Daniel J Schaid

List of Publications by Year
in descending order

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214 papers	16,228 citations	22153 59 h-index	18647 119 g-index
220 all docs	220 docs citations	220 times ranked	21322 citing authors

#	Article	IF	Citations
1	Penalized mediation models for multivariate data. Genetic Epidemiology, 2022, 46, 32-50.	1.3	2
2	Mumps virus-specific immune response outcomes and sex-based differences in a cohort of healthy adolescents. Clinical Immunology, 2022, 234, 108912.	3.2	14
3	Uterine fibroid polygenic risk score (PRS) associates and predicts risk for uterine fibroid. Human Genetics, 2022, 141, 1739-1748.	3.8	4
4	A microRNA Transcriptome-wide Association Study of Prostate Cancer Risk. Frontiers in Genetics, 2022, 13, 836841.	2.3	3
5	Polygenic risk for prostate cancer: Decreasing relative risk with age but little impact on absolute risk. American Journal of Human Genetics, 2022, 109, 900-908.	6.2	10
6	A rare variant analysis framework using public genotype summary counts to prioritize disease-predisposition genes. Nature Communications, 2022, 13, 2592.	12.8	6
7	Identification of Two Genetic Loci Associated with Leukopenia after Chemotherapy in Patients with Breast Cancer. Clinical Cancer Research, 2022, 28, 3342-3355.	7.0	3
8	Antimullerian Hormone as a Serum Biomarker for Risk of Chemotherapy-Induced Amenorrhea. Journal of the National Cancer Institute, 2021, 113, 1105-1108.	6.3	5
9	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
10	Impact of Personalized Genetic Breast Cancer Risk Estimation With Polygenic Risk Scores on Preventive Endocrine Therapy Intention and Uptake. Cancer Prevention Research, 2021, 14, 175-184.	1.5	11
11	Trans-ancestry genome-wide association meta-analysis of prostate cancer identifies new susceptibility loci and informs genetic risk prediction. Nature Genetics, 2021, 53, 65-75.	21.4	264
12	Genetic Variations and Health-Related Quality of Life (HRQOL): A Genome-Wide Study Approach. Cancers, 2021, 13, 716.	3.7	3
13	Response to Li and Hopper. American Journal of Human Genetics, 2021, 108, 527-529.	6.2	5
14	Genetic Predictors of Chemotherapy-Induced Peripheral Neuropathy from Paclitaxel, Carboplatin and Oxaliplatin: NCCTG/Alliance N08C1, N08CA and N08CB Study. Cancers, 2021, 13, 1084.	3.7	11
15	Transcriptional signatures associated with rubella virusâ€specific humoral immunity after a third dose of MMR vaccine in women of childbearing age. European Journal of Immunology, 2021, 51, 1824-1838.	2.9	3
16	A unified framework identifies new links between plasma lipids and diseases from electronic medical records across large-scale cohorts. Nature Genetics, 2021, 53, 972-981.	21.4	17
17	2dFDR: a new approach to confounder adjustment substantially increases detection power in omics association studies. Genome Biology, 2021, 22, 208.	8.8	2
18	Rare Germline Variants in ATM Predispose to Prostate Cancer: A PRACTICAL Consortium Study. European Urology Oncology, 2021, 4, 570-579.	5.4	38

