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	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
2	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
3	Association analyses of more than 140,000 men identify 63 new prostate cancer susceptibility loci. Nature Genetics, 2018, 50, 928-936.	21.4	652
4	Evidence for a prostate cancer susceptibility locus on the X chromosome.. Nature Genetics, 1998, 20, 175-179.	21.4	641
5	From genome-wide associations to candidate causal variants by statistical fine-mapping. Nature Reviews Genetics, 2018, 19, 491-504.	16.3	611
6	A meta-analysis of 87,040 individuals identifies 23 new susceptibility loci for prostate cancer. Nature Genetics, 2014, 46, 1103-1109.	21.4	408
7	Anxiety disorders and depressive disorders preceding Parkinson's disease: A case-control study. Movement Disorders, 2000, 15, 669-677.	3.9	407
8	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
9	The complex genetic epidemiology of prostate cancer. Human Molecular Genetics, 2004, 13, 103R-121.	2.9	298
10	Evaluating associations of haplotypes with traits. Genetic Epidemiology, 2004, 27, 348-364.	1.3	293
11	General score tests for associations of genetic markers with disease using cases and their parents. Genetic Epidemiology, 1996, 13, 423-449.	1.3	286
12	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
13	Evidence for a Prostate Cancerâ€“Susceptibility Locus on Chromosome 20. American Journal of Human Genetics, 2000, 67, 82-91.	6.2	213
14	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
15	Fine Mapping Causal Variants with an Approximate Bayesian Method Using Marginal Test Statistics. Genetics, 2015, 200, 719-736.	2.9	202
16	A controlled trial of cyproheptadine in cancer patients with anorexia and/or cachexia. Cancer, 1990, 65, 2657-2662.	4.1	200
17	Evidence for Autosomal Dominant Inheritance of Prostate Cancer. American Journal of Human Genetics, 1998, 62, 1425-1438.	6.2	198
18	Incorporating a Genetic Risk Score Into Coronary Heart Disease Risk Estimates. Circulation, 2016, 133, 1181-1188.	1.6	198

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19	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
20	Hysterectomy, menopause, and estrogen use preceding Parkinson's disease: An exploratory caseâ€control study. Movement Disorders, 2001, 16, 830-837.	3.9	194
21	Human Aromatase: Gene Resequencing and Functional Genomics. Cancer Research, 2005, 65, 11071-11082.	0.9	185
22	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	3.2	174
23	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
24	The kinship2 R Package for Pedigree Data. Human Heredity, 2014, 78, 91-93.	0.8	151
25	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
26	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
27	Genome-wide Modeling of Polygenic Risk Score in Colorectal Cancer Risk. American Journal of Human Genetics, 2020, 107, 432-444.	6.2	124
28	Human Arsenic Methyltransferase (AS3MT) Pharmacogenetics. Journal of Biological Chemistry, 2006, 281, 7364-7373.	3.4	119
29	Nonparametric Tests of Association of Multiple Genes with Human Disease. American Journal of Human Genetics, 2005, 76, 780-793.	6.2	117
30	Transmission Disequilibrium, Family Controls, and Great Expectations. American Journal of Human Genetics, 1998, 63, 935-941.	6.2	115
31	Use of Parents, Sibs, and Unrelated Controls for Detection of Associations between Genetic Markers and Disease. American Journal of Human Genetics, 1998, 63, 1492-1506.	6.2	115
32	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
33	Complete responses and long-term survivals after systemic chemotherapy for patients with advanced malignant melanoma. Cancer, 1989, 63, 224-227.	4.1	106
34	Analysis of the RNASEL Gene in Familial and Sporadic Prostate Cancer. American Journal of Human Genetics, 2002, 71, 116-123.	6.2	105
35	Where are the prostate cancer genes?â€”A summary of eight genome wide searches. Prostate, 2003, 57, 261-269.	2.3	104
36	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

