

Nilanjan Chatterjee

List of Publications by Year in descending order

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Version: 2024-02-01

156
papers

15,590
citations

34076

52
h-index

20343

116
g-index

182
all docs

182
docs citations

182
times ranked

24148
citing authors

#	ARTICLE	IF	CITATIONS
1	Logistic regression analysis of two-phase studies using generalized method of moments. <i>Biometrics</i> , 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. <i>International Journal of Epidemiology</i> , 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 case-control study in India. <i>International Journal of Epidemiology</i> , 2022, 51, 789-798.	0.9	2
4	Utilizing patient information to identify subtype heterogeneity of cancer driver genes. <i>Statistical Methods in Medical Research</i> , 2022, 31, 510-519.	0.7	2
5	Genome-wide association studies of 27 accelerometry-derived physical activity measurements identified novel loci and genetic mechanisms. <i>Genetic Epidemiology</i> , 2022, 46, 122-138.	0.6	7
6	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. <i>Breast Cancer Research</i> , 2022, 24, 2.	2.2	15
7	Trans-ethnic genome-wide association study of blood metabolites in the Chronic Renal Insufficiency Cohort (CRIC) study. <i>Kidney International</i> , 2022, 101, 814-823.	2.6	8
8	Rare Genetic Variants Associated With Myocardial Fibrosis: Multi-Ethnic Study of Atherosclerosis. <i>Frontiers in Cardiovascular Medicine</i> , 2022, 9, 804788.	1.1	6
9	Polygenic scores in biomedical research. <i>Nature Reviews Genetics</i> , 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 –the German Chronic Kidney Disease Study. <i>Nephrology Dialysis Transplantation</i> , 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. <i>Nature Genetics</i> , 2022, 54, 593-602.	9.4	98
12	Meta-analysis under imbalance in measurement of confounders in cohort studies using only summary-level data. <i>BMC Medical Research Methodology</i> , 2022, 22, 143.	1.4	2
13	Distinct Reproductive Risk Profiles for Intrinsic-Like Breast Cancer Subtypes: Pooled Analysis of Population-Based Studies. <i>Journal of the National Cancer Institute</i> , 2022, 114, 1706-1719.	3.0	14
14	Breast Cancer Risk in Women from Ghana Carrying Rare Germline Pathogenic Mutations. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2022, 31, 1593-1601.	1.1	3
15	Quantifying the Predictive Performance of Objectively Measured Physical Activity on Mortality in the UK Biobank. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 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. <i>Journal of the American Statistical Association</i> , 2021, 116, 133-143.	1.8	13
17	Combined Associations of a Polygenic Risk Score and Classical Risk Factors With Breast Cancer Risk. <i>Journal of the National Cancer Institute</i> , 2021, 113, 329-337.	3.0	45
18	Linear and Nonlinear Mendelian Randomization Analyses of the Association Between Diastolic Blood Pressure and Cardiovascular Events. <i>Circulation</i> , 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. <i>Nature Medicine</i> , 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. <i>American Journal of Epidemiology</i> , 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. <i>International Journal of Epidemiology</i> , 2021, 50, 1335-1349.	0.9	15
22	Assessing Lung Cancer Absolute Risk Trajectory Based on a Polygenic Risk Model. <i>Cancer Research</i> , 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. <i>Environment International</i> , 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. <i>Breast Cancer Research</i> , 2021, 23, 22.	2.2	49
25	Smoking Modifies Pancreatic Cancer Risk Loci on 2q21.3. <i>Cancer Research</i> , 2021, 81, 3134-3143.	0.4	8
26	Improving reporting standards for polygenic scores in risk prediction studies. <i>Nature</i> , 2021, 591, 211-219.	13.7	265
27	Provider and Patient Characteristics of Medicare Beneficiaries Who Are High-Risk for COVID-19 Mortality. <i>Journal of General Internal Medicine</i> , 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. <i>American Journal of Epidemiology</i> , 2021, 190, 1948-1960.	1.6	0