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19	Polymorphisms in STING Affect Human Innate Immune Responses to Poxviruses. Frontiers in Immunology, 2020, 11, 567348.	4.8	15
20	Genome-wide Modeling of Polygenic Risk Score in Colorectal Cancer Risk. American Journal of Human Genetics, 2020, 107, 432-444.	6.2	124
21	Penalized variance components for association of multiple genes with traits. Genetic Epidemiology, 2020, 44, 665-675.	1.3	1
22	Penalized models for analysis of multiple mediators. Genetic Epidemiology, 2020, 44, 408-424.	1.3	9
23	The effect of sample size on polygenic hazard models for prostate cancer. European Journal of Human Genetics, 2020, 28, 1467-1475.	2.8	14
24	Predictive Utility of Polygenic Risk Scores for Coronary Heart Disease in Three Major Racial and Ethnic Groups. American Journal of Human Genetics, 2020, 106, 707-716.	6.2	93
25	Minority-centric meta-analyses of blood lipid levels identify novel loci in the Population Architecture using Genomics and Epidemiology (PAGE) study. PLoS Genetics, 2020, 16, e1008684.	3.5	17
26	A Genetic Risk Score to Personalize Prostate Cancer Screening, Applied to Population Data. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 1731-1738.	2.5	27
27	Title is missing!. , 2020, 16, e1008684.		0
28	Title is missing!. , 2020, 16, e1008684.		0
29	Title is missing!. , 2020, 16, e1008684.		0
30	Title is missing!. , 2020, 16, e1008684.		0
31	Title is missing!. , 2020, 16, e1008684.		0
32	Title is missing!. , 2020, 16, e1008684.		0
33	Genetic predictors of chemotherapy-related amenorrhea inÂwomen with breast cancer. Fertility and Sterility, 2019, 112, 731-739.e1.	1.0	10
34	Genome analysis and pleiotropy assessment using causal networks with loss of function mutation and metabolomics. BMC Genomics, 2019, 20, 395.	2.8	19
35	Targeted Sequencing Study to Uncover Shared Genetic Susceptibility Between Peripheral Artery Disease and Coronary Heart Diseaseâ€"Brief Report. Arteriosclerosis, Thrombosis, and Vascular Biology, 2019, 39, 1227-1233.	2.4	12
36	Atlas-CNV: a validated approach to call single-exon CNVs in the eMERGESeq gene panel. Genetics in Medicine, 2019, 21, 2135-2144.	2.4	19

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37	An expanded variant list and assembly annotation identifies multiple novel coding and noncoding genes for prostate cancer risk using a normal prostate tissue eQTL data set. PLoS ONE, 2019, 14, e0214588.	2.5	5
38	Familial recurrence risk with varying amount of family history. Genetic Epidemiology, 2019, 43, 440-448.	1.3	0
39	A phenome-wide association study to discover pleiotropic effects of PCSK9, APOB, and LDLR. Npj Genomic Medicine, 2019, 4, 3.	3.8	26
40	Current perspectives in assessing humoral immunity after measles vaccination. Expert Review of Vaccines, 2019, 18, 75-87.	4.4	39
41	A review of kernel methods for genetic association studies. Genetic Epidemiology, 2019, 43, 122-136.	1.3	24
42	Detecting potential pleiotropy across cardiovascular and neurological diseases using univariate, bivariate, and multivariate methods on 43,870 individuals from the eMERGE network. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2019, 24, 272-283.	0.7	6
43	Germline variation at 8q24 and prostate cancer risk in men of European ancestry. Nature Communications, 2018, 9, 4616.	12.8	43
44	A smallâ€sample kernel association test for correlated data with application to microbiome association studies. Genetic Epidemiology, 2018, 42, 772-782.	1.3	30
45	From genome-wide associations to candidate causal variants by statistical fine-mapping. Nature Reviews Genetics, 2018, 19, 491-504.	16.3	611
46	Association analyses of more than 140,000 men identify 63 new prostate cancer susceptibility loci. Nature Genetics, 2018, 50, 928-936.	21.4	652
47	Fine-mapping of prostate cancer susceptibility loci in a large meta-analysis identifies candidate causal variants. Nature Communications, 2018, 9, 2256.	12.8	88
48	Detecting potential pleiotropy across cardiovascular and neurological diseases using univariate, bivariate, and multivariate methods on 43,870 individuals from the eMERGE network. , 2018, , .		6
49	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
50	Heritability of vaccine-induced measles neutralizing antibody titers. Vaccine, 2017, 35, 1390-1394.	3.8	13
51	Genome-wide associations of CD46 and IFI44L genetic variants with neutralizing antibody response to measles vaccine. Human Genetics, 2017, 136, 421-435.	3.8	59
52	Immunoglobulin GM and KM genes and measles vaccine-induced humoral immunity. Vaccine, 2017, 35, 5444-5447.	3.8	1
53	Mapping Complex Traits in a Diversity Outbred F1 Mouse Population Identifies Germline Modifiers of Metastasis in Human Prostate Cancer. Cell Systems, 2017, 4, 31-45.e6.	6.2	44
54	Breast cancer chemoprevention pharmacogenomics: Deep sequencing and functional genomics of the ZNF423 and CTSO genes. Npj Breast Cancer, 2017, 3, 30.	5.2	18