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37	Two Common Chromosome 8q24 Variants Are Associated with Increased Risk for Prostate Cancer. Cancer Research, 2007, 67, 2944-2950.	0.9	100
38	Combination hormonal therapy with tamoxifen plus fluoxymesteroneversus tamoxifen alone in postmenopausal women with metastatic breast cancer. An updated analysis. Cancer, 1991, 67, 886-891.	4.1	95
39	Identification of an association between HLA class II alleles and low antibody levels after measles immunization. Vaccine, 2001, 20, 430-438.	3.8	95
40	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
41	Likelihoods andTDT for the case-parents design. Genetic Epidemiology, 1999, 16, 250-260.	1.3	91
42	Linkage Analyses at the Chromosome 1 Loci 1q24-25 (HPC1), 1q42.2-43 (PCAP), and 1p36 (CAPB) in Families with Hereditary Prostate Cancer. American Journal of Human Genetics, 2000, 66, 539-546.	6.2	91
43	Base of tongue carcinoma: Patterns of failure and predictors of recurrence after surgery alone. Head and Neck, 1993, 15, 300-307.	2.0	88
44	Caution on Pedigree Haplotype Inference with Software That Assumes Linkage Equilibrium. American Journal of Human Genetics, 2002, 71, 992-995.	6.2	88
45	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
46	Fine-mapping of prostate cancer susceptibility loci in a large meta-analysis identifies candidate causal variants. Nature Communications, 2018, 9, 2256.	12.8	88
47	Patterns of tumor relapse following mastectomy and adjuvant systemic therapy in patients with axillary lymph node-positive breast cancer. Impact of clinical, histopathologic, and flow cytometric factors. Cancer, 1993, 72, 1247-1260.	4.1	87
48	Case-parents design for gene-environment interaction. Genetic Epidemiology, 1999, 16, 261-273.	1.3	87
49	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
50	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
51	Genomic Similarity and Kernel Methods I: Advancements by Building on Mathematical and Statistical Foundations. Human Heredity, 2010, 70, 109-131.	0.8	80
52	GLUTATHIONE S-TRANSFERASE OMEGA 1 AND OMEGA 2 PHARMACOGENOMICS. Drug Metabolism and Disposition, 2006, 34, 1237-1246.	3.3	77
53	GlutathioneS-Transferase P1: Gene Sequence Variation and Functional Genomic Studies. Cancer Research, 2008, 68, 4791-4801.	0.9	74
54	Microsatellite instability and hMLH1/hMSH2 expression in young endometrial carcinoma patients: Associations with family history and histopathology. , 2000, 86, 60-66.		73

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55	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
56	GlutathioneS-Transferase T1 and M1: Gene Sequence Variation and Functional Genomics. Clinical Cancer Research, 2007, 13, 7207-7216.	7.0	69
57	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
58	Genomic Similarity and Kernel Methods II: Methods for Genomic Information. Human Heredity, 2010, 70, 132-140.	0.8	67
59	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
60	Linkage Disequilibrium Testing When Linkage Phase Is Unknown. Genetics, 2004, 166, 505-512.	2.9	64
61	Exact Tests of Hardy-Weinberg Equilibrium and Homogeneity of Disequilibrium across Strata. American Journal of Human Genetics, 2006, 79, 1071-1080.	6.2	61
62	No association of germline alteration of MSR1 with prostate cancer risk. Nature Genetics, 2003, 35, 128-129.	21.4	60
63	Relative efficiency of ambiguous vs. directly measured haplotype frequencies. Genetic Epidemiology, 2002, 23, 426-443.	1.3	59
64	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
65	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
66	Human methylenetetrahydrofolate reductase pharmacogenomics: gene resequencing and functional genomics. Pharmacogenetics and Genomics, 2006, 16, 265-277.	1.5	58
67	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
68	Fast and robust adjustment of cell mixtures in epigenome-wide association studies with SmartSVA. BMC Genomics, 2017, 18, 413.	2.8	54
69	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
70	Incorporating Functional Annotations for Fine-Mapping Causal Variants in a Bayesian Framework Using Summary Statistics. Genetics, 2016, 204, 933-958.	2.9	51
71	Statistical Methods for Testing Genetic Pleiotropy. Genetics, 2016, 204, 483-497.	2.9	50
72	A prospective trial of midwest breast cancer patients: Ap53 gene mutation is the most important predictor of adverse outcome. International Journal of Cancer, 2000, 89, 32-38.	5.1	49

