Yudi Pawitan

List of Publications by Year
in descending order

172 papers	12,734 citations	50170 46 h-index	26548 107 g-index
179 all docs	179 docs citations	179 times ranked	22282 citing authors

#	Article	IF	Citations
1	Common genetic determinants of schizophrenia and bipolar disorder in Swedish families: a population-based study. Lancet, The, 2009, 373, 234-239.	6.3	1,785
2	From The Cover: An expression signature for p53 status in human breast cancer predicts mutation status, transcriptional effects, and patient survival. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 13550-13555.	3.3	1,109
3	Most genetic risk for autism resides with common variation. Nature Genetics, 2014, 46, 881-885.	9.4	977
4	Gene expression profiling spares early breast cancer patients from adjuvant therapy: derived and validated in two population-based cohorts. Breast Cancer Research, 2005, 7, R953-64.	2.2	659
5	Genetic Reclassification of Histologic Grade Delineates New Clinical Subtypes of Breast Cancer. Cancer Research, 2006, 66, 10292-10301.	0.4	606
6	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. Nature Genetics, 2013, 45, 501-512.	9.4	578
7	An interferon-related gene signature for DNA damage resistance is a predictive marker for chemotherapy and radiation for breast cancer. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 18490-18495.	3.3	484
8	False discovery rate, sensitivity and sample size for microarray studies. Bioinformatics, 2005, 21, 3017-3024.	1.8	410
9	Estrogen-Dependent Signaling in a Molecularly Distinct Subclass of Aggressive Prostate Cancer. Journal of the National Cancer Institute, 2008, 100, 815-825.	3.0	286
10	Generalized Linear Models with Random Effects. , 0, , .		284
11	Revisiting Mendelian disorders through exome sequencing. Human Genetics, 2011, 129, 351-370.	1.8	206
12	The pursuit of genome-wide association studies: where are we now?. Journal of Human Genetics, 2010, 55, 195-206.	1.1	191
13	Validation of a Radiosensitivity Molecular Signature in Breast Cancer. Clinical Cancer Research, 2012, 18, 5134-5143.	3.2	174
14	Familial aggregation of small-for-gestational-age births: The importance of fetal genetic effects. American Journal of Obstetrics and Gynecology, 2006, 194, 475-479.	0.7	155
15	Beta-Poisson model for single-cell RNA-seq data analyses. Bioinformatics, 2016, 32, 2128-2135.	1.8	151
16	Parental age and risk of childhood cancers: a population-based cohort study from Sweden. International Journal of Epidemiology, 2006, 35, 1495-1503.	0.9	146
17	mRNA Expression Signature of Gleason Grade Predicts Lethal Prostate Cancer. Journal of Clinical Oncology, 2011, 29, 2391-2396.	0.8	140
18	Maternal Effects for Preterm Birth: A Genetic Epidemiologic Study of 630,000 Families. American Journal of Epidemiology, 2009, 170, 1365-1372.	1.6	116

#	Article	IF	Citations
19	High-definition likelihood inference of genetic correlations across human complex traits. Nature Genetics, 2020, 52, 859-864.	9.4	114
20	Genetic and Shared Environmental Factors Do Not Confound the Association Between Birth Weight and Hypertension. Circulation, 2007, 115, 2931-2938.	1.6	112
21	Strategies and issues in the detection of pathway enrichment in genome-wide association studies. Human Genetics, 2009, 126, 289-301.	1.8	112
22	Congestive heart failure symptoms in patients with preserved left ventricular systolic function: Analysis of the CASS registry. Journal of the American College of Cardiology, 1991, 18, 377-382.	1.2	111
23	Profound changes in breast cancer incidence may reflect changes into a Westernized lifestyle: A comparative population-based study in Singapore and Sweden. International Journal of Cancer, 2005, 113, 302-306.	2.3	107
24	Network enrichment analysis: extension of gene-set enrichment analysis to gene networks. BMC Bioinformatics, 2012, 13, 226.	1.2	102
25	Psychosocial predictors of mortality in the Cardiac Arrhythmia Suppression Trial-1 (CAST-1). American Journal of Cardiology, 1993, 71, 263-267.	0.7	100
26	Nonparametric Spectral Density Estimation Using Penalized Whittle Likelihood. Journal of the American Statistical Association, 1994, 89, 600-610.	1.8	98
27	Regions of homozygosity and their impact on complex diseases and traits. Human Genetics, 2011, 129, 1-15.	1.8	98
28	Increased risk of death and cardiac arrest from encainide and flecainide in patients after non-Q-wave acute myocardial infarction in the Cardiac Arrhythmia Suppression Trial. American Journal of Cardiology, 1991, 68, 1551-1555.	0.7	94
29	VEGF-A Expression Correlates with TP53 Mutations in Nonâ€“Small Cell Lung Cancer: Implications for Antiangiogenesis Therapy. Cancer Research, 2015, 75, 1187-1190.	0.4	92
30	Analysis of p53 mutation status in human cancer cell lines: a paradigm for cell line cross-contamination. Cancer Biology and Therapy, 2008, 7, 699-708.	1.5	91
31	The discovery of human genetic variations and their use as disease markers: past, present and future. Journal of Human Genetics, 2010, 55, 403-415.	1.1	89
32	Improved Grading of Breast Adenocarcinomas Based on Genomic Instability. Cancer Research, 2004, 64, 904-909.	0.4	86
33	Modeling Disease Marker Processes in AIDS. Journal of the American Statistical Association, 1993, 88, 719-726.	1.8	81
34	A clinical model for identifying the short-term risk of breast cancer. Breast Cancer Research, 2017, 19, 29.	2.2	79
35	Crowdsourced estimation of cognitive decline and resilience in Alzheimer's disease. Alzheimer's and Dementia, 2016, 12, 645-653.	0.4	72
36	Bias in the estimation of false discovery rate in microarray studies. Bioinformatics, 2005, 21, 3865-3872.	1.8	70