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55	A Dab2Ip Genotype: Sex Interaction is Associated with Abdominal Aortic Aneurysm Expansion. Journal of Investigative Medicine, 2017, 65, 1077-1082.	1.6	7
56	Fast and robust adjustment of cell mixtures in epigenome-wide association studies with SmartSVA. BMC Genomics, 2017, 18, 413.	2.8	54
57	Multivariate generalized linear model for genetic pleiotropy. Biostatistics, 2017, 20, 111-128.	1.5	9
58	Whole exome sequencing in 75 high-risk families with validation and replication in independent case-control studies identifies TANGO2, OR5H14, and CHAD as new prostate cancer susceptibility genes. Oncotarget, 2017, 8, 1495-1507.	1.8	11
59	A large population-based association study between HLA and KIR genotypes and measles vaccine antibody responses. PLoS ONE, 2017, 12, e0171261.	2.5	23
60	Network-directed cis-mediator analysis of normal prostate tissue expression profiles reveals downstream regulatory associations of prostate cancer susceptibility loci. Oncotarget, 2017, 8, 85896-85908.	1.8	2
61	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
62	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	3.2	174
63	Incorporating Functional Annotations for Fine-Mapping Causal Variants in a Bayesian Framework Using Summary Statistics. Genetics, 2016, 204, 933-958.	2.9	51
64	Statistical Methods for Testing Genetic Pleiotropy. Genetics, 2016, 204, 483-497.	2.9	50
65	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
66	Small Sample Kernel Association Tests for Human Genetic and Microbiome Association Studies. Genetic Epidemiology, 2016, 40, 5-19.	1.3	45
67	The Role of Cardiovascular Risk Factors and Stroke in Familial Alzheimer Disease. JAMA Neurology, 2016, 73, 1231.	9.0	49
68	Genetically defined race, but not sex, is associated with higher humoral and cellular immune responses to measles vaccination. Vaccine, 2016, 34, 4913-4919.	3.8	24
69	Genome-wide association of familial prostate cancer cases identifies evidence for a rare segregating haplotype at 8q24.21. Human Genetics, 2016, 135, 923-938.	3.8	37
70	Incorporating a Genetic Risk Score Into Coronary Heart Disease Risk Estimates. Circulation, 2016, 133, 1181-1188.	1.6	198
71	Genetic variants associated with susceptibility to psychosis inÂlate-onset Alzheimerâ€™s disease families. Neurobiology of Aging, 2015, 36, 3116.e9-3116.e16.	3.1	14
72	Comprehensively Evaluating cis -Regulatory Variation in the Human Prostate Transcriptome by Using Gene-Level Allele-Specific Expression. American Journal of Human Genetics, 2015, 96, 869-882.	6.2	37

