of Thrombosis and Haemostasis</i> , 2011, 9, 33-38.	1.9	12
2069	Glucuronic Acid Epimerase is Associated with Plasma Triglyceride and High-Density Lipoprotein Cholesterol Levels in Turks. <i>Annals of Human Genetics</i> , 2011, 75, 398-417.	0.3	15
2070	Unbiased and Locally Efficient Estimation of Genetic Effect on Quantitative Trait in the Presence of Population Admixture. <i>Biometrics</i> , 2011, 67, 331-343.	0.8	2
2071	Genetic study of families affected with aggressive periodontitis. <i>Periodontology 2000</i> , 2011, 56, 87-101.	6.3	33
2072	Common variants in DGKK are strongly associated with risk of hypospadias. <i>Nature Genetics</i> , 2011, 43, 48-50.	9.4	99
2073	Family-based designs for genome-wide association studies. <i>Nature Reviews Genetics</i> , 2011, 12, 465-474.	7.7	251
2074	A novel approach for small sample size family-based association studies: sequential tests. <i>European Journal of Human Genetics</i> , 2011, 19, 915-920.	1.4	3
2075	Gene-ontology enrichment analysis in two independent family-based samples highlights biologically plausible processes for autism spectrum disorders. <i>European Journal of Human Genetics</i> , 2011, 19, 1082-1089.	1.4	39
2076	A targeted association study in systemic lupus erythematosus identifies multiple susceptibility alleles. <i>Genes and Immunity</i> , 2011, 12, 51-58.	2.2	40

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2078	Overview of techniques to account for confounding due to population stratification and cryptic relatedness in genomic data association analyses. <i>Heredity</i> , 2011, 106, 511-519.	1.2	70
2079	A family-based study of common polygenic variation and risk of schizophrenia. <i>Molecular Psychiatry</i> , 2011, 16, 887-888.	4.1	27
2080	Replication and further characterization of a Type 1 diabetes-associated locus at the telomeric end of the major histocompatibility complex. <i>Journal of Diabetes</i> , 2011, 3, 238-247.	0.8	8
2081	A meta-analysis of two genome-wide association studies identifies 3 new loci for alcohol dependence. <i>Journal of Psychiatric Research</i> , 2011, 45, 1419-1425.	1.5	74
2082	MMP1 and MMP20 contribute to tooth agenesis in humans. <i>Archives of Oral Biology</i> , 2011, 56, 506-511.	0.8	20
2083	William Allan Award Address: On the Role and Soul of a Statistical Geneticist. <i>American Journal of Human Genetics</i> , 2011, 88, 264-268.	2.6	1
2084	Association of ADAM10 and CAMK2A Polymorphisms with Conduct Disorder: Evidence from Family-Based Studies. <i>Journal of Abnormal Child Psychology</i> , 2011, 39, 773-782.	3.5	11
2085	Family-based association analysis of alcohol dependence in the COGA sample and replication in the Australian twin-family study. <i>Journal of Neural Transmission</i> , 2011, 118, 1293-1299.	1.4	18
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2087	SNP Variations in the 7q33 Region Containing DGKI are Associated with Dyslexia in the Finnish and German Populations. <i>Behavior Genetics</i> , 2011, 41, 134-140.	1.4	25
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2089	Evidence of association with type 1 diabetes in the SLC11A1 gene region. <i>BMC Medical Genetics</i> , 2011, 12, 59.	2.1	24
2090	Association of Rad51 polymorphism with DNA repair in BRCA1 mutation carriers and sporadic breast cancer risk. <i>BMC Cancer</i> , 2011, 11, 278.	1.1	22
2091	Exploration and comparison of methods for combining population- and family-based genetic association using the Genetic Analysis Workshop 17 mini-exome. <i>BMC Proceedings</i> , 2011, 5, S28.	1.8	11
2092	Identifying variants that contribute to linkage for dichotomous and quantitative traits in extended pedigrees. <i>BMC Proceedings</i> , 2011, 5, S68.	1.8	1
2093	MI-GWAS: a SAS platform for the analysis of inherited and maternal genetic effects in genome-wide association studies using log-linear models. <i>BMC Bioinformatics</i> , 2011, 12, 117.	1.2	6
