Joan E Bailey-Wilson

List of Publications by Year
in descending order

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248 papers	16,668 citations	26630 56 h-index	18130 120 g-index
263 all docs	263 docs citations	263 times ranked	20347 citing authors

#	Article	IF	Citations
1	What makes a good prediction? Feature importance and beginning to open the black box of machine learning in genetics. Human Genetics, 2022, 141, 1515-1528.	3.8	18
2	Whole exome sequence analysis in 51â€‰624 participants identifies novel genes and variants associated with refractive error and myopia. Human Molecular Genetics, 2022, , .	2.9	10
3	Geneâ€level association analysis of ordinal traits with functional ordinal logistic regressions. Genetic Epidemiology, 2022, 46, 234-255.	1.3	3
4	Complex N-Linked Glycosylation: A Potential Modifier of Niemannâ€“Pick Disease, Type C1 Pathology. International Journal of Molecular Sciences, 2022, 23, 5082.	4.1	2
5	Two-stage Study of Familial Prostate Cancer by Whole-exome Sequencing and Custom Capture Identifies 10 Novel Genes Associated with the Risk of Prostate Cancer. European Urology, 2021, 79, 353-361.	1.9	28
6	Gene-Based Association Testing of Dichotomous Traits With Generalized Functional Linear Mixed Models Using Extended Pedigrees: Applications to Age-Related Macular Degeneration. Journal of the American Statistical Association, 2021, 116, 531-545.	3.1	3
7	Increased Burden of Rare Sequence Variants in GnRH-Associated Genes in Women With Hypothalamic Amenorrhea. Journal of Clinical Endocrinology and Metabolism, 2021, 106, e1441-e1452.	3.6	13
8	Rare deleterious germline variants and risk of lung cancer. Npj Precision Oncology, 2021, 5, 12.	5.4	19
9	Geneâ€based analysis of biâ€variate survival traits via functional regressions with applications to eye diseases. Genetic Epidemiology, 2021, 45, 455-470.	1.3	1
10	IMI 2021 Yearly Digest. , 2021, 62, 7.		36
11	Genetic Variation and Recurrent Haplotypes on Chromosome 6q23-25 Risk Locus in Familial Lung Cancer. Cancer Research, 2021, 81, 3162-3173.	0.9	5
12	Evaluation of Shared Genetic Susceptibility to High and Low Myopia and Hyperopia. JAMA Ophthalmology, 2021, 139, 601.	2.5	22
13	Myopia in African Americans Is Significantly Linked to Chromosome 7p15.2-14.2. , 2021, 62, 16.		2
14	Sterol and lipid analyses identifies hypolipidemia and apolipoprotein disorders in autism associated with adaptive functioning deficits. Translational Psychiatry, 2021, 11, 471.	4.8	9
15	A powerful new method for rare-variant analysis of quantitative traits in families. European Journal of Human Genetics, 2020, 28, 1629-1630.	2.8	0
16	Whole Exome Sequencing of Highly Aggregated Lung Cancer Families Reveals Linked Loci for Increased Cancer Risk on Chromosomes 12q, 7p, and 4q. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 434-442.	2.5	11
17	Linear mixed models for association analysis of quantitative traits with nextâ€generation sequencing data. Genetic Epidemiology, 2019, 43, 189-206.	1.3	5
18	Geneâ€based association analysis of survival traits via functional regressionâ€based mixed effect cox models for related samples. Genetic Epidemiology, 2019, 43, 952-965.	1.3	4

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19	Small posterior fossa in Chiari I malformation affected families is significantly linked to 1q43-44 and 12q23-24.11 using whole exome sequencing. European Journal of Human Genetics, 2019, 27, 1599-1610.	2.8	15
20	Genome-wide scans of myopia in Pennsylvania Amish families reveal significant linkage to 12q15, 8q21.3 and 5p15.33. Human Genetics, 2019, 138, 339-354.	3.8	8
21	Exome genotyping and linkage analysis identifies two novel linked regions and replicates two others for myopia in Ashkenazi Jewish families. BMC Medical Genetics, 2019, 20, 27.	2.1	5
22	Analysis of the CDKN2A Gene in FAMMM Syndrome Families Reveals Early Age of Onset for Additional Syndromic Cancers. Cancer Research, 2019, 79, 2992-3000.	0.9	10