29	Large-scale plasma proteomic analysis identifies proteins and pathways associated with dementia risk. <i>Nature Aging</i> , 2021, 1, 473-489.	5.3	69
30	Proteins Associated with Risk of Kidney Function Decline in the General Population. <i>Journal of the American Society of Nephrology: JASN</i> , 2021, 32, 2291-2302.	3.0	23
31	Polygenic Risk Scores for Kidney Function and Their Associations with Circulating Proteome, and Incident Kidney Diseases. <i>Journal of the American Society of Nephrology: JASN</i> , 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. <i>Circulation</i> , 2021, 144, .	1.6	0
33	Interaction of Cigarette Smoking and Polygenic Risk Score on Reduced Lung Function. <i>JAMA Network Open</i> , 2021, 4, e2139525.	2.8	22
34	Predicting Lung Cancer Occurrence in Never-Smoking Females in Asia: TNSF-SQ, a Prediction Model. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020, 29, 452-459.	1.1	31
35	Comparative Validation of Breast Cancer Risk Prediction Models and Projections for Future Risk Stratification. <i>Journal of the National Cancer Institute</i> , 2020, 112, 278-285.	3.0	61
36	Effect of non-normality and low count variants on cross-phenotype association tests in GWAS. <i>European Journal of Human Genetics</i> , 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. <i>Genomics</i> , 2020, 112, 1223-1232.	1.3	15
38	A Transcriptome-Wide Association Study Identifies Novel Candidate Susceptibility Genes for Pancreatic Cancer. <i>Journal of the National Cancer Institute</i> , 2020, 112, 1003-1012.	3.0	59
39	Diesel exhaust and bladder cancer risk by pathologic stage and grade subtypes. <i>Environment International</i> , 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. <i>American Journal of Human Genetics</i> , 2020, 107, 418-431.	2.6	55
41	Isolated Diastolic Hypertension in the UK Biobank. <i>Hypertension</i> , 2020, 76, 699-706.	1.3	32
42	Cancer therapy shapes the fitness landscape of clonal hematopoiesis. <i>Nature Genetics</i> , 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. <i>Nature Genetics</i> , 2020, 52, 572-581.	9.4	265
44	A bidirectional Mendelian randomization study supports causal effects of kidney function on blood pressure. <i>Kidney International</i> , 2020, 98, 708-716.	2.6	70
45	Genome-Wide Gene-Diabetes and Gene-Obesity Interaction Scan in 8,255 Cases and 11,900 Controls from PanScan and PanC4 Consortia. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020, 29, 1784-1791.	1.1	5
46	A mixed-model approach for powerful testing of genetic associations with cancer risk incorporating tumor characteristics. <i>Biostatistics</i> , 2020, 22, 772-788.	0.9	11
47	Mustard oil consumption, cooking method, diet and gallbladder cancer risk in high- and low-risk regions of India. <i>International Journal of Cancer</i> , 2020, 147, 1621-1628.	2.3	15
48	Assessment of polygenic architecture and risk prediction based on common variants across fourteen cancers. <i>Nature Communications</i> , 2020, 11, 3353.	5.8	75
49	iCARE: An R package to build, validate and apply absolute risk models. <i>PLoS ONE</i> , 2020, 15, e0228198.	1.1	61
50	Genome-wide association and multi-omic analyses reveal ACTN2 as a gene linked to heart failure. <i>Nature Communications</i> , 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. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 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. <i>PLoS Genetics</i> , 2020, 16, e1009218.	1.5	49
53	Case-Only Analysis of Gene-Environment Interactions Using Polygenic Risk Scores. <i>American Journal of Epidemiology</i> , 2019, 188, 2013-2020.	1.6	15
54	Generalized meta-analysis for multiple regression models across studies with disparate covariate information. <i>Biometrika</i> , 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. <i>Breast Cancer Research</i> , 2019, 21, 68.	2.2	31
56	Mendelian randomization analysis using mixture models for robust and efficient estimation of causal effects. <i>Nature Communications</i> , 2019, 10, 1941.	5.8	118
57	Assessment of breast cancer risk: which tools to use?. <i>Lancet Oncology</i> , The, 2019, 20, 463-464.	5.1	9
58	Retinal transcriptome and eQTL analyses identify genes associated with age-related macular degeneration. <i>Nature Genetics</i> , 2019, 51, 606-610.	9.4	201