2094	Association and haplotype analysis of candidate genes in five genomic regions linked to sow maternal infanticide in a white Duroc × Erhualian resource population. <i>BMC Genetics</i> , 2011, 12, 24.	2.7	9

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2096	Perspectives on genome-wide multi-stage family-based association studies. <i>Statistics in Medicine</i> , 2011, 30, 2201-2221.	0.8	3
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2098	Rare variants in the <i>CYP27B1</i> gene are associated with multiple sclerosis. <i>Annals of Neurology</i> , 2011, 70, 881-886.	2.8	204
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2266	Summary of Results and Discussions From the Gene-Based Tests Group at Genetic Analysis Workshop 18. <i>Genetic Epidemiology</i> , 2014, 38, S44-8.	0.6	6
2267	Effects of RET and NRG1 polymorphisms in Indonesian patients with Hirschsprung disease. <i>Journal of Pediatric Surgery</i> , 2014, 49, 1614-1618.	0.8	37
2268	A General Efficient and Flexible Approach for Genome-Wide Association Analyses of Imputed Genotypes in Family-Based Designs. <i>Genetic Epidemiology</i> , 2014, 38, 560-571.	0.6	23
2269	Testing gene-environment interactions in family-based association studies using trait-based ascertained samples. <i>Statistics in Medicine</i> , 2014, 33, 304-318.	0.8	1
2270	A data-smoothing approach to explore and test gene-environment interaction in case-parent trios. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2014, 13, 159-71.	0.2	3
2271	Association of the tumor necrosis factor α 308 A/G promoter polymorphism with Tourette syndrome. <i>International Journal of Immunogenetics</i> , 2014, 41, 493-498.	0.8	13
2272	Comparing barriers to mental health treatment and substance use disorder treatment among individuals with comorbid major depression and substance use disorders. <i>Journal of Substance Abuse Treatment</i> , 2014, 46, 268-273.	1.5	81
2273	A unified GMDR method for detecting gene-gene interactions in family and unrelated samples with application to nicotine dependence. <i>Human Genetics</i> , 2014, 133, 139-150.	1.8	23
2274	Genome-wide association study of bipolar disorder in Canadian and UK populations corroborates disease loci including SYNE1 and CSMD1. <i>BMC Medical Genetics</i> , 2014, 15, 2.	2.1	106
2275	The FOXE1 locus is a major genetic determinant for familial nonmedullary thyroid carcinoma. <i>International Journal of Cancer</i> , 2014, 134, 2098-2107.	2.3	39
2276	Rare-Variant Extensions of the Transmission Disequilibrium Test: Application to Autism Exome Sequence Data. <i>American Journal of Human Genetics</i> , 2014, 94, 33-46.	2.6	69
2277	FARVAT: a family-based rare variant association test. <i>Bioinformatics</i> , 2014, 30, 3197-3205.	1.8	34
2278	Cytochrome P450 gene CYP337 and heritability of fitness traits in the <i>Glanville</i> fritillary butterfly. <i>Molecular Ecology</i> , 2014, 23, 1994-2005.	2.0	16
2279	Utilising Family-Based Designs for Detecting Rare Variant Disease Associations. <i>Annals of Human Genetics</i> , 2014, 78, 129-140.	0.3	12
2280	A new genome scan for primary nonsyndromic vesicoureteric reflux emphasizes high genetic heterogeneity and shows linkage and association with various genes already implicated in urinary tract development. <i>Molecular Genetics & Genomic Medicine</i> , 2014, 2, 7-29.	0.6	23
2281	Twin studies in inherited eye disease. <i>Clinical and Experimental Ophthalmology</i> , 2014, 42, 84-93.	1.3	3
2282	Disentangling Pooled Triad Genotypes for Association Studies. <i>Annals of Human Genetics</i> , 2014, 78, 345-356.	0.3	1

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2283	Fine Mapping and Functional Studies of Risk Variants for Type 1 Diabetes at Chromosome 16p13.13. <i>Diabetes</i> , 2014, 63, 4360-4368.	0.3	17
2284	Remind me again what disease we are studying? A population genetics, genetic analysis, and real data perspective on why progress on identifying genetic influences on common epilepsies has been so slow. <i>Progress in Brain Research</i> , 2014, 213, 199-221.	0.9	8