23	ComPaSSâ€GWAS: A method to reduce type I error in genomeâ€wide association studies when replication data are not available. Genetic Epidemiology, 2019, 43, 102-111.	1.3	7
24	Inferring disease risk genes from sequencing data in multiplex pedigrees through sharing of rare variants. Genetic Epidemiology, 2019, 43, 37-49.	1.3	6
25	Phenotypic and genotypic heterogeneity of Lynch syndrome: a complex diagnostic challenge. Familial Cancer, 2018, 17, 403-414.	1.9	20
26	Genetic Susceptibility to Lung Cancer. , 2018, , 46-51.e2.		5
27	The 677Câ†'T variant of MTHFR is the major genetic modifier of biomarkers of folate status in a young, healthy Irish population. American Journal of Clinical Nutrition, 2018, 108, 1334-1341.	4.7	18
28	Genome-wide association meta-analysis highlights light-induced signaling as a driver for refractive error. Nature Genetics, 2018, 50, 834-848.	21.4	239
29	Rare Variants in Known Susceptibility Loci and Their Contribution to Risk of Lung Cancer. Journal of Thoracic Oncology, 2018, 13, 1483-1495.	1.1	22
30	A genome-wide association study identifies a susceptibility locus for biliary atresia on 2p16.1 within the gene EFEMP1. PLoS Genetics, 2018, 14, e1007532.	3.5	51
31	Genome-wide association study of familial lung cancer. Carcinogenesis, 2018, 39, 1135-1140.	2.8	42
32	Myopia in Chinese families shows linkage to 10q26.13. Molecular Vision, 2018, 24, 29-42.	1.1	3
33	A genome-wide association study of corneal astigmatism: The CREAM Consortium. Molecular Vision, 2018, 24, 127-142.	1.1	10
34	gsSKAT: Rapid gene set analysis and multiple testing correction for rareâ€variant association studies using weighted linear kernels. Genetic Epidemiology, 2017, 41, 297-308.	1.3	9
35	Rare copy number variants in patients with congenital conotruncal heart defects. Birth Defects Research, 2017, 109, 271-295.	1.5	15
36	Genome-wide association study identifies three novel loci in Fuchs endothelial corneal dystrophy. Nature Communications, 2017, 8, 14898.	12.8	101

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37	A comparison study of multivariate fixed models and Gene Association with Multiple Traits (GAMuT) for nextâ€generation sequencing. Genetic Epidemiology, 2017, 41, 18-34.	1.3	3
38	Analysis of sequence data to identify potential risk variants for oral clefts in multiplex families. Molecular Genetics & Genomic Medicine, 2017, 5, 570-579.	1.2	13
39	The FUT2 secretor variant p.Trp154Ter influences serum vitamin B12 concentration via holo-haptocorrin, but not holo-transcobalamin, and is associated with haptocorrin glycosylation. Human Molecular Genetics, 2017, 26, 4975-4988.	2.9	16
40	Caucasian Families Exhibit Significant Linkage of Myopia to Chromosome 11p. , 2017, 58, 3547.		11
41	Familial Lung Cancer: A Brief History from the Earliest Work to the Most Recent Studies. Genes, 2017, 8, 36.	2.4	22
42	Post hoc Analysis for Detecting Individual Rare Variant Risk Associations Using Probit Regression Bayesian Variable Selection Methods in Caseâ€Control Sequencing Studies. Genetic Epidemiology, 2016, 40, 461-469.	1.3	5
43	A Common Polymorphism in HIBCH Influences Methylmalonic Acid Concentrations in Blood Independently of Cobalamin. American Journal of Human Genetics, 2016, 98, 869-882.	6.2	43
44	REVEL: An Ensemble Method for Predicting the Pathogenicity of Rare Missense Variants. American Journal of Human Genetics, 2016, 99, 877-885.	6.2	1,555
45	Assessing the Genetic Predisposition of Education on Myopia: A Mendelian Randomization Study. Genetic Epidemiology, 2016, 40, 66-72.	1.3	56
46	A Comparison Study of Fixed and Mixed Effect Models for Gene Level Association Studies of Complex Traits. Genetic Epidemiology, 2016, 40, 702-721.	1.3	10
47	Childhood gene-environment interactions and age-dependent effects of genetic variants associated with refractive error and myopia: The CREAM Consortium. Scientific Reports, 2016, 6, 25853.	3.3	80
48	Comparison of parametric and machine methods for variable selection in simulated Genetic Analysis Workshop 19 data. BMC Proceedings, 2016, 10, 147-152.	1.6	1