59	BOADICEA: a comprehensive breast cancer risk prediction model incorporating genetic and nongenetic risk factors. <i>Genetics in Medicine</i> , 2019, 21, 1708-1718.	1.1	415
60	Genetically Determined Height and Risk of Non-hodgkin Lymphoma. <i>Frontiers in Oncology</i> , 2019, 9, 1539.	1.3	6
61	Etiology of hormone receptor positive breast cancer differs by levels of histologic grade and proliferation. <i>International Journal of Cancer</i> , 2018, 143, 746-757.	2.3	19
62	Review of Statistical Methods for Gene-Environment Interaction Analysis. <i>Current Epidemiology Reports</i> , 2018, 5, 39-45.	1.1	10
63	Power Analysis for Genetic Association Test (PAGEANT) provides insights to challenges for rare variant association studies. <i>Bioinformatics</i> , 2018, 34, 1506-1513.	1.8	18
64	Using imputed genotype data in the joint score tests for genetic association and gene-environment interactions in case-control studies. <i>Genetic Epidemiology</i> , 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. <i>International Journal of Epidemiology</i> , 2018, 47, 526-536.	0.9	88
66	Characterising cis-regulatory variation in the transcriptome of histologically normal and tumour-derived pancreatic tissues. <i>Gut</i> , 2018, 67, 521-533.	6.1	26
67	Post-Selection Inference Following Aggregate Level Hypothesis Testing in Large-Scale Genomic Data. <i>Journal of the American Statistical Association</i> , 2018, 113, 1770-1783.	1.8	14
68	Heritability informed power optimization (HIPO) leads to enhanced detection of genetic associations across multiple traits. <i>PLoS Genetics</i> , 2018, 14, e1007549.	1.5	36
69	Two high-risk susceptibility loci at 6p25.3 and 14q32.13 for Waldenström macroglobulinemia. <i>Nature Communications</i> , 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. <i>Nature Genetics</i> , 2018, 50, 1318-1326.	9.4	225
71	A subregion-based burden test for simultaneous identification of susceptibility loci and subregions within. <i>Genetic Epidemiology</i> , 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. <i>Scientific Reports</i> , 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. <i>Lancet Oncology</i> , 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. <i>Nature Communications</i> , 2017, 8, 15034.	5.8	40
75	Genetics of gallbladder cancer – Authors' reply. <i>Lancet Oncology</i> , The, 2017, 18, e297.	5.1	1
76	Comparison of approaches for incorporating new information into existing risk prediction models. <i>Statistics in Medicine</i> , 2017, 36, 1134-1156.	0.8	11
77	Update on the State of the Science for Analytical Methods for Gene-Environment Interactions. <i>American Journal of Epidemiology</i> , 2017, 186, 762-770.	1.6	79
78	Opportunities and Challenges for Environmental Exposure Assessment in Population-Based Studies. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017, 26, 1370-1380.	1.1	27
79	Lessons Learned From Past Gene-Environment Interaction Successes. <i>American Journal of Epidemiology</i> , 2017, 186, 778-786.	1.6	53
80	Integrating Clinical and Multiple Omics Data for Prognostic Assessment across Human Cancers. <i>Scientific Reports</i> , 2017, 7, 16954.	1.6	79
81	Increasing mapping precision of genome-wide association studies: to genotype and impute, sequence, or both?. <i>Genome Biology</i> , 2017, 18, 118.	3.8	16
82	Association between breast cancer genetic susceptibility variants and terminal duct lobular unit involution of the breast. <i>International Journal of Cancer</i> , 2017, 140, 825-832.	2.3	9
83	Current Challenges and New Opportunities for Gene-Environment Interaction Studies of Complex Diseases. <i>American Journal of Epidemiology</i> , 2017, 186, 753-761.	1.6	150
84	Association between GWAS-identified lung adenocarcinoma susceptibility loci and EGFR mutations in never-smoking Asian women, and comparison with findings from Western populations. <i>Human Molecular Genetics</i> , 2016, 26, ddw414.	1.4	50
85	Breast Cancer Risk From Modifiable and Nonmodifiable Risk Factors Among White Women in the United States. <i>JAMA Oncology</i> , 2016, 2, 1295.	3.4	285
86	Developing and evaluating polygenic risk prediction models for stratified disease prevention. <i>Nature Reviews Genetics</i> , 2016, 17, 392-406.	7.7	559