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73	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
74	Behavioral Risk Exposure and Host Genetics of Susceptibility to HIVâ€1 Infection. Journal of Infectious Diseases, 2006, 193, 16-26.	4.0	49
75	The Role of Cardiovascular Risk Factors and Stroke in Familial Alzheimer Disease. JAMA Neurology, 2016, 73, 1231.	9.0	49
76	Heritability of plasma amyloid ? in typical late-onset Alzheimer?s disease pedigrees. Genetic Epidemiology, 2001, 21, 19-30.	1.3	48
77	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
78	Polymorphisms in Mitochondrial Genes and Prostate Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2008, 17, 3558-3566.	2.5	48
79	Age-Specific Incidence Rates for Dementia and Alzheimer Disease in NIA-LOAD/NCRAD and EFIGA Families. JAMA Neurology, 2014, 71, 315.	9.0	48
80	Methods to impute missing genotypes for population data. Human Genetics, 2007, 122, 495-504.	3.8	47
81	Prostate cancer and genetic susceptibility: A genome scan incorporating disease aggressiveness. Prostate, 2006, 66, 317-325.	2.3	45
82	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
83	Small Sample Kernel Association Tests for Human Genetic and Microbiome Association Studies. Genetic Epidemiology, 2016, 40, 5-19.	1.3	45
84	Case-control study of debrisoquine 4-hydroxylase, n-acetyltransferase 2, and apolipoprotein e gene polymorphisms in Parkinson's disease. Movement Disorders, 2000, 15, 714-719.	3.9	44
85	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
86	Germline variation at 8q24 and prostate cancer risk in men of European ancestry. Nature Communications, 2018, 9, 4616.	12.8	43
87	Regression Models for Linkage: Issues of Traits, Covariates, Heterogeneity, and Interaction. Human Heredity, 2003, 55, 86-96.	0.8	42
88	Glutathione Pathway Genetic Polymorphisms and Lung Cancer Survival After Platinum-Based Chemotherapy. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 811-821.	2.5	42
89	Sibâ€pair linkage tests for disease susceptibility loci: Common tests vs. the asymptotically most powerful test. Genetic Epidemiology, 1990, 7, 359-370.	1.3	40
90	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

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91	Current perspectives in assessing humoral immunity after measles vaccination. Expert Review of Vaccines, 2019, 18, 75-87.	4.4	39
92	A double-blind trial of tamoxifen plus prednisolone versus tamoxifen plus placebo in postmenopausal women with metastatic breast cancer. A collaborative trial of the north central cancer treatment group and mayo clinic. Cancer, 1991, 68, 34-39.	4.1	38
93	Rare Germline Variants in ATM Predispose to Prostate Cancer: A PRACTICAL Consortium Study. European Urology Oncology, 2021, 4, 570-579.	5.4	38
94	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
95	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
96	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
97	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
98	Kernel methods for large-scale genomic data analysis. Briefings in Bioinformatics, 2015, 16, 183-192.	6.5	33
99	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
100	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
101	Genotype relative-risks and association tests for nuclear families with missing parental data. Genetic Epidemiology, 1997, 14, 1113-1118.	1.3	31
102	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
103	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
104	Power comparisons between similarityâ€based multilocus association methods, logistic regression, and score tests for haplotypes. Genetic Epidemiology, 2009, 33, 183-197.	1.3	30
105	A smallâ€sample kernel association test for correlated data with application to microbiome association studies. Genetic Epidemiology, 2018, 42, 772-782.	1.3	30
106	Power and Sample Size for Testing Associations of Haplotypes with Complex Traits. Annals of Human Genetics, 2006, 70, 116-130.	0.8	29
107	Human Hydroxysteroid Sulfotransferase SULT2B1 Pharmacogenomics: Gene Sequence Variation and Functional Genomics. Journal of Pharmacology and Experimental Therapeutics, 2007, 322, 529-540.	2.5	29
108	The genomic organization of human dystrobrevin. Neurogenetics, 1997, 1, 37-42.	1.4	28