49	Parametric Linkage Analysis Identifies Five Novel Genome-Wide Significant Loci for Familial Lung Cancer. Human Heredity, 2016, 82, 64-74.	0.8	13
50	r2VIM: A new variable selection method for random forests in genome-wide association studies. BioData Mining, 2016, 9, 7.	4.0	53
51	High incidence of unrecognized visceral/neurological late-onset Niemann-Pick disease, type C1, predicted by analysis of massively parallel sequencing data sets. Genetics in Medicine, 2016, 18, 41-48.	2.4	171
52	Focused Analysis of Exome Sequencing Data for Rare Germline Mutations in Familial and Sporadic Lung Cancer. Journal of Thoracic Oncology, 2016, 11, 52-61.	1.1	27
53	Ancestry of the Timorese: age-related macular degeneration associated genotype and allele sharing among human populations from throughout the world. Frontiers in Genetics, 2015, 6, 238.	2.3	9
54	Lessons Learned from Whole Exome Sequencing in Multiplex Families Affected by a Complex Genetic Disorder, Intracranial Aneurysm. PLoS ONE, 2015, 10, e0121104.	2.5	32

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55	Tiled regression reduces type I error rates in tests of association of rare single nucleotide variants with non-normally distributed traits, compared with simple linear regression. , 2015, , .		1
56	A Recurrent Mutation in PARK2 Is Associated with Familial Lung Cancer. American Journal of Human Genetics, 2015, 96, 301-308.	6.2	61
57	A Hereditary Form of Small Intestinal Carcinoid Associated With a Germline Mutation in Inositol Polyphosphate Multikinase. Gastroenterology, 2015, 149, 67-78.	1.3	96
58	Common Variants at Putative Regulatory Sites of the Tissue Nonspecific Alkaline Phosphatase Gene Influence Circulating Pyridoxal 5â€²-Phosphate Concentration in Healthy Adults. Journal of Nutrition, 2015, 145, 1386-1393.	2.9	19
59	Geneâ€Gene Interaction Among WNT Genes for Oral Cleft in Trios. Genetic Epidemiology, 2015, 39, 385-394.	1.3	30
60	Genome-wide association study for refractive astigmatism reveals genetic co-determination with spherical equivalent refractive error: the CREAM consortium. Human Genetics, 2015, 134, 131-146.	3.8	24
61	Determination of the allelic frequency in Smithâ€“Lemliâ€“Opitz syndrome by analysis of massively parallel sequencing data sets. Clinical Genetics, 2015, 87, 570-575.	2.0	43
62	Copy number variants encompassing Mendelian disease genes in a large multigenerational family segregating bipolar disorder. BMC Genetics, 2015, 16, 27.	2.7	18
63	Pleiotropy Analysis of Quantitative Traits at Gene Level by Multivariate Functional Linear Models. Genetic Epidemiology, 2015, 39, 259-275.	1.3	52
64	Variable selection method for the identification of epistatic models. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2015, , 195-206.	0.7	6
65	Genome-Wide Meta-Analysis of Myopia and Hyperopia Provides Evidence for Replication of 11 Loci. PLoS ONE, 2014, 9, e107110.	2.5	40
66	Generalized Functional Linear Models for Geneâ€Based Caseâ€Control Association Studies. Genetic Epidemiology, 2014, 38, 622-637.	1.3	22
67	8q24 risk alleles and prostate cancer in African-Barbadian men. Prostate, 2014, 74, 1579-1588.	2.3	20
68	George Bonney (1947â€“2013) Remembered. Genetic Epidemiology, 2014, 38, 95-96.	1.3	0
69	Association analysis of 9,560 prostate cancer cases from the International Consortium of Prostate Cancer Genetics confirms the role of reported prostate cancer associated SNPs for familial disease. Human Genetics, 2014, 133, 347-356.	3.8	24
70	Inferring rare disease risk variants based on exact probabilities of sharing by multiple affected relatives. Bioinformatics, 2014, 30, 2189-2196.	4.1	30
71	Genome-wide analysis of multi-ancestry cohorts identifies new loci influencing intraocular pressure and susceptibility to glaucoma. Nature Genetics, 2014, 46, 1126-1130.	21.4	212
72	False-positive rates in two-point parametric linkage analysis. BMC Proceedings, 2014, 8, S110.	1.6	1