87	Telomere structure and maintenance gene variants and risk of five cancer types. <i>International Journal of Cancer</i> , 2016, 139, 2655-2670.	2.3	43
88	An investigation of the association of genetic susceptibility risk with somatic mutation burden in breast cancer. <i>British Journal of Cancer</i> , 2016, 115, 752-760.	2.9	16
89	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. <i>Nature Communications</i> , 2016, 7, 11843.	5.8	86
90	Meta-analysis of genome-wide association studies discovers multiple loci for chronic lymphocytic leukemia. <i>Nature Communications</i> , 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. <i>Breast Cancer Research and Treatment</i> , 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. <i>Human Molecular Genetics</i> , 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. <i>Human Molecular Genetics</i> , 2016, 25, 1203-1214.	1.4	38
94	Constrained Maximum Likelihood Estimation for Model Calibration Using Summary-Level Information From External Big Data Sources. <i>Journal of the American Statistical Association</i> , 2016, 111, 107-117.	1.8	87
95	MEGSA: A Powerful and Flexible Framework for Analyzing Mutual Exclusivity of Tumor Mutations. <i>American Journal of Human Genetics</i> , 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. <i>PLoS Genetics</i> , 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. <i>PLoS Genetics</i> , 2016, 12, e1006493.	1.5	98
98	Further Confirmation of Germline Glioma Risk Variant rs78378222 in <i>TP53</i> and Its Implication in Tumor Tissues via Integrative Analysis of TCGA Data. <i>Human Mutation</i> , 2015, 36, 684-688.	1.1	19
99	Genetic variants associated with longer telomere length are associated with increased lung cancer risk among never-smoking women in Asia: a report from the female lung cancer consortium in Asia. <i>International Journal of Cancer</i> , 2015, 137, 311-319.	2.3	72
100	An exposure-weighted score test for genetic associations integrating environmental risk factors. <i>Biometrics</i> , 2015, 71, 596-605.	0.8	11
101	Characterization of Large Structural Genetic Mosaicism in Human Autosomes. <i>American Journal of Human Genetics</i> , 2015, 96, 487-497.	2.6	101
102	Testing calibration of risk models at extremes of disease risk. <i>Biostatistics</i> , 2015, 16, 143-154.	0.9	26
103	Modification of Occupational Exposures on Bladder Cancer Risk by Common Genetic Polymorphisms. <i>Journal of the National Cancer Institute</i> , 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. <i>Human Molecular Genetics</i> , 2014, 23, 6616-6633.	1.4	90
105	Combined Associations of Genetic and Environmental Risk Factors: Implications for Prevention of Breast Cancer. <i>Journal of the National Cancer Institute</i> , 2014, 106, dju305-dju305.	3.0	101
106	Genome-wide interaction study of smoking and bladder cancer risk. <i>Carcinogenesis</i> , 2014, 35, 1737-1744.	1.3	50
107	The 19q12 Bladder Cancer GWAS Signal: Association with Cyclin E Function and Aggressive Disease. <i>Cancer Research</i> , 2014, 74, 5808-5818.	0.4	24
108	Genetic polymorphisms in the 9p21 region associated with risk of multiple cancers. <i>Carcinogenesis</i> , 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. <i>Nature Genetics</i> , 2014, 46, 1233-1238.	9.4	147
110	Characterizing the genetic basis of methylome diversity in histologically normal human lung tissue. <i>Nature Communications</i> , 2014, 5, 3365.	5.8	123
111	Rare variants of large effect in BRCA2 and CHEK2 affect risk of lung cancer. <i>Nature Genetics</i> , 2014, 46, 736-741.	9.4	360
112	Projecting the performance of risk prediction based on polygenic analyses of genome-wide association studies. <i>Nature Genetics</i> , 2013, 45, 400-405.	9.4	350
113	Common Genetic Polymorphisms Modify the Effect of Smoking on Absolute Risk of Bladder Cancer. <i>Cancer Research</i> , 2013, 73, 2211-2220.	0.4	107
114	Using shared genetic controls in studies of gene-environment interactions. <i>Biometrika</i> , 2013, 100, 319-338.	1.3	4
115	Testing Gene-Environment Interaction in Large-Scale Case-Control Association Studies: Possible Choices and Comparisons. <i>American Journal of Epidemiology</i> , 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. <i>American Journal of Epidemiology</i> , 2012, 175, 191-202.	1.6	102