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109	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
110	Regression Models for Linkage Heterogeneity Applied to Familial Prostate Cancer. American Journal of Human Genetics, 2001, 68, 1189-1196.	6.2	27
111	Genetic epidemiology and haplotypes. Genetic Epidemiology, 2004, 27, 317-320.	1.3	27
112	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
113	Sequential haplotype scan methods for association analysis. Genetic Epidemiology, 2007, 31, 553-564.	1.3	26
114	A phenome-wide association study to discover pleiotropic effects of PCSK9, APOB, and LDLR. Npj Genomic Medicine, 2019, 4, 3.	3.8	26
115	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
116	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
117	Lessons learned in the analysis of high-dimensional data in vaccinomics. Vaccine, 2015, 33, 5262-5270.	3.8	24
118	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
119	A review of kernel methods for genetic association studies. Genetic Epidemiology, 2019, 43, 122-136.	1.3	24
120	Genome-wide linkage scan of prostate cancer Gleason score and confirmation of chromosome 19q. Human Genetics, 2007, 121, 729-735.	3.8	23
121	Case-only exome sequencing and complex disease susceptibility gene discovery: study design considerations. Journal of Medical Genetics, 2015, 52, 10-16.	3.2	23
122	A large population-based association study between HLA and KIR genotypes and measles vaccine antibody responses. PLoS ONE, 2017, 12, e0171261.	2.5	23
123	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
124	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
125	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
126	Discovery of Cancer Susceptibility Genes: Study Designs, Analytic Approaches, and Trends in Technology. Journal of the National Cancer Institute Monographs, 1999, 1999, 1-16.	2.1	20

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127	A Kernel Regression Approach to Geneâ€Gene Interaction Detection for Caseâ€Control Studies. Genetic Epidemiology, 2013, 37, 695-703.	1.3	20
128	Genome analysis and pleiotropy assessment using causal networks with loss of function mutation and metabolomics. BMC Genomics, 2019, 20, 395.	2.8	19
129	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
130	A phase I-II trial of the combination of recombinant leukocyte a interferon and recombinant human interferon-Î³ in patients with metastatic malignant melanoma. Cancer, 1988, 62, 2472-2474.	4.1	18
131	Breast cancer chemoprevention pharmacogenomics: Deep sequencing and functional genomics of the ZNF423 and CTSO genes. Npj Breast Cancer, 2017, 3, 30.	5.2	18
132	Quantitative trait transmission disequilibrium test: Allowance for missing parents. Genetic Epidemiology, 1999, 17, S307-12.	1.3	17
133	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
134	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
135	Relative-risk regression models using cases and their parents. Genetic Epidemiology, 1995, 12, 813-818.	1.3	16
136	Polymorphisms in STING Affect Human Innate Immune Responses to Poxviruses. Frontiers in Immunology, 2020, 11, 567348.	4.8	15
137	Linkage of nonspecific X-linked mental retardation to Xq21.31. American Journal of Medical Genetics Part A, 1992, 43, 436-442.	2.4	14
138	Robust Multipoint Identical-by-Descent Mapping for Affected Relative Pairs. American Journal of Human Genetics, 2005, 76, 128-138.	6.2	14
139	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
140	Detecting genomic clustering of risk variants from sequence data: cases versus controls. Human Genetics, 2013, 132, 1301-1309.	3.8	14
141	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
142	The effect of sample size on polygenic hazard models for prostate cancer. European Journal of Human Genetics, 2020, 28, 1467-1475.	2.8	14
143	Mumps virus-specific immune response outcomes and sex-based differences in a cohort of healthy adolescents. Clinical Immunology, 2022, 234, 108912.	3.2	14
144	Estimation of genotype relative risks from pedigree data by retrospective likelihoods. Genetic Epidemiology, 2010, 34, 287-298.	1.3	13

