

Nilanjan Chatterjee

List of Publications by Year in descending order

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Version: 2024-02-01

156
papers

15,590
citations

34105

52
h-index

20358

116
g-index

182
all docs

182
docs citations

182
times ranked

24148
citing authors

#	ARTICLE	IF	CITATIONS
1	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. <i>Nature Genetics</i> , 2010, 42, 937-948.	21.4	2,634
2	Hundreds of variants clustered in genomic loci and biological pathways affect human height. <i>Nature</i> , 2010, 467, 832-838.	27.8	1,789
3	Estimation of effect size distribution from genome-wide association studies and implications for future discoveries. <i>Nature Genetics</i> , 2010, 42, 570-575.	21.4	609
4	Developing and evaluating polygenic risk prediction models for stratified disease prevention. <i>Nature Reviews Genetics</i> , 2016, 17, 392-406.	16.8	559
5	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.	6.2	489
6	BOADICEA: a comprehensive breast cancer risk prediction model incorporating genetic and nongenetic risk factors. <i>Genetics in Medicine</i> , 2019, 21, 1708-1718.	2.4	415
7	Cancer therapy shapes the fitness landscape of clonal hematopoiesis. <i>Nature Genetics</i> , 2020, 52, 1219-1226.	21.4	367
8	Rare variants of large effect in BRCA2 and CHEK2 affect risk of lung cancer. <i>Nature Genetics</i> , 2014, 46, 736-741.	21.4	360
9	Projecting the performance of risk prediction based on polygenic analyses of genome-wide association studies. <i>Nature Genetics</i> , 2013, 45, 400-405.	21.4	350
10	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.	3.5	332
11	Breast Cancer Risk From Modifiable and Nonmodifiable Risk Factors Among White Women in the United States. <i>JAMA Oncology</i> , 2016, 2, 1295.	7.1	285
12	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.	21.4	265
13	Improving reporting standards for polygenic scores in risk prediction studies. <i>Nature</i> , 2021, 591, 211-219.	27.8	265
14	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.	7.1	249
15	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.	6.2	242
16	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.	21.4	225
17	Retinal transcriptome and eQTL analyses identify genes associated with age-related macular degeneration. <i>Nature Genetics</i> , 2019, 51, 606-610.	21.4	201
18	C-Reactive Protein and Risk of Lung Cancer. <i>Journal of Clinical Oncology</i> , 2010, 28, 2719-2726.	1.6	188

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19	Semiparametric maximum likelihood estimation exploiting gene-environment independence in case-control studies. <i>Biometrika</i> , 2005, 92, 399-418.	2.4	185
20	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.	1.4	169
21	Current Challenges and New Opportunities for Gene-Environment Interaction Studies of Complex Diseases. <i>American Journal of Epidemiology</i> , 2017, 186, 753-761.	3.4	150
22	Genome-wide association study identifies multiple susceptibility loci for diffuse large B cell lymphoma. <i>Nature Genetics</i> , 2014, 46, 1233-1238.	21.4	147
23	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.	6.2	139
24	Characterizing the genetic basis of methylome diversity in histologically normal human lung tissue. <i>Nature Communications</i> , 2014, 5, 3365.	12.8	123
25	Mendelian randomization analysis using mixture models for robust and efficient estimation of causal effects. <i>Nature Communications</i> , 2019, 10, 1941.	12.8	118
26	A Pseudoscore Estimator for Regression Problems With Two-Phase Sampling. <i>Journal of the American Statistical Association</i> , 2003, 98, 158-168.	3.1	113
27	Common Genetic Polymorphisms Modify the Effect of Smoking on Absolute Risk of Bladder Cancer. <i>Cancer Research</i> , 2013, 73, 2211-2220.	0.9	107
28	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.	3.4	102
29	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.	6.3	101
30	Characterization of Large Structural Genetic Mosaicism in Human Autosomes. <i>American Journal of Human Genetics</i> , 2015, 96, 487-497.	6.2	101
31	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.	3.5	98
32	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.	21.4	98
33	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.	3.4	97
34	Meta-analysis of genome-wide association studies discovers multiple loci for chronic lymphocytic leukemia. <i>Nature Communications</i> , 2016, 7, 10933.	12.8	94
35	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.	2.9	90
36	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.	1.9	88