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73	Whole Exome Sequencing of Distant Relatives in Multiplex Families Implicates Rare Variants in Candidate Genes for Oral Clefts. Genetics, 2014, 197, 1039-1044.	2.9	79
74	VARIABLE SELECTION METHOD FOR THE IDENTIFICATION OF EPISTATIC MODELS. , 2014, , .		7
75	Risk estimation using probability machines. BioData Mining, 2014, 7, 2.	4.0	14
76	Genetic heterogeneity in Finnish hereditary prostate cancer using ordered subset analysis. European Journal of Human Genetics, 2013, 21, 437-443.	2.8	4
77	Meta-analysis of genome-wide association studies in five cohorts reveals common variants in RBFOX1, a regulator of tissue-specific splicing, associated with refractive error. Human Molecular Genetics, 2013, 22, 2754-2764.	2.9	60
78	HOXB13 is a susceptibility gene for prostate cancer: results from the International Consortium for Prostate Cancer Genetics (ICPCG). Human Genetics, 2013, 132, 5-14.	3.8	166
79	Nine Loci for Ocular Axial Length Identified through Genome-wide Association Studies, Including Shared Loci with Refractive Error. American Journal of Human Genetics, 2013, 93, 264-277.	6.2	139
80	Matrix Metalloproteinases and Educational Attainment in Refractive Error. Ophthalmology, 2013, 120, 298-305.	5.2	38
81	Genome-wide meta-analyses of multiancestry cohorts identify multiple new susceptibility loci for refractive error and myopia. Nature Genetics, 2013, 45, 314-318.	21.4	398
82	Functional Linear Models for Association Analysis of Quantitative Traits. Genetic Epidemiology, 2013, 37, 726-742.	1.3	53
83	Linkage analysis identifies a locus for plasma von Willebrand factor undetected by genome-wide association. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 588-593.	7.1	85
84	Regional replication of association with refractive error on 15q14 and 15q25 in the Age-Related Eye Disease Study cohort. Molecular Vision, 2013, 19, 2173-86.	1.1	12
85	A founder mutation in LEPRE1 carried by 1.5% of West Africans and 0.4% of African Americans causes lethal recessive osteogenesis imperfecta. Genetics in Medicine, 2012, 14, 543-551.	2.4	49
86	Large scale international replication and meta-analysis study confirms association of the 15q14 locus with myopia. The CREAM consortium. Human Genetics, 2012, 131, 1467-1480.	3.8	67
87	Genome-Wide Association Study of Intracranial Aneurysms Confirms Role of Anril and SOX17 in Disease Risk. Stroke, 2012, 43, 2846-2852.	2.0	106
88	Analysis of Xq27-28 linkage in the international consortium for prostate cancer genetics (ICPCG) families. BMC Medical Genetics, 2012, 13, 46.	2.1	5
89	Chromosomes 4 and 8 implicated in a genome wide SNP linkage scan of 762 prostate cancer families collected by the ICPCG. Prostate, 2012, 72, 410-426.	2.3	14
90	Suggestive evidence of linkage identified at chromosomes 12q24 and 2p16 in African American prostate cancer families from louisiana. Prostate, 2012, 72, 938-947.	2.3	16

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91	A cooperative interaction between LPHN3 and 11q doubles the risk for ADHD. Molecular Psychiatry, 2012, 17, 741-747.	7.9	52
92	Identifying rare variants from exome scans: the GAW17 experience. BMC Proceedings, 2011, 5, S1.	1.6	6
93	Performance of random forests and logic regression methods using mini-exome sequence data. BMC Proceedings, 2011, 5, S104.	1.6	2
94	Comparison of results from tests of association in unrelated individuals with uncollapsed and collapsed sequence variants using tiled regression. BMC Proceedings, 2011, 5, S15.	1.6	10
95	Old lessons learned anew: family-based methods for detecting genes responsible for quantitative and qualitative traits in the Genetic Analysis Workshop 17 mini-exome sequence data. BMC Proceedings, 2011, 5, S83.	1.6	10
96	Brief review of regressionâ€based and machine learning methods in genetic epidemiology: the Genetic Analysis Workshop 17 experience. Genetic Epidemiology, 2011, 35, S5-11.	1.3	93
97	Regression and data mining methods for analyses of multiple rare variants in the Genetic Analysis Workshop 17 miniâ€exome data. Genetic Epidemiology, 2011, 35, S92-100.	1.3	5