2285	Trio study and meta-analysis support the association of genetic variation at the serotonin transporter with early-onset obsessive-compulsive disorder. <i>Neuroscience Letters</i> , 2014, 580, 100-103.	1.0	39
2286	A novel transmission-based test of association for multivariate phenotypes: an application to systolic and diastolic blood pressure levels. <i>BMC Proceedings</i> , 2014, 8, S71.	1.8	2
2287	Genome-wide association and linkage analyses localize a progressive retinal atrophy locus in Persian cats. <i>Mammalian Genome</i> , 2014, 25, 354-362.	1.0	24
2288	Examination of Genetic Variation in GABRA2 with Conduct Disorder and Alcohol Abuse and Dependence in a Longitudinal Study. <i>Behavior Genetics</i> , 2014, 44, 356-367.	1.4	13
2289	Family-based association study of ZNF533, DOCK4 and IMMP2L gene polymorphisms linked to autism in a northeastern Chinese Han population. <i>Journal of Zhejiang University: Science B</i> , 2014, 15, 264-271.	1.3	29
2290	Analysis of Genetic Linkage Data for Mendelian Traits. <i>Current Protocols in Human Genetics</i> , 2014, 83, 1.4.1-31.	3.5	6
2291	The HLA-B*39 allele increases type 1 diabetes risk conferred by HLA-DRB1*04:04-DQB1*03:02 and HLA-DRB1*08-DQB1*04 class II haplotypes. <i>Human Immunology</i> , 2014, 75, 65-70.	1.2	30
2292	Genetic studies of Crohn's disease: Past, present and future. <i>Bailliere's Best Practice and Research in Clinical Gastroenterology</i> , 2014, 28, 373-386.	1.0	87
2293	APOE polymorphism and diabetic nephropathy. <i>Clinical and Experimental Nephrology</i> , 2014, 18, 230-233.	0.7	10
2294	Association Mapping in Crop Plants. <i>Advances in Genetics</i> , 2014, 85, 109-147.	0.8	127
2296	Analytic power and sample size calculation for the genotypic transmission/disequilibrium test in case-parent trio studies. <i>Biometrical Journal</i> , 2014, 56, 1076-1092.	0.6	6
2297	Association and Mutation Analyses of the <i>IRF6</i> Gene in Families with Nonsyndromic and Syndromic Cleft Lip and/or Cleft Palate. <i>Cleft Palate-Craniofacial Journal</i> , 2014, 51, 49-55.	0.5	20
2298	Rare-Variant Kernel Machine Test for Longitudinal Data from Population and Family Samples. <i>Human Heredity</i> , 2015, 80, 126-138.	0.4	9
2300	Increased Power for Detection of Parent-of-Origin Effects via the Use of Haplotype Estimation. <i>American Journal of Human Genetics</i> , 2015, 97, 419-434.	2.6	15
2301	Statistical equivalent of the classical TDT for quantitative traits and multivariate phenotypes. <i>Journal of Genetics</i> , 2015, 94, 619-628.	0.4	7
2302	Novel evidence of association with nonsyndromic cleft lip with or without cleft palate was shown for single nucleotide polymorphisms in <i>FOXF2</i> gene in an Asian population. <i>Birth Defects Research Part A: Clinical and Molecular Teratology</i> , 2015, 103, 857-862.	1.6	11

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2304	ACN9 and alcohol dependence: Family-based association analysis in multiplex alcohol dependence families. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2015, 168, 179-187.	1.1	4
2305	On the use of the transmission disequilibrium test to detect pseudo-autosomal variants affecting traits with sex-limited expression. <i>Animal Genetics</i> , 2015, 46, 395-402.	0.6	4
2306	Adaptive robust genetic association tests using case-parents triad families. <i>Biometrical Journal</i> , 2015, 57, 453-467.	0.6	1
2307	Detecting gene-environment interactions in human birth defects: Study designs and statistical methods. <i>Birth Defects Research Part A: Clinical and Molecular Teratology</i> , 2015, 103, 692-702.	1.6	5
2308	Association between Tourette Syndrome and the Dopamine D3 Receptor Gene Rs6280. <i>Chinese Medical Journal</i> , 2015, 128, 654-658.	0.9	9
2309	Using parental phenotypes in case-parent studies. <i>Frontiers in Genetics</i> , 2015, 6, 221.	1.1	2