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73	A Large Multiethnic Genome-Wide Association Study of Prostate Cancer Identifies Novel Risk Variants and Substantial Ethnic Differences. Cancer Discovery, 2015, 5, 878-891.	9.4	111
74	Kernel methods for large-scale genomic data analysis. Briefings in Bioinformatics, 2015, 16, 183-192.	6.5	33
75	Associations of prostate cancer risk variants with disease aggressiveness: results of the NCI-SPORE Genetics Working Group analysis of 18,343 cases. Human Genetics, 2015, 134, 439-450.	3.8	45
76	Fine Mapping Causal Variants with an Approximate Bayesian Method Using Marginal Test Statistics. Genetics, 2015, 200, 719-736.	2.9	202
77	A Powerful Nonparametric Statistical Framework for Family-Based Association Analyses. Genetics, 2015, 200, 69-78.	2.9	2
78	Lessons learned in the analysis of high-dimensional data in vaccinomics. Vaccine, 2015, 33, 5262-5270.	3.8	24
79	Multiple novel prostate cancer susceptibility signals identified by fine-mapping of known risk loci among Europeans. Human Molecular Genetics, 2015, 24, 5589-5602.	2.9	67
80	Case-only exome sequencing and complex disease susceptibility gene discovery: study design considerations. Journal of Medical Genetics, 2015, 52, 10-16.	3.2	23
81	PedBLIMP: Extending Linear Predictors to Impute Genotypes in Pedigrees. Genetic Epidemiology, 2014, 38, 531-541.	1.3	5
82	Regularized Rare Variant Enrichment Analysis for Caseâ€Control Exome Sequencing Data. Genetic Epidemiology, 2014, 38, 104-113.	1.3	7
83	Age-Specific Incidence Rates for Dementia and Alzheimer Disease in NIA-LOAD/NCRAD and EFIGA Families. JAMA Neurology, 2014, 71, 315.	9.0	48
84	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
85	Prospective Validation of HLA-DRB1*07:01 Allele Carriage As a Predictive Risk Factor for Lapatinib-Induced Liver Injury. Journal of Clinical Oncology, 2014, 32, 2296-2303.	1.6	69
86	A meta-analysis of 87,040 individuals identifies 23 new susceptibility loci for prostate cancer. Nature Genetics, 2014, 46, 1103-1109.	21.4	408
87	The kinship2 R Package for Pedigree Data. Human Heredity, 2014, 78, 91-93.	0.8	151
88	A WeightedU-Statistic for Genetic Association Analyses of Sequencing Data. Genetic Epidemiology, 2014, 38, 699-708.	1.3	10
89	Detecting genomic clustering of risk variants from sequence data: cases versus controls. Human Genetics, 2013, 132, 1301-1309.	3.8	14
90	A Kernel Regression Approach to Geneâ€Gene Interaction Detection for Caseâ€Control Studies. Genetic Epidemiology, 2013, 37, 695-703.	1.3	20

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91	Multiple Genetic Variant Association Testing by Collapsing and Kernel Methods With Pedigree or Population Structured Data. Genetic Epidemiology, 2013, 37, 409-418.	1.3	87
92	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
93	Twoâ€Phase Designs to Followâ€Up Genomeâ€Wide Association Signals With DNA Resequencing Studies. Genetic Epidemiology, 2013, 37, 229-238.	1.3	11
94	Regression Modeling of Allele Frequencies and Testing Hardy Weinberg Equilibrium. Human Heredity, 2012, 74, 71-82.	0.8	5
95	Gemcitabine metabolic pathway genetic polymorphisms and response in patients with non-small cell lung cancer. Pharmacogenetics and Genomics, 2012, 22, 105-116.	1.5	33
96	Analysis of Xq27-28 linkage in the international consortium for prostate cancer genetics (ICPCG) families. BMC Medical Genetics, 2012, 13, 46.	2.1	5
97	Genetic association with overall survival of taxane-treated lung cancer patients - a genome-wide association study in human lymphoblastoid cell lines followed by a clinical association study. BMC Cancer, 2012, 12, 422.	2.6	40
98	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
99	Power of Singleâ€vs. Multiâ€Marker Tests of Association. Genetic Epidemiology, 2012, 36, 480-487.	1.3	12
100	Validation of prostate cancer risk-related loci identified from genome-wide association studies using family-based association analysis: evidence from the International Consortium for Prostate Cancer Genetics (ICPCG). Human Genetics, 2012, 131, 1095-1103.	3.8	21
101	Using the gene ontology to scan multilevel gene sets for associations in genome wide association studies. Genetic Epidemiology, 2012, 36, 3-16.	1.3	32
102	Genetic Variation Predicting Cisplatin Cytotoxicity Associated with Overall Survival in Lung Cancer Patients Receiving Platinum-Based Chemotherapy. Clinical Cancer Research, 2011, 17, 5801-5811.	7.0	87
103	Two-stage caseâ€“control designs for rare genetic variants. Human Genetics, 2010, 127, 659-668.	3.8	5
104	Estimation of genotype relative risks from pedigree data by retrospective likelihoods. Genetic Epidemiology, 2010, 34, 287-298.	1.3	13
105	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
106	Genome-wide linkage analyses of hereditary prostate cancer families with colon cancer provide further evidence for a susceptibility locus on 15q11â€“q14. European Journal of Human Genetics, 2010, 18, 1141-1147.	2.8	7
107	Glutathione Pathway Genetic Polymorphisms and Lung Cancer Survival After Platinum-Based Chemotherapy. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 811-821.	2.5	42
108	Genome-Wide Associations and Functional Genomic Studies of Musculoskeletal Adverse Events in Women Receiving Aromatase Inhibitors. Journal of Clinical Oncology, 2010, 28, 4674-4682.	1.6	196