98	Genomeâ€wide linkage scan for prostate cancer susceptibility in Finland: Evidence for a novel locus on 2q37.3 and confirmation of signal on 17q21â€q22. International Journal of Cancer, 2011, 129, 2400-2407.	5.1	18
99	Linkage Analysis of Quantitative Refraction and Refractive Errors in the Beaver Dam Eye Study. , 2011, 52, 5220.		18
100	Linkage Analysis in the Next-Generation Sequencing Era. Human Heredity, 2011, 72, 228-236.	0.8	89
101	Dissecting the genetic heterogeneity of myopia susceptibility in an Ashkenazi Jewish population using ordered subset analysis. Molecular Vision, 2011, 17, 1641-51.	1.1	3
102	Genomeâ€wide linkage analysis of 1,233 prostate cancer pedigrees from the International Consortium for prostate cancer Genetics using novel sumLINK and sumLOD analyses. Prostate, 2010, 70, 735-744.	2.3	22
103	Contribution of HPC1 (RNASEL) and HPCX variants to prostate cancer in a founder population. Prostate, 2010, 70, 1716-1727.	2.3	29
104	Genomeâ€wide Linkage Analysis of Multiple Metabolic Factors: Evidence of Genetic Heterogeneity. Obesity, 2010, 18, 146-152.	3.0	6
105	Admixture Mapping of Obesityâ€related Traits in African Americans: The Atherosclerosis Risk in Communities (ARIC) Study. Obesity, 2010, 18, 563-572.	3.0	44
106	A common variant of the latrophilin 3 gene, LPHN3, confers susceptibility to ADHD and predicts effectiveness of stimulant medication. Molecular Psychiatry, 2010, 15, 1053-1066.	7.9	245
107	Association of Matrix Metalloproteinase Gene Polymorphisms with Refractive Error in Amish and Ashkenazi Families. , 2010, 51, 4989.		34
108	A Susceptibility Locus on Chromosome 6q Greatly Increases Lung Cancer Risk among Light and Never Smokers. Cancer Research, 2010, 70, 2359-2367.	0.9	52

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109	A Second Genetic Variant on Chromosome 15q24-25.1 Associates with Lung Cancer. Cancer Research, 2010, 70, 3128-3135.	0.9	5
110	Cumulative Effect of Multiple Loci on Genetic Susceptibility to Familial Lung Cancer. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 517-524.	2.5	24
111	Ordered Subset Analysis Identifies Loci Influencing Lung Cancer Risk on Chromosomes 6q and 12q. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 3157-3166.	2.5	10
112	The Relationship Between Smoking and Replicated Sequence Variants on Chromosomes 8 and 9 With Familial Intracranial Aneurysm. Stroke, 2010, 41, 1132-1137.	2.0	47
113	Structureâ€"Function Correlations Using Scanning Laser Polarimetry in Primary Angle-Closure Glaucoma and Primary Open-Angle Glaucoma. American Journal of Ophthalmology, 2010, 149, 817-825.e1.	3.3	16
114	Genomewide Linkage Scans for Ocular Refraction and Meta-analysis of Four Populations in the Myopia Family Study. , 2009, 50, 2024.		30
115	Fine Mapping of Chromosome 6q23-25 Region in Familial Lung Cancer Families Reveals RGS17 as a Likely Candidate Gene. Clinical Cancer Research, 2009, 15, 2666-2674.	7.0	80
116	Evaluation of random forests performance for genome-wide association studies in the presence of interaction effects. BMC Proceedings, 2009, 3, S64.	1.6	21
117	Haplotype and Cell Proliferation Analyses of Candidate Lung Cancer Susceptibility Genes on Chromosome 15q24-25.1. Cancer Research, 2009, 69, 7844-7850.	0.9	49
118	Polymorphisms in the neural nicotinic acetylcholine receptor Î±4 subunit (CHRNA4) are associated with ADHD in a genetic isolate. ADHD Attention Deficit and Hyperactivity Disorders, 2009, 1, 19-24.	1.7	19
119	Genome screen in familial intracranial aneurysm. BMC Medical Genetics, 2009, 10, 3.	2.1	26
120	Genome-wide Scan of African-American and White Families for Linkage to Myopia. American Journal of Ophthalmology, 2009, 147, 512-517.e2.	3.3	30
121	Heritability Analysis of Spherical Equivalent, Axial Length, Corneal Curvature, and Anterior Chamber Depth in the Beaver Dam Eye Study. JAMA Ophthalmology, 2009, 127, 649.	2.4	91
