Nilanjan Chatterjee

List of Publications by Year
in descending order

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156	15,590	39113 52	23173 116
papers	citations	h-index	g-index

182	182	182	26600
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Logistic regression analysis of twoâ€phase studies using generalized method of moments. Biometrics, 2023, 79, 241-252.	0.8	1
2	Prospective evaluation of a breast-cancer risk model integrating classical risk factors and polygenic risk in 15 cohorts from six countries. International Journal of Epidemiology, 2022, 50, 1897-1911.	0.9	43
3	Reproductive factors and gall-bladder cancer, and the effect of common genetic variants on these associations: a caseâ€“control study in India. International Journal of Epidemiology, 2022, 51, 789-798.	0.9	2
4	Utilizing patient information to identify subtype heterogeneity of cancer driver genes. Statistical Methods in Medical Research, 2022, 31, 510-519.	0.7	2
5	Genomeâ€wide association studies of 27 accelerometryâ€derived physical activity measurements identified novel loci and genetic mechanisms. Genetic Epidemiology, 2022, 46, 122-138.	0.6	7
6	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. Breast Cancer Research, 2022, 24, 2.	2.2	15
7	Trans-ethnic genome-wide association study of blood metabolites in the Chronic Renal Insufficiency Cohort (CRIC) study. Kidney International, 2022, 101, 814-823.	2.6	8
8	Rare Genetic Variants Associated With Myocardial Fibrosis: Multi-Ethnic Study of Atherosclerosis. Frontiers in Cardiovascular Medicine, 2022, 9, 804788.	1.1	6
9	Polygenic scores in biomedical research. Nature Reviews Genetics, 2022, 23, 524-532.	7.7	69
10	MO517: A Polygenic Risk Score for Reduced EGFR is Associated With Adverse Events in a Chronic Kidney Disease Cohort â€"the German Chronic Kidney Disease Study. Nephrology Dialysis Transplantation, 2022, 37, .	0.4	2
11	Plasma proteome analyses in individuals of European and African ancestry identify cis-pQTLs and models for proteome-wide association studies. Nature Genetics, 2022, 54, 593-602.	9.4	98
12	Meta-analysis under imbalance in measurement of confounders in cohort studies using only summary-level data. BMC Medical Research Methodology, 2022, 22, 143.	1.4	2
13	Distinct Reproductive Risk Profiles for Intrinsic-Like Breast Cancer Subtypes: Pooled Analysis of Population-Based Studies. Journal of the National Cancer Institute, 2022, 114, 1706-1719.	3.0	14
14	Breast Cancer Risk in Women from Ghana Carrying Rare Germline Pathogenic Mutations. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 1593-1601.	1.1	3
15	Quantifying the Predictive Performance of Objectively Measured Physical Activity on Mortality in the UK Biobank. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2021, 76, 1486-1494.	1.7	37
16	A Penalized Regression Framework for Building Polygenic Risk Models Based on Summary Statistics From Genome-Wide Association Studies and Incorporating External Information. Journal of the American Statistical Association, 2021, 116, 133-143.	1.8	13
17	Combined Associations of a Polygenic Risk Score and Classical Risk Factors With Breast Cancer Risk. Journal of the National Cancer Institute, 2021, 113, 329-337.	3.0	45
18	Linear and Nonlinear Mendelian Randomization Analyses of the Association Between Diastolic Blood Pressure and Cardiovascular Events. Circulation, 2021, 143, 895-906.	1.6	73

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19	Individual and community-level risk for COVID-19 mortality in the United States. Nature Medicine, 2021, 27, 264-269.	15.2	70
20	A Likelihood Ratio Test for Gene-Environment Interaction Based on the Trend Effect of Genotype Under an Additive Risk Model Using the Gene-Environment Independence Assumption. American Journal of Epidemiology, 2021, 190, 129-141.	1.6	2