2310	Fine Mapping of a GWAS-Derived Obesity Candidate Region on Chromosome 16p11.2. <i>PLoS ONE</i> , 2015, 10, e0125660.	1.1	12
2311	Porcine SOX9 Gene Expression Is Influenced by an 18bp Indel in the 5'-UTR. <i>PLoS ONE</i> , 2015, 10, e0139583.	1.1	16
2312	No Evidence for Enrichment in Schizophrenia for Common Allelic Associations at Imprinted Loci. <i>PLoS ONE</i> , 2015, 10, e0144172.	1.1	4
2313	Fine mapping analysis confirms and strengthens linkage of four chromosomal regions in familial hypospadias. <i>European Journal of Human Genetics</i> , 2015, 23, 516-522.	1.4	16
2314	Population variation in total genetic risk of Hirschsprung disease from common RET, SEMA3 and NRG1 susceptibility polymorphisms. <i>Human Molecular Genetics</i> , 2015, 24, 2997-3003.	1.4	66
2315	Heritability of IL-1A Gene Promoter Polymorphism in Patients With Coronary Artery Disease: A Trio-Family Study. <i>Laboratory Medicine</i> , 2015, 46, 20-25.	0.8	2
2316	A multi-SNP association test for complex diseases incorporating an optimal P-value threshold algorithm in nuclear families. <i>BMC Genomics</i> , 2015, 16, 381.	1.2	20
2317	Review of statistical methodologies for the detection of parent-of-origin effects in family trio genome-wide association data with binary disease traits. <i>Briefings in Bioinformatics</i> , 2015, 16, 429-448.	3.2	23
2318	Bayes factors based on robust TDT-type tests for family trio design. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2015, 14, 253-64.	0.2	0
2319	IRF6 polymorphisms in Mexican patients with non-syndromic cleft lip. <i>Meta Gene</i> , 2015, 4, 8-16.	0.3	9
2320	A Sequence Kernel Association Test for Dichotomous Traits in Family Samples under a Generalized Linear Mixed Model. <i>Human Heredity</i> , 2015, 79, 60-68.	0.4	29

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2322	Methylenetetrahydrofolate Reductase Gene A1298C Polymorphism in Pediatric Stroke—Case—Control and Family-based Study. <i>Journal of Stroke and Cerebrovascular Diseases</i> , 2015, 24, 61-65.	0.7	7
2323	TNF-alpha-308G>A polymorphism and the risk of familial CAD in a Pakistani population. <i>Human Immunology</i> , 2015, 76, 13-18.	1.2	13
2324	Family-based association study of HLA class II with type 1 diabetes in Moroccans. <i>Pathologie Et Biologie</i> , 2015, 63, 80-84.	2.2	7
2325	Learning about the X from our parents. <i>Frontiers in Genetics</i> , 2015, 6, 15.	1.1	5
2326	Association Mapping. , 2015, , 217-256.		3
2327	A Powerful Nonparametric Statistical Framework for Family-Based Association Analyses. <i>Genetics</i> , 2015, 200, 69-78.	1.2	2
2328	Distribution-free tolerance intervals with nomination samples: Applications to mercury contamination in fish. <i>Statistical Methodology</i> , 2015, 26, 16-33.	0.5	8
2329	Whole genome analysis of a Vietnamese trio. <i>Journal of Biosciences</i> , 2015, 40, 113-124.	0.5	4
2330	Rare variant association studies: considerations, challenges and opportunities. <i>Genome Medicine</i> , 2015, 7, 16.	3.6	176
2331	Genome-wide association mapping in plants. <i>Theoretical and Applied Genetics</i> , 2015, 128, 1163-1174.	1.8	23
2332	A haplotype-based framework for group-wise transmission/disequilibrium tests for rare variant association analysis. <i>Bioinformatics</i> , 2015, 31, 1452-1459.	1.8	14
2333	Genetic linkage analysis in the age of whole-genome sequencing. <i>Nature Reviews Genetics</i> , 2015, 16, 275-284.	7.7	225
2334	On Ranked Set Sampling Variation and Its Applications to Public Health Research. <i>ICSA Book Series in Statistics</i> , 2015, , 291-313.	0.0	1
2335	Associating Multivariate Quantitative Phenotypes with Genetic Variants in Family Samples with a Novel Kernel Machine Regression Method. <i>Genetics</i> , 2015, 201, 1329-1339.	1.2	14
2336	Genetic Modifiers and Oligogenic Inheritance. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2015, 5, a017145-a017145.	2.9	84