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37	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.	3.1	87
38	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. <i>Nature Communications</i> , 2016, 7, 11843.	12.8	86
39	Update on the State of the Science for Analytical Methods for Gene-Environment Interactions. <i>American Journal of Epidemiology</i> , 2017, 186, 762-770.	3.4	79
40	Integrating Clinical and Multiple Omics Data for Prognostic Assessment across Human Cancers. <i>Scientific Reports</i> , 2017, 7, 16954.	3.3	79
41	Assessment of polygenic architecture and risk prediction based on common variants across fourteen cancers. <i>Nature Communications</i> , 2020, 11, 3353.	12.8	75
42	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
43	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.	5.1	72
44	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.	1.3	70
45	A bidirectional Mendelian randomization study supports causal effects of kidney function on blood pressure. <i>Kidney International</i> , 2020, 98, 708-716.	5.2	70
46	Individual and community-level risk for COVID-19 mortality in the United States. <i>Nature Medicine</i> , 2021, 27, 264-269.	30.7	70
47	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.	2.5	70
48	Common genetic variation and risk of gallbladder cancer in India: a case-control genome-wide association study. <i>Lancet Oncology</i> , 2017, 18, 535-544.	10.7	69
49	Large-scale plasma proteomic analysis identifies proteins and pathways associated with dementia risk. <i>Nature Aging</i> , 2021, 1, 473-489.	11.6	69
50	Polygenic scores in biomedical research. <i>Nature Reviews Genetics</i> , 2022, 23, 524-532.	16.3	69
51	Genetic polymorphisms in the 9p21 region associated with risk of multiple cancers. <i>Carcinogenesis</i> , 2014, 35, 2698-2705.	2.8	67
52	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.	6.3	61
53	iCARE: An R package to build, validate and apply absolute risk models. <i>PLoS ONE</i> , 2020, 15, e0228198.	2.5	61
54	A Marginal Likelihood Approach for Estimating Penetrance from Kin-Cohort Designs. <i>Biometrics</i> , 2001, 57, 245-252.	1.4	60

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55	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.	6.3	59
56	Genome-wide association and multi-omic analyses reveal ACTN2 as a gene linked to heart failure. <i>Nature Communications</i> , 2020, 11, 1122.	12.8	57
57	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.	3.1	56
58	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.	6.2	55
59	Lessons Learned From Past Gene-Environment Interaction Successes. <i>American Journal of Epidemiology</i> , 2017, 186, 778-786.	3.4	53
60	Genome-wide interaction study of smoking and bladder cancer risk. <i>Carcinogenesis</i> , 2014, 35, 1737-1744.	2.8	50
61	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.	2.9	50
62	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.	2.9	50
63	Assessing Lung Cancer Absolute Risk Trajectory Based on a Polygenic Risk Model. <i>Cancer Research</i> , 2021, 81, 1607-1615.	0.9	50
64	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.	5.0	49
65	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.	3.5	49
66	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.	1.3	48
67	A Bivariate Cure-Mixture Approach for Modeling Familial Association in Diseases. <i>Biometrics</i> , 2001, 57, 779-786.	1.4	46
68	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.	3.1	45
69	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.	6.3	45
70	Telomere structure and maintenance gene variants and risk of five cancer types. <i>International Journal of Cancer</i> , 2016, 139, 2655-2670.	5.1	43
71	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.	1.9	43
72	MEGSA: A Powerful and Flexible Framework for Analyzing Mutual Exclusivity of Tumor Mutations. <i>American Journal of Human Genetics</i> , 2016, 98, 442-455.	6.2	40