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109	Family-based association analysis of 42 hereditary prostate cancer families identifies the Apolipoprotein L3 region on chromosome 22q12 as a risk locus. Human Molecular Genetics, 2010, 19, 3852-3862.	2.9	21
110	Genomic Similarity and Kernel Methods II: Methods for Genomic Information. Human Heredity, 2010, 70, 132-140.	0.8	67
111	Genomic Similarity and Kernel Methods I: Advancements by Building on Mathematical and Statistical Foundations. Human Heredity, 2010, 70, 109-131.	0.8	80
112	Human Glucocorticoid Receptor Î± Gene (NR3C1) Pharmacogenomics: Gene Resequencing and Functional Genomics. Journal of Clinical Endocrinology and Metabolism, 2009, 94, 3072-3084.	3.6	32
113	Dense genome-wide SNP linkage scan in 301 hereditary prostate cancer families identifies multiple regions with suggestive evidence for linkage. Human Molecular Genetics, 2009, 18, 1839-1848.	2.9	25
114	Genotype determination for polymorphisms in linkage disequilibrium. BMC Bioinformatics, 2009, 10, 63.	2.6	7
115	Power comparisons between similarityâ€based multilocus association methods, logistic regression, and score tests for haplotypes. Genetic Epidemiology, 2009, 33, 183-197.	1.3	30
116	Catechol O-methyltransferase pharmacogenomics: human liver genotypeâ€“phenotype correlation and proximal promoter studies. Pharmacogenetics and Genomics, 2009, 19, 577-587.	1.5	11
117	Fine mapping of familial prostate cancer families narrows the interval for a susceptibility locus on chromosome 22q12.3 to 1.36ÂMb. Human Genetics, 2008, 123, 65-75.	3.8	9
118	Testing whether genetic variation explains correlation of quantitative measures of gene expression, and application to genetic network analysis. Statistics in Medicine, 2008, 27, 3847-3867.	1.6	1
119	Searching for epistasis and linkage heterogeneity by correlations of pedigreeâ€specific linkage scores. Genetic Epidemiology, 2008, 32, 464-475.	1.3	0
120	Human betaine-homocysteine methyltransferase (BHMT) and BHMT2: Common gene sequence variation and functional characterization. Molecular Genetics and Metabolism, 2008, 94, 326-335.	1.1	59
121	GlutathioneS-Transferase P1: Gene Sequence Variation and Functional Genomic Studies. Cancer Research, 2008, 68, 4791-4801.	0.9	74
122	Human phenylethanolamineN-methyltransferase genetic polymorphisms and exercise-induced epinephrine release. Physiological Genomics, 2008, 33, 323-332.	2.3	11
123	Polymorphisms in Mitochondrial Genes and Prostate Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2008, 17, 3558-3566.	2.5	48
124	Testing Genetic Linkage with Relative Pairs and Covariates by Quasi-Likelihood Score Statistics. Human Heredity, 2007, 64, 220-233.	0.8	5
125	Robust Multipoint Simultaneous Identical-by-Descent Mapping for Two Linked Loci. Human Heredity, 2007, 63, 35-46.	0.8	4
126	Two Common Chromosome 8q24 Variants Are Associated with Increased Risk for Prostate Cancer. Cancer Research, 2007, 67, 2944-2950.	0.9	100