2337	An HLA-G—14bp insertion/deletion polymorphism associates with the development of autistic spectrum disorders. <i>Brain, Behavior, and Immunity</i> , 2015, 44, 207-212.	2.0	32
2338	Polymorphisms within ASTN2 gene are associated with age at onset of Alzheimer’s disease. <i>Journal of Neural Transmission</i> , 2015, 122, 701-708.	1.4	24

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2340	Family-based association study of interleukin 6 (IL6) and its receptor (IL6R) functional polymorphisms in schizophrenia in the Polish population. <i>Journal of Neuroimmunology</i> , 2015, 285, 62-67.	1.1	6
2341	Likelihood Ratio Test for Multi-Sample Mixture Model and Its Application to Genetic Imprinting. <i>Journal of the American Statistical Association</i> , 2015, 110, 867-877.	1.8	8
2342	Relationship between SNPs and expression level for candidate genes in rheumatoid arthritis. <i>Scandinavian Journal of Rheumatology</i> , 2015, 44, 2-7.	0.6	8
2343	A Killer Immunoglobulin - Like Receptor Gene - Content Haplotype and A Cognate Human Leukocyte Antigen Ligand are Associated with Autism. <i>Autism-open Access</i> , 2016, 06, .	0.2	5
2344	Using Incomplete Trios to Boost Confidence in Family Based Association Studies. <i>Frontiers in Genetics</i> , 2016, 7, 34.	1.1	1
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2346	Testing Allele Transmission of an SNP Set Using a Family-Based Generalized Genetic Random Field Method. <i>Genetic Epidemiology</i> , 2016, 40, 341-351.	0.6	4
2347	Test for association of common variants in GRM7 with alcohol consumption. <i>Alcohol</i> , 2016, 55, 43-50.	0.8	1
2348	Software for Genome-Wide Association Studies in Autopolyploids and Its Application to Potato. <i>Plant Genome</i> , 2016, 9, plantgenome2015.08.0073.	1.6	191
2349	Discovery of rare variants for complex phenotypes. <i>Human Genetics</i> , 2016, 135, 625-634.	1.8	40
2350	Detecting multi-way epistasis in family-based association studies. <i>Briefings in Bioinformatics</i> , 2016, 18, bbw039.	3.2	4
2351	A Method to Exploit the Structure of Genetic Ancestry Space to Enhance Case-Control Studies. <i>American Journal of Human Genetics</i> , 2016, 98, 857-868.	2.6	21
2352	Risk and resistance perspectives in translation-oriented etiology research. <i>Translational Behavioral Medicine</i> , 2016, 6, 44-54.	1.2	14
2353	Excess maternal transmission of variants in the THADA gene to offspring with type 2 diabetes. <i>Diabetologia</i> , 2016, 59, 1702-1713.	2.9	19
2354	A multi-ethnic genome-wide association study identifies novel loci for non-syndromic cleft lip with or without cleft palate on 2p24.2, 17q23 and 19q13. <i>Human Molecular Genetics</i> , 2016, 25, ddw104.	1.4	163
2355	Lipid phenotype and heritage pattern in families with genetic hypercholesterolemia not related to LDLR, APOB, PCSK9, or APOE. <i>Journal of Clinical Lipidology</i> , 2016, 10, 1397-1405.e2.	0.6	12
2357	Effects of SEMA3 polymorphisms in Hirschsprung disease patients. <i>Pediatric Surgery International</i> , 2016, 32, 1025-1028.	0.6	23

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2359	MSX1 gene polymorphisms in Mexican patients with non-syndromic cleft lip/palate. <i>International Journal of Pediatric Otorhinolaryngology</i> , 2016, 90, 119-124.	0.4	7
2360	Conditioning adaptive combination of P-values method to analyze case-parent trios with or without population controls. <i>Scientific Reports</i> , 2016, 6, 28389.	1.6	1
2361	The impact of genotype calling errors on family-based studies. <i>Scientific Reports</i> , 2016, 6, 28323.	1.6	12
2362	Assessing transmission ratio distortion in extended families: a comparison of analysis methods. <i>BMC Proceedings</i> , 2016, 10, 197-202.	1.8	1
2363	Gene Mapping in Admixed Families: A Cautionary Note on the Interpretation of the Transmission Disequilibrium Test and a Possible Solution. <i>Human Heredity</i> , 2016, 81, 106-116.	0.4	3