21	A comprehensive evaluation of methods for Mendelian randomization using realistic simulations and an analysis of 38 biomarkers for risk of type 2 diabetes. International Journal of Epidemiology, 2021, 50, 1335-1349.	0.9	15
22	Assessing Lung Cancer Absolute Risk Trajectory Based on a Polygenic Risk Model. Cancer Research, 2021, 81, 1607-1615.	0.4	50
23	Sub-multiplicative interaction between polygenic risk score and household coal use in relation to lung adenocarcinoma among never-smoking women in Asia. Environment International, 2021, 147, 105975.	4.8	12
24	Comparative validation of the BOADICEA and Tyrer-Cuzick breast cancer risk models incorporating classical risk factors and polygenic risk in a population-based prospective cohort of women of European ancestry. Breast Cancer Research, 2021, 23, 22.	2.2	49
25	Smoking Modifies Pancreatic Cancer Risk Loci on 2q21.3. Cancer Research, 2021, 81, 3134-3143.	0.4	8
26	Improving reporting standards for polygenic scores in risk prediction studies. Nature, 2021, 591, 211-219.	13.7	265
27	Provider and Patient Characteristics of Medicare Beneficiaries Who Are High-Risk for COVID-19 Mortality. Journal of General Internal Medicine, 2021, 36, 2189-2190.	1.3	0
28	A Robust Test for Additive Gene-Environment Interaction Under the Trend Effect of Genotype Using an Empirical Bayes-Type Shrinkage Estimator. American Journal of Epidemiology, 2021, 190, 1948-1960.	1.6	0
29	Large-scale plasma proteomic analysis identifies proteins and pathways associated with dementia risk. Nature Aging, 2021, 1, 473-489.	5.3	69
30	Proteins Associated with Risk of Kidney Function Decline in the General Population. Journal of the American Society of Nephrology: JASN, 2021, 32, 2291-2302.	3.0	23
31	Polygenic Risk Scores for Kidney Function and Their Associations with Circulating Proteome, and Incident Kidney Diseases. Journal of the American Society of Nephrology: JASN, 2021, 32, 3161-3173.	3.0	27
32	Abstract 11049: Rare Genetic Variants in Individuals with Low ASCVD Risk and Hard Chd or High Coronary Artery Disease: Multi-Ethnic Study of Atherosclerosis. Circulation, 2021, 144, .	1.6	0
33	Interaction of Cigarette Smoking and Polygenic Risk Score on Reduced Lung Function. JAMA Network Open, 2021, 4, e2139525.	2.8	22
34	Predicting Lung Cancer Occurrence in Never-Smoking Females in Asia: TNSF-SQ, a Prediction Model. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 452-459.	1.1	31
35	Comparative Validation of Breast Cancer Risk Prediction Models and Projections for Future Risk Stratification. Journal of the National Cancer Institute, 2020, 112, 278-285.	3.0	61
36	Effect of non-normality and low count variants on cross-phenotype association tests in GWAS. European Journal of Human Genetics, 2020, 28, 300-312.	1.4	12

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37	Tuberculosis infection and lung adenocarcinoma: Mendelian randomization and pathway analysis of genome-wide association study data from never-smoking Asian women. Genomics, 2020, 112, 1223-1232.	1.3	15
38	A Transcriptome-Wide Association Study Identifies Novel Candidate Susceptibility Genes for Pancreatic Cancer. Journal of the National Cancer Institute, 2020, 112, 1003-1012.	3.0	59
39	Diesel exhaust and bladder cancer risk by pathologic stage and grade subtypes. Environment International, 2020, 135, 105346.	4.8	25
40	Combined Utility of 25 Disease and Risk Factor Polygenic Risk Scores for Stratifying Risk of All-Cause Mortality. American Journal of Human Genetics, 2020, 107, 418-431.	2.6	55
41	Isolated Diastolic Hypertension in the UK Biobank. Hypertension, 2020, 76, 699-706.	1.3	32