122	EPHA2 Is Associated with Age-Related Cortical Cataract in Mice and Humans. PLoS Genetics, 2009, 5, e1000584.	3.5	140
123	Fine-mapping of candidate region in Amish and Ashkenazi families confirms linkage of refractive error to a QTL on 1p34-p36. Molecular Vision, 2009, 15, 1398-406.	1.1	10
124	Examining the effect of linkage disequilibrium between markers on the Type I error rate and power of nonparametric multipoint linkage analysis of twoâ€generation and multigenerational pedigrees in the presence of missing genotype data. Genetic Epidemiology, 2008, 32, 41-51.	1.3	7
125	Genomewide scan of ocular refraction in Africanâ€American families shows significant linkage to chromosome 7p15. Genetic Epidemiology, 2008, 32, 454-463.	1.3	51
126	ARLTS1 germline variants and the risk for breast, prostate, and colorectal cancer. European Journal of Human Genetics, 2008, 16, 983-991.	2.8	12

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127	Establishing an adjusted p-value threshold to control the family-wide type 1 error in genome wide association studies. BMC Genomics, 2008, 9, 516.	2.8	287
128	Genome Screen to Detect Linkage to Intracranial Aneurysm Susceptibility Genes. Stroke, 2008, 39, 1434-1440.	2.0	47
129	Recruitment strategies and comparison of prostate cancer-specific clinical data on African-American and Caucasian males with and without family history. Prostate Cancer and Prostatic Diseases, 2008, 11, 274-279.	3.9	5
130	Familial Aggregation of Common Sequence Variants on 15q24-25.1 in Lung Cancer. Journal of the National Cancer Institute, 2008, 100, 1326-1330.	6.3	141
131	Identification of a Novel Tumor Suppressor Gene p34 on Human Chromosome 6q25.1. Cancer Research, 2007, 67, 93-99.	0.9	37
132	Familial aggregation of myopia in the Tehran eye study: estimation of the sibling and parent offspring recurrence risk ratios. British Journal of Ophthalmology, 2007, 91, 1440-1444.	3.9	18
133	The GLC1H Glaucoma Locus May Reflect Glaucoma With Elevated Intraocular Pressure. JAMA Ophthalmology, 2007, 125, 1716.	2.4	3
134	Compelling evidence for a prostate cancer gene at 22q12.3 by the International Consortium for Prostate Cancer Genetics. Human Molecular Genetics, 2007, 16, 1271-1278.	2.9	31
135	EGFR-T790M Is a Rare Lung Cancer Susceptibility Allele with Enhanced Kinase Activity. Cancer Research, 2007, 67, 4665-4670.	0.9	92
136	Confirmation of Linkage to Ocular Refraction on Chromosome 22q and Identification of a Novel Linkage Region on 1q. JAMA Ophthalmology, 2007, 125, 80.	2.4	47
137	Attention-Deficit/Hyperactivity Disorder and Comorbid Disruptive Behavior Disorders: Evidence of Pleiotropy and New Susceptibility Loci. Biological Psychiatry, 2007, 61, 1329-1339.	1.3	69
138	Identification of Novel Genetic Loci for Intraocular Pressure. JAMA Ophthalmology, 2007, 125, 74.	2.4	47
139	Heritability and Familial Aggregation of Refractive Error in the Old Order Amish. , 2007, 48, 4002.		47
140	Genome-wide linkage of 77 families from the African American Hereditary Prostate Cancer Study (AAHPC). Prostate, 2007, 67, 22-31.	2.3	23
141	Replicating genotypeâ€“phenotype associations. Nature, 2007, 447, 655-660.	27.8	1,509
142	KLF6 IVS1 -27G>A Variant and the Risk of Prostate Cancer in Finland. European Urology, 2007, 52, 1076-1081.	1.9	14
143	Segregation analysis of 1,546 prostate cancer families in Finland shows recessive inheritance. Human Genetics, 2007, 121, 257-267.	3.8	26
144	The Value of Molecular Haplotypes in a Family-Based Linkage Study. American Journal of Human Genetics, 2006, 79, 458-468.	6.2	10

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145	Pooled genome linkage scan of aggressive prostate cancer: results from the International Consortium for Prostate Cancer Genetics. Human Genetics, 2006, 120, 471-485.	3.8	57
146	Segregation analysis of urothelial cell carcinoma. European Journal of Cancer, 2006, 42, 1428-1433.	2.8	30
147	Allele frequency misspecification: effect on power and Type I error of model-dependent linkage analysis of quantitative traits under random ascertainment. BMC Genetics, 2006, 7, 21.	2.7	11