2364	Evaluation of proton-coupled folate transporter (<i>SLC46A1</i>) polymorphisms as risk factors for neural tube defects and oral clefts. <i>American Journal of Medical Genetics, Part A</i> , 2016, 170, 1007-1016.	0.7	7
2365	Detecting multiple variants associated with disease based on sequencing data of case-parent trios. <i>Journal of Human Genetics</i> , 2016, 61, 851-860.	1.1	4
2366	Family-based approaches: design, imputation, analysis, and beyond. <i>BMC Genetics</i> , 2016, 17, 9.	2.7	13
2367	Paternal transmission of <i>MTHFD1</i> G1958A variant predisposes to neural tube defects in the offspring. <i>Developmental Medicine and Child Neurology</i> , 2016, 58, 625-631.	1.1	9
2368	Genetics of Lung Disease. , 2016, , 32-43.e3.		0
2369	Statistical Analysis of GWAS. <i>Computational Biology</i> , 2016, , 105-161.	0.1	0
2370	An efficient gene-gene interaction test for genome-wide association studies in trio families. <i>Bioinformatics</i> , 2016, 32, 1848-1855.	1.8	10
2371	Polymorphisms in Wnt signaling pathway genes are associated with peak bone mineral density, lean mass, and fat mass in Chinese male nuclear families. <i>Osteoporosis International</i> , 2016, 27, 1805-1815.	1.3	15
2372	Accuracy of polymerase chain reaction-restriction fragment length polymorphism for RET rs2435357 genotyping as Hirschsprung risk. <i>Journal of Surgical Research</i> , 2016, 203, 91-94.	0.8	14
2373	The top 100 most cited scientific reports focused on diabetes research. <i>Acta Diabetologica</i> , 2016, 53, 13-26.	1.2	36
2374	The Genetics of Allergic Disease and Asthma. , 2016, , 18-30.e4.		0
2375	PRINCESS: Privacy-protecting Rare disease International Network Collaboration via Encryption through Software guard extensionS. <i>Bioinformatics</i> , 2017, 33, 871-878.	1.8	75

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2378	Components of the folate metabolic pathway and ADHD core traits: an exploration in eastern Indian probands. <i>Journal of Human Genetics</i> , 2017, 62, 687-695.	1.1	19
2380	Association of candidate gene polymorphisms with clinical subtypes of preterm birth in a Latin American population. <i>Pediatric Research</i> , 2017, 82, 554-559.	1.1	8
2381	Polymorphisms of STS gene and SULT2A1 gene and neurosteroid levels in Han Chinese boys with attention-deficit/hyperactivity disorder: an exploratory investigation. <i>Scientific Reports</i> , 2017, 7, 45595.	1.6	9
2382	Polygenic transmission disequilibrium confirms that common and rare variation act additively to create risk for autism spectrum disorders. <i>Nature Genetics</i> , 2017, 49, 978-985.	9.4	401
2383	Interaction between Maternal and Paternal <i>SHMT1</i> C1420T Predisposes to Neural Tube Defects in the Fetus: Evidence from Case-Control and Family-Based Triad Approaches. <i>Birth Defects Research</i> , 2017, , .	0.8	0
2384	Polymorphisms in CYP2C9 are associated with response to indomethacin among neonates with patent ductus arteriosus. <i>Pediatric Research</i> , 2017, 82, 776-780.	1.1	21
2385	Analysis of case-parent trios for imprinting effect using a loglinear model with adjustment for sex-of-parent-specific transmission ratio distortion. <i>Human Genetics</i> , 2017, 136, 951-961.	1.8	2
2386	The Rare-Variant Generalized Disequilibrium Test for Association Analysis of Nuclear and Extended Pedigrees with Application to Alzheimer Disease WGS Data. <i>American Journal of Human Genetics</i> , 2017, 100, 193-204.	2.6	26
2387	Single Marker Family-Based Association Analysis Conditional on Parental Information. <i>Methods in Molecular Biology</i> , 2017, 1666, 391-407.	0.4	0
2388	Population Stratification in Genetic Association Studies. <i>Current Protocols in Human Genetics</i> , 2017, 95, 1.22.1-1.22.23.	3.5	108
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2390	Joint genotype- and ancestry-based genome-wide association studies in admixed populations. <i>Genetic Epidemiology</i> , 2017, 41, 555-566.	0.6	11