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127	A Comprehensive Examination of CYP19 Variation and Breast Density. Cancer Epidemiology Biomarkers and Prevention, 2007, 16, 623-625.	2.5	12
128	Strong Evidence of a Genetic Determinant for Mammographic Density, a Major Risk Factor for Breast Cancer. Cancer Research, 2007, 67, 8412-8418.	0.9	69
129	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
130	Human Hydroxysteroid Sulfotransferase SULT2B1 Pharmacogenomics: Gene Sequence Variation and Functional Genomics. Journal of Pharmacology and Experimental Therapeutics, 2007, 322, 529-540.	2.5	29
131	Confirmation of a Positive Association between Prostate Cancer Risk and a Locus at Chromosome 8q24. Cancer Epidemiology Biomarkers and Prevention, 2007, 16, 809-814.	2.5	88
132	Application of sequential haplotype scan methods to case-control data. BMC Proceedings, 2007, 1, S21.	1.6	2
133	GlutathioneS-Transferase T1 and M1: Gene Sequence Variation and Functional Genomics. Clinical Cancer Research, 2007, 13, 7207-7216.	7.0	69
134	Evaluation of Genetic Variations in the Androgen and Estrogen Metabolic Pathways as Risk Factors for Sporadic and Familial Prostate Cancer. Cancer Epidemiology Biomarkers and Prevention, 2007, 16, 969-978.	2.5	101
135	One- and two-locus models for mapping rheumatoid arthritis-susceptibility genes on chromosome 6. BMC Proceedings, 2007, 1, S103.	1.6	1
136	Affected relative pairs and simultaneous search for twoâ€locus linkage in the presence of epistasis. Genetic Epidemiology, 2007, 31, 431-449.	1.3	3
137	Sequential haplotype scan methods for association analysis. Genetic Epidemiology, 2007, 31, 553-564.	1.3	26
138	Linkage analyses of rheumatoid arthritis and related quantitative phenotypes: the GAW15 experience. Genetic Epidemiology, 2007, 31, S86-S95.	1.3	1
139	A comprehensive examination of CYP19 variation and risk of breast cancer using two haplotype-tagging approaches. Breast Cancer Research and Treatment, 2007, 102, 237-247.	2.5	31
140	Genome-wide linkage scan of prostate cancer Gleason score and confirmation of chromosome 19q. Human Genetics, 2007, 121, 729-735.	3.8	23
141	Methods to impute missing genotypes for population data. Human Genetics, 2007, 122, 495-504.	3.8	47
142	Exact Tests of Hardy-Weinberg Equilibrium and Homogeneity of Disequilibrium across Strata. American Journal of Human Genetics, 2006, 79, 1071-1080.	6.2	61
143	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
144	Human methylenetetrahydrofolate reductase pharmacogenomics: gene resequencing and functional genomics. Pharmacogenetics and Genomics, 2006, 16, 265-277.	1.5	58

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145	Prostate cancer and genetic susceptibility: A genome scan incorporating disease aggressiveness. Prostate, 2006, 66, 317-325.	2.3	45
146	Power and Sample Size for Testing Associations of Haplotypes with Complex Traits. Annals of Human Genetics, 2006, 70, 116-130.	0.8	29
147	Human Arsenic Methyltransferase (AS3MT) Pharmacogenetics. Journal of Biological Chemistry, 2006, 281, 7364-7373.	3.4	119
148	Role of the Nijmegen Breakage Syndrome 1 Gene in Familial and Sporadic Prostate Cancer. Cancer Epidemiology Biomarkers and Prevention, 2006, 15, 935-938.	2.5	49
149	Behavioral Risk Exposure and Host Genetics of Susceptibility to HIVâ€1 Infection. Journal of Infectious Diseases, 2006, 193, 16-26.	4.0	49
150	Methylenetetrahydrofolate Reductase Haplotype Tag Single-Nucleotide Polymorphisms and Risk of Breast Cancer. Cancer Epidemiology Biomarkers and Prevention, 2006, 15, 2322-2324.	2.5	10
151	GLUTATHIONE S-TRANSFERASE OMEGA 1 AND OMEGA 2 PHARMACOGENOMICS. Drug Metabolism and Disposition, 2006, 34, 1237-1246.	3.3	77
152	Truncating Variants in p53AIP1 Disrupting DNA Damageâ€“Induced Apoptosis Are Associated with Prostate Cancer Risk. Cancer Research, 2006, 66, 10302-10307.	0.9	9
153	Description of the international consortium for prostate cancer genetics, and failure to replicate linkage of hereditary prostate cancer to 20q13. Prostate, 2005, 63, 276-290.	2.3	33
154	Human Aromatase: Gene Resequencing and Functional Genomics. Cancer Research, 2005, 65, 11071-11082.	0.9	185
155	A Germline DNA Polymorphism Enhances Alternative Splicing of the KLF6 Tumor Suppressor Gene and Is Associated with Increased Prostate Cancer Risk. Cancer Research, 2005, 65, 1213-1222.	0.9	202
156	Robust Multipoint Identical-by-Descent Mapping for Affected Relative Pairs. American Journal of Human Genetics, 2005, 76, 128-138.	6.2	14
157	Nonparametric Tests of Association of Multiple Genes with Human Disease. American Journal of Human Genetics, 2005, 76, 780-793.	6.2	117
158	A Combined Genomewide Linkage Scan of 1,233 Families for Prostate Cancerâ€“Susceptibility Genes Conducted by the International Consortium for Prostate Cancer Genetics. American Journal of Human Genetics, 2005, 77, 219-229.	6.2	138
159	Linkage Disequilibrium Testing When Linkage Phase Is Unknown. Genetics, 2004, 166, 505-512.	2.9	64
160	The complex genetic epidemiology of prostate cancer. Human Molecular Genetics, 2004, 13, 103R-121.	2.9	298
161	Evaluating associations of haplotypes with traits. Genetic Epidemiology, 2004, 27, 348-364.	1.3	293
162	Genetic epidemiology and haplotypes. Genetic Epidemiology, 2004, 27, 317-320.	1.3	27