42	Cancer therapy shapes the fitness landscape of clonal hematopoiesis. Nature Genetics, 2020, 52, 1219-1226.	9.4	367
43	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. Nature Genetics, 2020, 52, 572-581.	9.4	265
44	A bidirectional Mendelian randomization study supports causal effects of kidney function onÂbloodÂpressure. Kidney International, 2020, 98, 708-716.	2.6	70
45	Genome-Wide Geneâ€“Diabetes and Geneâ€“Obesity Interaction Scan in 8,255 Cases and 11,900 Controls from PanScan and PanC4 Consortia. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 1784-1791.	1.1	5
46	A mixed-model approach for powerful testing of genetic associations with cancer risk incorporating tumor characteristics. Biostatistics, 2020, 22, 772-788.	0.9	11
47	Mustard oil consumption, cooking method, diet and gallbladder cancer risk in highâ€•and lowâ€risk regions of India. International Journal of Cancer, 2020, 147, 1621-1628.	2.3	15
48	Assessment of polygenic architecture and risk prediction based on common variants across fourteen cancers. Nature Communications, 2020, 11, 3353.	5.8	75
49	iCARE: An R package to build, validate and apply absolute risk models. PLoS ONE, 2020, 15, e0228198.	1.1	61
50	Genome-wide association and multi-omic analyses reveal ACTN2 as a gene linked to heart failure. Nature Communications, 2020, 11, 1122.	5.8	57
51	Evaluating Discrimination of a Lung Cancer Risk Prediction Model Using Partial Risk-Score in a Two-Phase Study. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 1196-1203.	1.1	3
52	A powerful method for pleiotropic analysis under composite null hypothesis identifies novel shared loci between Type 2 Diabetes and Prostate Cancer. PLoS Genetics, 2020, 16, e1009218.	1.5	49
53	Case-Only Analysis of Gene-Environment Interactions Using Polygenic Risk Scores. American Journal of Epidemiology, 2019, 188, 2013-2020.	1.6	15
54	Generalized meta-analysis for multiple regression models across studies with disparate covariate information. Biometrika, 2019, 106, 567-585.	1.3	35

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55	Joint association of mammographic density adjusted for age and body mass index and polygenic risk score with breast cancer risk. Breast Cancer Research, 2019, 21, 68.	2.2	31
56	Mendelian randomization analysis using mixture models for robust and efficient estimation of causal effects. Nature Communications, 2019, 10, 1941.	5.8	118
57	Assessment of breast cancer risk: which tools to use?. Lancet Oncology, The, 2019, 20, 463-464.	5.1	9
58	Retinal transcriptome and eQTL analyses identify genes associated with age-related macular degeneration. Nature Genetics, 2019, 51, 606-610.	9.4	201
59	BOADICEA: a comprehensive breast cancer risk prediction model incorporating genetic and nongenetic risk factors. Genetics in Medicine, 2019, 21, 1708-1718.	1.1	415
60	Genetically Determined Height and Risk of Non-hodgkin Lymphoma. Frontiers in Oncology, 2019, 9, 1539.	1.3	6
61	Etiology of hormone receptor positive breast cancer differs by levels of histologic grade and proliferation. International Journal of Cancer, 2018, 143, 746-757.	2.3	19
62	Review of Statistical Methods for Gene-Environment Interaction Analysis. Current Epidemiology Reports, 2018, 5, 39-45.	1.1	10
63	Power Analysis for Genetic Association Test (PAGEANT) provides insights to challenges for rare variant association studies. Bioinformatics, 2018, 34, 1506-1513.	1.8	18
64	Using imputed genotype data in the joint score tests for genetic association and geneâ€“environment interactions in caseâ€control studies. Genetic Epidemiology, 2018, 42, 146-155.	0.6	8
65	Joint associations of a polygenic risk score and environmental risk factors for breast cancer in the Breast Cancer Association Consortium. International Journal of Epidemiology, 2018, 47, 526-536.	0.9	88