2391	Interaction between Maternal and Paternal <i>SHMT1</i> C1420T Predisposes to Neural Tube Defects in the Fetus: Evidence from Case-Control and Family-Based Triad Approaches. <i>Birth Defects Research</i> , 2017, 109, 1020-1029.	0.8	10
2392	Adaptive combination of Bayes factors as a powerful method for the joint analysis of rare and common variants. <i>Scientific Reports</i> , 2017, 7, 13858.	1.6	4
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2396	An informative intragenic microsatellite marker suggests the IL-1 receptor as a genetic modifier in cystic fibrosis. <i>European Respiratory Journal</i> , 2017, 50, 1700426.	3.1	8
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2398	Genetics of Rheumatic Diseases. , 2017, , 327-343.		0
2399	A Pragmatic Test for Detecting Association between a Dichotomous Trait and the Genotypes of Affected Families, Controls and Independent Cases. <i>Frontiers in Genetics</i> , 2017, 8, 49.	1.1	2
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2402	Genes and microRNAs associated with mouse cleft palate: A systematic review and bioinformatics analysis. <i>Mechanisms of Development</i> , 2018, 150, 21-27.	1.7	27
2403	Possible effect of SNAIL family transcriptional repressor 1 polymorphisms in non-syndromic cleft lip with or without cleft palate. <i>Clinical Oral Investigations</i> , 2018, 22, 2535-2541.	1.4	8
2404	Evidence of interaction between genes in the folate/homocysteine metabolic pathway in controlling risk of non-syndromic oral cleft. <i>Oral Diseases</i> , 2018, 24, 820-828.	1.5	14
2405	The nature of nurture: Effects of parental genotypes. <i>Science</i> , 2018, 359, 424-428.	6.0	720
2406	Maternal association and influence of DHFR 19bp deletion variant predisposes foetus to anencephaly susceptibility: a family-based triad study. <i>Biomarkers</i> , 2018, 23, 640-646.	0.9	7
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2408	Efficient Monte Carlo evaluation of resampling-based hypothesis tests with applications to genetic epidemiology. <i>Statistical Methods in Medical Research</i> , 2018, 27, 1437-1450.	0.7	0
2409	Investigation of previously implicated genetic variants in chronic tic disorders: a transmission disequilibrium test approach. <i>European Archives of Psychiatry and Clinical Neuroscience</i> , 2018, 268, 301-316.	1.8	23
2410	Family-based analysis of GGT1 and HNF1A gene polymorphisms in patients with polycystic ovary syndrome. <i>Reproductive BioMedicine Online</i> , 2018, 36, 115-119.	1.1	6
2411	Weighted Transmission Disequilibrium Test for Family Trio Association Design. <i>Human Heredity</i> , 2018, 83, 196-209.	0.4	0
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2415	Replication of a rare risk haplotype on 1p36.33 for autism spectrum disorder. <i>Human Genetics</i> , 2018, 137, 807-815.	1.8	4
2416	FUT2 Variants Confer Susceptibility to Familial Otitis Media. <i>American Journal of Human Genetics</i> , 2018, 103, 679-690.	2.6	40
2417	Genetic Determinants of IgA Nephropathy: Eastern Perspective. <i>Seminars in Nephrology</i> , 2018, 38, 455-460.	0.6	24
2418	Pedigree Selection and Information Content. <i>Current Protocols in Human Genetics</i> , 2018, 97, e56.	3.5	3
2419	Association between a common missense variant in <i>LOXL3</i> gene and the risk of non-syndromic cleft palate. <i>Congenital Anomalies (discontinued)</i> , 2018, 58, 136-140.	0.3	7
2420	A Bayesian Gene-Based Genome-Wide Association Study Analysis of Osteosarcoma Trio Data Using a Hierarchically Structured Prior. <i>Cancer Informatics</i> , 2018, 17, 117693511877510.	0.9	12
2421	Investigating the shared genetics of non-syndromic cleft lip/palate and facial morphology. <i>PLoS Genetics</i> , 2018, 14, e1007501.	1.5	44
2422	Evaluation of Gene-Based Family-Based Methods to Detect Novel Genes Associated With Familial Late Onset Alzheimer Disease. <i>Frontiers in Neuroscience</i> , 2018, 12, 209.	1.4	21
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