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163	Comparison of Microsatellites Versus Single-Nucleotide Polymorphisms in a Genome Linkage Screen for Prostate Cancerâ€“Susceptibility Loci. American Journal of Human Genetics, 2004, 75, 948-965.	6.2	129
164	Where are the prostate cancer genes?â€”A summary of eight genome wide searches. Prostate, 2003, 57, 261-269.	2.3	104
165	Genome linkage screen for prostate cancer susceptibility loci: Results from the Mayo Clinic familial prostate cancer study. Prostate, 2003, 57, 335-346.	2.3	48
166	No association of germline alteration of MSR1 with prostate cancer risk. Nature Genetics, 2003, 35, 128-129.	21.4	60
167	Regression Models for Linkage: Issues of Traits, Covariates, Heterogeneity, and Interaction. Human Heredity, 2003, 55, 86-96.	0.8	42
168	Caution on Pedigree Haplotype Inference with Software That Assumes Linkage Equilibrium. American Journal of Human Genetics, 2002, 71, 992-995.	6.2	88
169	Score Tests for Association between Traits and Haplotypes when Linkage Phase Is Ambiguous. American Journal of Human Genetics, 2002, 70, 425-434.	6.2	1,656
170	Analysis of the RNASEL Gene in Familial and Sporadic Prostate Cancer. American Journal of Human Genetics, 2002, 71, 116-123.	6.2	105
171	Genetic epidemiology and microarrays. Genetic Epidemiology, 2002, 23, 1-3.	1.3	8
172	Relative efficiency of ambiguous vs. directly measured haplotype frequencies. Genetic Epidemiology, 2002, 23, 426-443.	1.3	59
173	?Reply to Fallin et al.?. Genetic Epidemiology, 2002, 23, 462-464.	1.3	4
174	Lack of Referral Bias in Genetic Studies of Prostate Cancer. Epidemiology, 2002, 13, 612-613.	2.7	1
175	Analysis of the Prostate Cancerâ€“Susceptibility Locus HPC20 in 172 Families Affected by Prostate Cancer. American Journal of Human Genetics, 2001, 68, 795-801.	6.2	51
176	Regression Models for Linkage Heterogeneity Applied to Familial Prostate Cancer. American Journal of Human Genetics, 2001, 68, 1189-1196.	6.2	27
177	Identification of an association between HLA class II alleles and low antibody levels after measles immunization. Vaccine, 2001, 20, 430-438.	3.8	95
178	Hysterectomy, menopause, and estrogen use preceding Parkinson's disease: An exploratory caseâ€control study. Movement Disorders, 2001, 16, 830-837.	3.9	194
179	Heritability of plasma amyloid ? in typical late-onset Alzheimer?s disease pedigrees. Genetic Epidemiology, 2001, 21, 19-30.	1.3	48
180	Major Histocompatibility Complex Class Iâ€“Recognizing Receptors Are Disease Risk Genes in Rheumatoid Arthritis. Journal of Experimental Medicine, 2001, 193, 1159-1168.	8.5	316

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