148	A genetic model for determining MSH2 and MLH1 carrier probabilities based on family history and tumor microsatellite instability. Clinical Genetics, 2006, 69, 254-262.	2.0	20
149	Population Isolates in South Tyrol and Their Value for Genetic Dissection of Complex Diseases. Annals of Human Genetics, 2006, 70, 812-821.	0.8	15
150	Genes, environment and the value of prospective cohort studies. Nature Reviews Genetics, 2006, 7, 812-820.	16.3	276
151	Covariate-based linkage analysis: application of a propensity score as the single covariate consistently improves power to detect linkage. European Journal of Human Genetics, 2006, 14, 1018-1026.	2.8	9
152	Two-locus genome-wide linkage scan for prostate cancer susceptibility genes with an interaction effect. Human Genetics, 2006, 118, 716-724.	3.8	16
153	Genomewide scan in Ashkenazi Jewish families demonstrates evidence of linkage of ocular refraction to a QTL on chromosome 1p36. Human Genetics, 2006, 119, 389-399.	3.8	84
154	Identification of genetic loci for basal cell nevus syndrome and inflammatory bowel disease in a single large pedigree. Human Genetics, 2006, 120, 31-41.	3.8	4
155	Profiling Genetic Variation along the Androgen Biosynthesis and Metabolism Pathways Implicates Several Single Nucleotide Polymorphisms and Their Combinations as Prostate Cancer Risk Factors. Cancer Research, 2006, 66, 743-747.	0.9	54
156	A common nonsense mutation in EphB2 is associated with prostate cancer risk in African American men with a positive family history. Journal of Medical Genetics, 2006, 43, 507-511.	3.2	65
157	Genome-wide scan of additional Jewish families confirms linkage of a myopia susceptibility locus to chromosome 22q12. Molecular Vision, 2006, 12, 1499-505.	1.1	17
158	Parametric versus nonparametric and two-point versus multipoint: controversies in gene mapping. , 2005, , .		0
159	Genetic Analysis Workshop 14: Introduction to Workshop Summaries. Genetic Epidemiology, 2005, 29, S1-S6.	1.3	5
160	Haplotypes and haplotype-tagging single-nucleotide polymorphism: Presentation Group 8 of Genetic Analysis Workshop 14. Genetic Epidemiology, 2005, 29, S59-S71.	1.3	11
161	Hereditary prostate cancer in Finland: fine-mapping validates 3p26 as a major predisposition locus. Human Genetics, 2005, 116, 43-50.	3.8	25
162	A major locus for hereditary prostate cancer in Finland: localization by linkage disequilibrium of a haplotype in the HPCX region. Human Genetics, 2005, 117, 307-316.	3.8	30

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163	Genetic Analysis Workshop 14: microsatellite and single-nucleotide polymorphism marker loci for genome-wide scans. BMC Genetics, 2005, 6, S1.	2.7	10
164	Investigation of altering single-nucleotide polymorphism density on the power to detect trait loci and frequency of false positive in nonparametric linkage analyses of qualitative traits. BMC Genetics, 2005, 6, S20.	2.7	5
165	Application of the propensity score in a covariate-based linkage analysis of the Collaborative Study on the Genetics of Alcoholism. BMC Genetics, 2005, 6, S33.	2.7	6
166	Identification of tag single-nucleotide polymorphisms in regions with varying linkage disequilibrium. BMC Genetics, 2005, 6, S73.	2.7	7
167	Haplotypic structure of the X chromosome in the COGA population sample and the quality of its reconstruction by extant software packages. BMC Genetics, 2005, 6, S77.	2.7	8
168	A Genetic Contribution to Intraocular Pressure: The Beaver Dam Eye Study. , 2005, 46, 555.		50
169	Support for Polygenic Influences on Ocular Refractive Error. , 2005, 46, 442.		51
170	EPIDEMIOLOGY: Enhanced: DNA Identifications After the 9/11 World Trade Center Attack. Science, 2005, 310, 1122-1123.	12.6	147
171	Polygenic Effects and Cigarette Smoking Account for a Portion of the Familial Aggregation of Nuclear Sclerosis. American Journal of Epidemiology, 2005, 161, 707-713.	3.4	17
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