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73	Functional characterization of a multi-cancer risk locus on chr5p15.33 reveals regulation of TERT by ZNF148. <i>Nature Communications</i> , 2017, 8, 15034.	12.8	40
74	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.	2.9	38
75	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.	3.4	37
76	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.	3.6	37
77	Heritability informed power optimization (HIPO) leads to enhanced detection of genetic associations across multiple traits. <i>PLoS Genetics</i> , 2018, 14, e1007549.	3.5	36
78	Generalized meta-analysis for multiple regression models across studies with disparate covariate information. <i>Biometrika</i> , 2019, 106, 567-585.	2.4	35
79	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.	1.4	34
80	Modification of Occupational Exposures on Bladder Cancer Risk by Common Genetic Polymorphisms. <i>Journal of the National Cancer Institute</i> , 2015, 107, djv223.	6.3	34
81	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.	3.5	34
82	Isolated Diastolic Hypertension in the UK Biobank. <i>Hypertension</i> , 2020, 76, 699-706.	2.7	32
83	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.	5.0	31
84	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.	2.5	31
85	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.	1.3	27
86	Opportunities and Challenges for Environmental Exposure Assessment in Population-Based Studies. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017, 26, 1370-1380.	2.5	27
87	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.	6.1	27
88	Testing calibration of risk models at extremes of disease risk. <i>Biostatistics</i> , 2015, 16, 143-154.	1.5	26
89	Characterising cis-regulatory variation in the transcriptome of histologically normal and tumour-derived pancreatic tissues. <i>Gut</i> , 2018, 67, 521-533.	12.1	26
90	Diesel exhaust and bladder cancer risk by pathologic stage and grade subtypes. <i>Environment International</i> , 2020, 135, 105346.	10.0	25

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91	The 19q12 Bladder Cancer GWAS Signal: Association with Cyclin E Function and Aggressive Disease. <i>Cancer Research</i> , 2014, 74, 5808-5818.	0.9	24
92	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.	6.1	23
93	Analysis of cohort studies with multivariate and partially observed disease classification data. <i>Biometrika</i> , 2010, 97, 683-698.	2.4	22
94	Interaction of Cigarette Smoking and Polygenic Risk Score on Reduced Lung Function. <i>JAMA Network Open</i> , 2021, 4, e2139525.	5.9	22
95	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.	1.3	21
96	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.	1.4	21
97	Analysis of Case-Control Association Studies: SNPs, Imputation and Haplotypes. <i>Statistical Science</i> , 2009, 24, 489-502.	2.8	19
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.	2.5	19
99	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.	5.1	19
100	Power Analysis for Genetic Association Test (PAGEANT) provides insights to challenges for rare variant association studies. <i>Bioinformatics</i> , 2018, 34, 1506-1513.	4.1	18
101	Invited Commentary: Efficient Testing of Gene-Environment Interaction. <i>American Journal of Epidemiology</i> , 2008, 169, 231-233.	3.4	17
102	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.	6.4	16
103	Increasing mapping precision of genome-wide association studies: to genotype and impute, sequence, or both?. <i>Genome Biology</i> , 2017, 18, 118.	8.8	16
104	Two high-risk susceptibility loci at 6p25.3 and 14q32.13 for Waldenström macroglobulinemia. <i>Nature Communications</i> , 2018, 9, 4182.	12.8	15
105	Case-Only Analysis of Gene-Environment Interactions Using Polygenic Risk Scores. <i>American Journal of Epidemiology</i> , 2019, 188, 2013-2020.	3.4	15
106	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.	2.9	15
107	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.	5.1	15
108	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.	1.9	15