66	Characterising cis-regulatory variation in the transcriptome of histologically normal and tumour-derived pancreatic tissues. Gut, 2018, 67, 521-533.	6.1	26
67	Post-Selection Inference Following Aggregate Level Hypothesis Testing in Large-Scale Genomic Data. Journal of the American Statistical Association, 2018, 113, 1770-1783.	1.8	14
68	Heritability informed power optimization (HIPO) leads to enhanced detection of genetic associations across multiple traits. PLoS Genetics, 2018, 14, e1007549.	1.5	36
69	Two high-risk susceptibility loci at 6p25.3 and 14q32.13 for WaldenstrÃ¶m macroglobulinemia. Nature Communications, 2018, 9, 4182.	5.8	15
70	Estimation of complex effect-size distributions using summary-level statistics from genome-wide association studies across 32 complex traits. Nature Genetics, 2018, 50, 1318-1326.	9.4	225
71	A subregionâ€based burden test for simultaneous identification of susceptibility loci and subregions within. Genetic Epidemiology, 2018, 42, 673-683.	0.6	6
72	Association of Genome-Wide Association Study (GWAS) Identified SNPs and Risk of Breast Cancer in an Indian Population. Scientific Reports, 2017, 7, 40963.	1.6	14

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73	Common genetic variation and risk of gallbladder cancer in India: a case-control genome-wide association study. Lancet Oncology, The, 2017, 18, 535-544.	5.1	69
74	Functional characterization of a multi-cancer risk locus on chr5p15.33 reveals regulation of TERT by ZNF148. Nature Communications, 2017, 8, 15034.	5.8	40
75	Genetics of gallbladder cancer â€“ Authors' reply. Lancet Oncology, The, 2017, 18, e297.	5.1	1
76	Comparison of approaches for incorporating new information into existing risk prediction models. Statistics in Medicine, 2017, 36, 1134-1156.	0.8	11
77	Update on the State of the Science for Analytical Methods for Gene-Environment Interactions. American Journal of Epidemiology, 2017, 186, 762-770.	1.6	79
78	Opportunities and Challenges for Environmental Exposure Assessment in Population-Based Studies. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 1370-1380.	1.1	27
79	Lessons Learned From Past Gene-Environment Interaction Successes. American Journal of Epidemiology, 2017, 186, 778-786.	1.6	53
80	Integrating Clinical and Multiple Omics Data for Prognostic Assessment across Human Cancers. Scientific Reports, 2017, 7, 16954.	1.6	79
81	Increasing mapping precision of genome-wide association studies: to genotype and impute, sequence, or both?. Genome Biology, 2017, 18, 118.	3.8	16
82	Association between breast cancer genetic susceptibility variants and terminal duct lobular unit involution of the breast. International Journal of Cancer, 2017, 140, 825-832.	2.3	9
83	Current Challenges and New Opportunities for Gene-Environment Interaction Studies of Complex Diseases. American Journal of Epidemiology, 2017, 186, 753-761.	1.6	150
84	Association between GWAS-identified lung adenocarcinoma susceptibility loci andEGFRmutations in never-smoking Asian women, and comparison with findings from Western populations. Human Molecular Genetics, 2016, 26, ddw414.	1.4	50
85	Breast Cancer Risk From Modifiable and Nonmodifiable Risk Factors Among White Women in the United States. JAMA Oncology, 2016, 2, 1295.	3.4	285
86	Developing and evaluating polygenic risk prediction models for stratified disease prevention. Nature Reviews Genetics, 2016, 17, 392-406.	7.7	559
87	Telomere structure and maintenance gene variants and risk of five cancer types. International Journal of Cancer, 2016, 139, 2655-2670.	2.3	43
88	An investigation of the association of genetic susceptibility risk with somatic mutation burden in breast cancer. British Journal of Cancer, 2016, 115, 752-760.	2.9	16