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145	Heritability of vaccine-induced measles neutralizing antibody titers. Vaccine, 2017, 35, 1390-1394.	3.8	13
146	A Comprehensive Examination of CYP19 Variation and Breast Density. Cancer Epidemiology Biomarkers and Prevention, 2007, 16, 623-625.	2.5	12
147	Power of Singleâ€•vs. Multiâ€Marker Tests of Association. Genetic Epidemiology, 2012, 36, 480-487.	1.3	12
148	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
149	Genetic heterogeneity in hereditary sensory and autonomic neuropathies: The need for improved ascertainment. Muscle and Nerve, 2000, 23, 1453-1455.	2.2	11
150	Human phenylethanolamineN-methyltransferase genetic polymorphisms and exercise-induced epinephrine release. Physiological Genomics, 2008, 33, 323-332.	2.3	11
151	Catechol O-methyltransferase pharmacogenomics: human liver genotypeâ€“phenotype correlation and proximal promoter studies. Pharmacogenetics and Genomics, 2009, 19, 577-587.	1.5	11
152	Twoâ€Phase Designs to Followâ€Up Genomeâ€Wide Association Signals With DNA Resequencing Studies. Genetic Epidemiology, 2013, 37, 229-238.	1.3	11
153	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
154	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
155	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
156	Randomized clinical trial of CFP versus CMFP in women with metastatic breast cancer. Cancer, 1989, 63, 1931-1937.	4.1	10
157	Methylenetetrahydrofolate Reductase Haplotype Tag Single-Nucleotide Polymorphisms and Risk of Breast Cancer. Cancer Epidemiology Biomarkers and Prevention, 2006, 15, 2322-2324.	2.5	10
158	A WeightedU-Statistic for Genetic Association Analyses of Sequencing Data. Genetic Epidemiology, 2014, 38, 699-708.	1.3	10
159	Genetic predictors of chemotherapy-related amenorrhea inÂwomen with breast cancer. Fertility and Sterility, 2019, 112, 731-739.e1.	1.0	10
160	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
161	Truncating Variants in p53AIP1 Disrupting DNA Damageâ€“Induced Apoptosis Are Associated with Prostate Cancer Risk. Cancer Research, 2006, 66, 10302-10307.	0.9	9
162	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

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163	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
164	Multivariate generalized linear model for genetic pleiotropy. Biostatistics, 2017, 20, 111-128.	1.5	9
165	Penalized models for analysis of multiple mediators. Genetic Epidemiology, 2020, 44, 408-424.	1.3	9
166	Genetic epidemiology and microarrays. Genetic Epidemiology, 2002, 23, 1-3.	1.3	8
167	Genotype determination for polymorphisms in linkage disequilibrium. BMC Bioinformatics, 2009, 10, 63.	2.6	7
168	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
169	Regularized Rare Variant Enrichment Analysis for Caseâ€Control Exome Sequencing Data. Genetic Epidemiology, 2014, 38, 104-113.	1.3	7
170	A Dab2Ip Genotype: Sex Interaction is Associated with Abdominal Aortic Aneurysm Expansion. Journal of Investigative Medicine, 2017, 65, 1077-1082.	1.6	7
171	Robust transmission regression models for linkage and association. Genetic Epidemiology, 2000, 19, S78-S84.	1.3	6
172	Model-free sib-pair linkage analysis: Combining full-sib and half-sib pairs. Genetic Epidemiology, 2000, 19, 30-51.	1.3	6
173	Detecting potential pleiotropy across cardiovascular and neurological diseases using univariate, bivariate, and multivariate methods on 43,870 individuals from the eMERGE network. , 2018, , .		6
174	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
175	A rare variant analysis framework using public genotype summary counts to prioritize disease-predisposition genes. Nature Communications, 2022, 13, 2592.	12.8	6
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177	Two-stage caseâ€“control designs for rare genetic variants. Human Genetics, 2010, 127, 659-668.	3.8	5
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