117	Testing for Gene-Environment and Gene-Gene Interactions Under Monotonicity Constraints. <i>Journal of the American Statistical Association</i> , 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. <i>American Journal of Epidemiology</i> , 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. <i>American Journal of Human Genetics</i> , 2012, 90, 821-835.	2.6	242
120	Alcohol and breast cancer risk in postmenopausal women: The PLCO experience.. <i>Journal of Clinical Oncology</i> , 2012, 30, 1521-1521.	0.8	0
121	Improved Imputation of Common and Uncommon Single Nucleotide Polymorphisms (SNPs) with a New Reference Set. <i>Nature Precedings</i> , 2011, , .	0.1	0
122	Predicting the Future of Genetic Risk Prediction: Table 1.. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2011, 20, 3-8.	1.1	13
123	Distribution of allele frequencies and effect sizes and their interrelationships for common genetic susceptibility variants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 18026-18031.	3.3	249
124	Hundreds of variants clustered in genomic loci and biological pathways affect human height. <i>Nature</i> , 2010, 467, 832-838.	13.7	1,789
125	Estimation of effect size distribution from genome-wide association studies and implications for future discoveries. <i>Nature Genetics</i> , 2010, 42, 570-575.	9.4	609
126	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. <i>Nature Genetics</i> , 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. <i>Biometrika</i> , 2010, 97, 683-698.	1.3	22
128	Inference in Semiparametric Regression Models Under Partial Questionnaire Design and Nonmonotone Missing Data. <i>Journal of the American Statistical Association</i> , 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. <i>PLoS Genetics</i> , 2010, 6, e1001053.	1.5	332
130	C-Reactive Protein and Risk of Lung Cancer. <i>Journal of Clinical Oncology</i> , 2010, 28, 2719-2726.	0.8	188
131	Analysis of Case-Control Association Studies: SNPs, Imputation and Haplotypes. <i>Statistical Science</i> , 2009, 24, 489-502.	1.6	19
132	Shrinkage Estimators for Robust and Efficient Inference in Haplotype-Based Case-Control Studies. <i>Journal of the American Statistical Association</i> , 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. <i>American Journal of Human Genetics</i> , 2009, 85, 679-691.	2.6	489
134	The use of the risk percentile curve in the analysis of epidemiologic data. <i>Statistics and Its Interface</i> , 2009, 2, 123-131.	0.2	2
135	Tests for gene-environment interaction from case-control data: a novel study of type I error, power and designs. <i>Genetic Epidemiology</i> , 2008, 32, 615-626.	0.6	70
136	Haplotype-Based Regression Analysis and Inference of Case-Control Studies with Unphased Genotypes and Measurement Errors in Environmental Exposures. <i>Biometrics</i> , 2008, 64, 673-684.	0.8	21
137	Exploiting Gene-Environment Independence for Analysis of Case-Control Studies: An Empirical Bayes-Type Shrinkage Estimator to Trade-Off between Bias and Efficiency. <i>Biometrics</i> , 2008, 64, 685-694.	0.8	169
138	Invited Commentary: Efficient Testing of Gene-Environment Interaction. <i>American Journal of Epidemiology</i> , 2008, 169, 231-233.	1.6	17
139	Breast Cancer Relative Hazard Estimates From Case-Control and Cohort Designs With Missing Data on Mammographic Density. <i>Journal of the American Statistical Association</i> , 2008, 103, 976-988.	1.8	6
140	<i>The authors replied as follows:</i>. <i>Biometrics</i> , 2007, 63, 965-966.	0.8	1
141	A semiparametric pseudo-score method for analysis of two-phase studies with continuous phase-I covariates. <i>Lifetime Data Analysis</i> , 2007, 13, 607-622.	0.4	5
142	Powerful Multilocus Tests of Genetic Association in the Presence of Gene-Gene and Gene-Environment Interactions. <i>American Journal of Human Genetics</i> , 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. <i>Biometrics</i> , 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. <i>Genetic Epidemiology</i> , 2005, 28, 138-156.	0.6	48

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