89	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. Nature Communications, 2016, 7, 11843.	5.8	86
90	Meta-analysis of genome-wide association studies discovers multiple loci for chronic lymphocytic leukemia. Nature Communications, 2016, 7, 10933.	5.8	94

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91	Ages at menarche- and menopause-related genetic variants in relation to terminal duct lobular unit involution in normal breast tissue. Breast Cancer Research and Treatment, 2016, 158, 341-350.	1.1	5
92	Meta-analysis of genome-wide association studies identifies multiple lung cancer susceptibility loci in never-smoking Asian women. Human Molecular Genetics, 2016, 25, 620-629.	1.4	50
93	Identification of a novel susceptibility locus at 13q34 and refinement of the 20p12.2 region as a multi-signal locus associated with bladder cancer risk in individuals of European ancestry. Human Molecular Genetics, 2016, 25, 1203-1214.	1.4	38
94	Constrained Maximum Likelihood Estimation for Model Calibration Using Summary-Level Information From External Big Data Sources. Journal of the American Statistical Association, 2016, 111, 107-117.	1.8	87
95	MEGSA: A Powerful and Flexible Framework for Analyzing Mutual Exclusivity of Tumor Mutations. American Journal of Human Genetics, 2016, 98, 442-455.	2.6	40
96	A Powerful Procedure for Pathway-Based Meta-analysis Using Summary Statistics Identifies 43 Pathways Associated with Type II Diabetes in European Populations. PLoS Genetics, 2016, 12, e1006122.	1.5	34
97	Winner's Curse Correction and Variable Thresholding Improve Performance of Polygenic Risk Modeling Based on Genome-Wide Association Study Summary-Level Data. PLoS Genetics, 2016, 12, e1006493.	1.5	98
98	Further Confirmation of Germline Glioma Risk Variant rs78378222 inTP53and Its Implication in Tumor Tissues via Integrative Analysis of TCGA Data. Human Mutation, 2015, 36, 684-688.	1.1	19
99	<scp>G</scp>enetic variants associated with longer telomere length are associated with increased lung cancer risk among neverâ€smoking women in Asia: a report from the female lung cancer consortium in Asia. International Journal of Cancer, 2015, 137, 311-319.	2.3	72
100	An exposureâ€weighted score test for genetic associations integrating environmental risk factors. Biometrics, 2015, 71, 596-605.	0.8	11
101	Characterization of Large Structural Genetic Mosaicism in Human Autosomes. American Journal of Human Genetics, 2015, 96, 487-497.	2.6	101
102	Testing calibration of risk models at extremes of disease risk. Biostatistics, 2015, 16, 143-154.	0.9	26
103	Modification of Occupational Exposures on Bladder Cancer Risk by Common Genetic Polymorphisms. Journal of the National Cancer Institute, 2015, 107, djv223.	3.0	34
104	Imputation and subset-based association analysis across different cancer types identifies multiple independent risk loci in the TERT-CLPTM1L region on chromosome 5p15.33. Human Molecular Genetics, 2014, 23, 6616-6633.	1.4	90
105	Combined Associations of Genetic and Environmental Risk Factors: Implications for Prevention of Breast Cancer. Journal of the National Cancer Institute, 2014, 106, dju305-dju305.	3.0	101
106	Genome-wide interaction study of smoking and bladder cancer risk. Carcinogenesis, 2014, 35, 1737-1744.	1.3	50
107	The 19q12 Bladder Cancer GWAS Signal: Association with Cyclin E Function and Aggressive Disease. Cancer Research, 2014, 74, 5808-5818.	0.4	24
108	Genetic polymorphisms in the 9p21 region associated with risk of multiple cancers. Carcinogenesis, 2014, 35, 2698-2705.	1.3	67

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109	Genome-wide association study identifies multiple susceptibility loci for diffuse large B cell lymphoma. Nature Genetics, 2014, 46, 1233-1238.	9.4	147