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109	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. <i>Breast Cancer Research</i> , 2022, 24, 2.	5.0	15
110	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.	3.3	14
111	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.	3.1	14
112	Validation Studies: Bias, Efficiency, and Exposure Assessment. <i>Epidemiology</i> , 2002, 13, 503-506.	2.7	14
113	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.	6.3	14
114	Adjustment for competing risk in kin-cohort estimation. <i>Genetic Epidemiology</i> , 2003, 25, 303-313.	1.3	13
115	Predicting the Future of Genetic Risk Prediction: Table 1.. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2011, 20, 3-8.	2.5	13
116	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.	3.1	13
117	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.	2.8	12
118	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.	10.0	12
119	An exposure-weighted score test for genetic associations integrating environmental risk factors. <i>Biometrics</i> , 2015, 71, 596-605.	1.4	11
120	Comparison of approaches for incorporating new information into existing risk prediction models. <i>Statistics in Medicine</i> , 2017, 36, 1134-1156.	1.6	11
121	A mixed-model approach for powerful testing of genetic associations with cancer risk incorporating tumor characteristics. <i>Biostatistics</i> , 2020, 22, 772-788.	1.5	11
122	Review of Statistical Methods for Gene-Environment Interaction Analysis. <i>Current Epidemiology Reports</i> , 2018, 5, 39-45.	2.4	10
123	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.	5.1	9
124	Assessment of breast cancer risk: which tools to use?. <i>Lancet Oncology</i> , The, 2019, 20, 463-464.	10.7	9
125	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.	1.3	8
126	Smoking Modifies Pancreatic Cancer Risk Loci on 2q21.3. <i>Cancer Research</i> , 2021, 81, 3134-3143.	0.9	8

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127	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.	5.2	8
128	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.	1.3	7
129	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.	3.1	6
130	Testing for Gene-Environment and Gene-Gene Interactions Under Monotonicity Constraints. <i>Journal of the American Statistical Association</i> , 2012, 107, 1441-1452.	3.1	6
131	A subregion-based burden test for simultaneous identification of susceptibility loci and subregions within. <i>Genetic Epidemiology</i> , 2018, 42, 673-683.	1.3	6
132	Genetically Determined Height and Risk of Non-hodgkin Lymphoma. <i>Frontiers in Oncology</i> , 2019, 9, 1539.	2.8	6
133	Rare Genetic Variants Associated With Myocardial Fibrosis: Multi-Ethnic Study of Atherosclerosis. <i>Frontiers in Cardiovascular Medicine</i> , 2022, 9, 804788.	2.4	6
134	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.	0.9	5
135	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.	2.5	5
136	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.	2.5	5
137	On Use of Bivariate Survival Models with Cure Fraction. <i>Biometrics</i> , 2003, 59, 1184-1185.	1.4	4
138	Using shared genetic controls in studies of gene-environment interactions. <i>Biometrika</i> , 2013, 100, 319-338.	2.4	4
139	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.	3.1	3
140	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.	2.5	3
141	Breast Cancer Risk in Women from Ghana Carrying Rare Germline Pathogenic Mutations. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2022, 31, 1593-1601.	2.5	3
142	COMMENTARY: Apportioning causes, targeting populations and predicting risks: Population attributable fractions. <i>European Journal of Epidemiology</i> , 2002, 18, 933-935.	5.7	2
143	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.	3.4	2
144	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.	1.9	2

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145	The use of the risk percentile curve in the analysis of epidemiologic data. <i>Statistics and Its Interface</i> , 2009, 2, 123-131.	0.3	2
146	Utilizing patient information to identify subtype heterogeneity of cancer driver genes. <i>Statistical Methods in Medical Research</i> , 2022, 31, 510-519.	1.5	2
147	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, .	0.7	2
148	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.	3.1	2
149	<i>The authors replied as follows:</i>. <i>Biometrics</i> , 2007, 63, 965-966.	1.4	1
150	Genetics of gallbladder cancer –“ Authors' reply. <i>Lancet Oncology</i> , The, 2017, 18, e297.	10.7	1
151	Logistic regression analysis of two–phase studies using generalized method of moments. <i>Biometrics</i> , 2023, 79, 241-252.	1.4	1
152	Improved Imputation of Common and Uncommon Single Nucleotide Polymorphisms (SNPs) with a New Reference Set. <i>Nature Precedings</i> , 2011, , .	0.1	0
153	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.	2.6	0
154	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.	3.4	0
155	Alcohol and breast cancer risk in postmenopausal women: The PLCO experience.. <i>Journal of Clinical Oncology</i> , 2012, 30, 1521-1521.	1.6	0
156	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