110	Characterizing the genetic basis of methylome diversity in histologically normal human lung tissue. Nature Communications, 2014, 5, 3365.	5.8	123
111	Rare variants of large effect in BRCA2 and CHEK2 affect risk of lung cancer. Nature Genetics, 2014, 46, 736-741.	9.4	360
112	Projecting the performance of risk prediction based on polygenic analyses of genome-wide association studies. Nature Genetics, 2013, 45, 400-405.	9.4	350
113	Common Genetic Polymorphisms Modify the Effect of Smoking on Absolute Risk of Bladder Cancer. Cancer Research, 2013, 73, 2211-2220.	0.4	107
114	Using shared genetic controls in studies of gene-environment interactions. Biometrika, 2013, 100, 319-338.	1.3	4
115	Testing Gene-Environment Interaction in Large-Scale Case-Control Association Studies: Possible Choices and Comparisons. American Journal of Epidemiology, 2012, 175, 177-190.	1.6	97
116	Gene-Environment Interactions in Genome-Wide Association Studies: A Comparative Study of Tests Applied to Empirical Studies of Type 2 Diabetes. American Journal of Epidemiology, 2012, 175, 191-202.	1.6	102
117	Testing for Geneâ€“Environment and Geneâ€“Gene Interactions Under Monotonicity Constraints. Journal of the American Statistical Association, 2012, 107, 1441-1452.	1.8	6
118	Likelihood Ratio Test for Detecting Gene (G)-Environment (E) Interactions Under an Additive Risk Model Exploiting G-E Independence for Case-Control Data. American Journal of Epidemiology, 2012, 176, 1060-1067.	1.6	37
119	A Subset-Based Approach Improves Power and Interpretation for the Combined Analysis of Genetic Association Studies of Heterogeneous Traits. American Journal of Human Genetics, 2012, 90, 821-835.	2.6	242
120	Alcohol and breast cancer risk in postmenopausal women: The PLCO experience.. Journal of Clinical Oncology, 2012, 30, 1521-1521.	0.8	0
121	Improved Imputation of Common and Uncommon Single Nucleotide Polymorphisms (SNPs) with a New Reference Set. Nature Precedings, 2011, , .	0.1	0
122	Predicting the Future of Genetic Risk Prediction: Table 1.. Cancer Epidemiology Biomarkers and Prevention, 2011, 20, 3-8.	1.1	13
123	Distribution of allele frequencies and effect sizes and their interrelationships for common genetic susceptibility variants. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 18026-18031.	3.3	249
124	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	13.7	1,789
125	Estimation of effect size distribution from genome-wide association studies and implications for future discoveries. Nature Genetics, 2010, 42, 570-575.	9.4	609
126	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nature Genetics, 2010, 42, 937-948.	9.4	2,634

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127	Analysis of cohort studies with multivariate and partially observed disease classification data. Biometrika, 2010, 97, 683-698.	1.3	22
128	Inference in Semiparametric Regression Models Under Partial Questionnaire Design and Nonmonotone Missing Data. Journal of the American Statistical Association, 2010, 105, 787-797.	1.8	3
129	Multiple Independent Loci at Chromosome 15q25.1 Affect Smoking Quantity: a Meta-Analysis and Comparison with Lung Cancer and COPD. PLoS Genetics, 2010, 6, e1001053.	1.5	332
130	C-Reactive Protein and Risk of Lung Cancer. Journal of Clinical Oncology, 2010, 28, 2719-2726.	0.8	188
131	Analysis of Case-Control Association Studies: SNPs, Imputation and Haplotypes. Statistical Science, 2009, 24, 489-502.	1.6	19
132	Shrinkage Estimators for Robust and Efficient Inference in Haplotype-Based Case-Control Studies. Journal of the American Statistical Association, 2009, 104, 220-233.	1.8	56
133	A Genome-wide Association Study of Lung Cancer Identifies a Region of Chromosome 5p15 Associated with Risk for Adenocarcinoma. American Journal of Human Genetics, 2009, 85, 679-691.	2.6	489
134	The use of the risk percentile curve in the analysis of epidemiologic data. Statistics and Its Interface, 2009, 2, 123-131.	0.2	2
135	Tests for geneâ€environment interaction from caseâ€control data: a novel study of type I error, power and designs. Genetic Epidemiology, 2008, 32, 615-626.	0.6	70
136	Haplotypeâ€Based Regression Analysis and Inference of Caseâ€“Control Studies with Unphased Genotypes and Measurement Errors in Environmental Exposures. Biometrics, 2008, 64, 673-684.	0.8	21
137	Exploiting Geneâ€Environment Independence for Analysis of Caseâ€“Control Studies: An Empirical Bayesâ€Type Shrinkage Estimator to Tradeâ€Off between Bias and Efficiency. Biometrics, 2008, 64, 685-694.	0.8	169
138	Invited Commentary: Efficient Testing of Gene-Environment Interaction. American Journal of Epidemiology, 2008, 169, 231-233.	1.6	17
139	Breast Cancer Relative Hazard Estimates From Caseâ€“Control and Cohort Designs With Missing Data on Mammographic Density. Journal of the American Statistical Association, 2008, 103, 976-988.	1.8	6
140	The authors replied as follows:. Biometrics, 2007, 63, 965-966.	0.8	1
141	A semiparametric pseudo-score method for analysis of two-phase studies with continuous phase-I covariates. Lifetime Data Analysis, 2007, 13, 607-622.	0.4	5
142	Powerful Multilocus Tests of Genetic Association in the Presence of Gene-Gene and Gene-Environment Interactions. American Journal of Human Genetics, 2006, 79, 1002-1016.	2.6	139
143	Case-Control and Case-Only Designs with Genotype and Family History Data: Estimating Relative Risk, Residual Familial Aggregation, and Cumulative Risk. Biometrics, 2006, 62, 36-48.	0.8	34
144	Exploiting gene-environment independence in family-based case-control studies: Increased power for detecting associations, interactions and joint effects. Genetic Epidemiology, 2005, 28, 138-156.	0.6	48

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145	Semiparametric maximum likelihood estimation exploiting gene-environment independence in case-control studies. Biometrika, 2005, 92, 399-418.	1.3	185
146	A Two-Stage Regression Model for Epidemiological Studies With Multivariate Disease Classification Data. Journal of the American Statistical Association, 2004, 99, 127-138.	1.8	45
147	Risk of non-Hodgkin's lymphoma and family history of lymphatic, hematologic, and other cancers. Cancer Epidemiology Biomarkers and Prevention, 2004, 13, 1415-21.	1.1	70
148	Adjustment for competing risk in kin-cohort estimation. Genetic Epidemiology, 2003, 25, 303-313.	0.6	13
149	On Use of Bivariate Survival Models with Cure Fraction. Biometrics, 2003, 59, 1184-1185.	0.8	4
150	A Pseudoscore Estimator for Regression Problems With Two-Phase Sampling. Journal of the American Statistical Association, 2003, 98, 158-168.	1.8	113
151	COMMENTARY: Apportioning causes, targeting populations and predicting risks: Population attributable fractions. European Journal of Epidemiology, 2002, 18, 933-935.	2.5	2
152	Validation Studies: Bias, Efficiency, and Exposure Assessment. Epidemiology, 2002, 13, 503-506.	1.2	14
153	Association and aggregation analysis using kin-cohort designs with applications to genotype and family history data from the Washington Ashkenazi Study. Genetic Epidemiology, 2001, 21, 123-138.	0.6	27
154	Pseudo-likelihood estimates of the cumulative risk of an autosomal dominant disease from a kin-cohort study. Genetic Epidemiology, 2001, 20, 210-227.	0.6	21
155	A Marginal Likelihood Approach for Estimating Penetrance from Kinâ€Cohort Designs. Biometrics, 2001, 57, 245-252.	0.8	60
156	A Bivariate Cure-Mixture Approach for Modeling Familial Association in Diseases. Biometrics, 2001, 57, 779-786.	0.8	46