#	Article	IF	Citations
37	Prevalence, characteristics and significance of ventricular premature complexes and ventricular tachycardia detected by 24-hour continuous electrocardiographic recording in the Cardiac Arrhythmia Suppression Trial. American Journal of Cardiology, 1991, 68, 887-896.	0.7	68
38	Tobacco Use, Body Mass Index, and the Risk of Leukemia and Multiple Myeloma: A Nationwide Cohort Study in Sweden. Cancer Research, 2007, 67, 5983-5986.	0.4	68
39	Sparse partial least-squares regression and its applications to high-throughput data analysis. Chemometrics and Intelligent Laboratory Systems, 2011, 109, 1-8.	1.8	65
40	Heritability, Assortative Mating and Gender Differences in Violent Crime: Results from a Total Population Sample Using Twin, Adoption, and Sibling Models. Behavior Genetics, 2012, 42, 3-18.	1.4	64
41	Reproducibility of Methods to Detect Differentially Expressed Genes from Single-Cell RNA Sequencing. Frontiers in Genetics, 2019, 10, 1331.	1.1	58
42	Model-based estimation of the attributable fraction for cross-sectional, caseâ€“control and cohort studies using the R package AF. European Journal of Epidemiology, 2016, 31, 575-582.	2.5	56
43	Identification of a secondary peak in myocardial infarction onset 11 to 12 hours after awakening: The cardiac arrhythmia suppression trial (CAST) experience. Journal of the American College of Cardiology, 1993, 22, 998-1003.	1.2	55
44	Gene-based meta-analysis of genome-wide association studies implicates new loci involved in obesity. Human Molecular Genetics, 2015, 24, 6849-6860.	1.4	55
45	Betweenâ€“within models for survival analysis. Statistics in Medicine, 2013, 32, 3067-3076.	0.8	54
46	Integrated molecular portrait of non-small cell lung cancers. BMC Medical Genomics, 2013, 6, 53.	0.7	51
47	Integration of somatic mutation, expression and functional data reveals potential driver genes predictive of breast cancer survival. Bioinformatics, 2015, 31, 2607-2613.	1.8	49
48	Correlation test to assess low-level processing of high-density oligonucleotide microarray data. BMC Bioinformatics, 2005, 6, 80.	1.2	47
49	How Many Genetic Variants Remain to Be Discovered?. PLoS ONE, 2009, 4, e7969.	1.1	47
50	Statistical interim monitoring of the cardiac arrhythmia suppression trial. Statistics in Medicine, 1990, 9, 1081-1090.	0.8	46
51	Effects of Advancing Age on the Efficacy and Side Effects of Antiarrhythmic Drugs in Post-Myocardial Infarction Patients with Ventricular Arrhythmias. Journal of the American Geriatrics Society, 1992, 40, 666-672.	1.3	45
52	Exome versus transcriptome sequencing in identifying coding region variants. Expert Review of Molecular Diagnostics, 2012, 12, 241-251.	1.5	43
53	Filtering genes to improve sensitivity in oligonucleotide microarray data analysis. Nucleic Acids Research, 2007, 35, e102-e102.	6.5	42
54	A Genome-Wide Assessment of Variability in Human Serum Metabolism. Human Mutation, 2013, 34, 515-524.	1.1	42

#	Article	IF	Citations
55	Parametric and penalized generalized survival models. Statistical Methods in Medical Research, 2018, 27, 1531-1546.	0.7	42
56	Quantitative Proteomics Profiling of Primary Lung Adenocarcinoma Tumors Reveals Functional Perturbations in Tumor Metabolism. Journal of Proteome Research, 2013, 12, 3934-3943.	1.8	40
57	Affinity Proteomics Reveals Elevated Muscle Proteins in Plasma of Children with Cerebral Malaria. PLoS Pathogens, 2014, 10, e1004038.	2.1	40
58	Finding regions of significance in SELDI measurements for identifying protein biomarkers. Bioinformatics, 2006, 22, 1515-1523.	1.8	39
59	Identification of differentially expressed genes and false discovery rate in microarray studies. Current Opinion in Lipidology, 2007, 18, 187-193.	1.2	39
60	ABO blood group and risk of cancer: A register-based cohort study of 1.6 million blood donors. Cancer Epidemiology, 2016, 44, 40-43.	0.8	38
61	Multidimensional Normalization to Minimize Plate Effects of Suspension Bead Array Data. Journal of Proteome Research, 2016, 15, 3473-3480.	1.8	38
62	Heritable Variation, With Little or No Maternal Effect, Accounts for Recurrence Risk to Autism Spectrum Disorder in Sweden. Biological Psychiatry, 2018, 83, 589-597.	0.7	38
63	Is the Association between General Cognitive Ability and Violent Crime Caused by Family-Level Confounders?. PLoS ONE, 2012, 7, e41783.	1.1	38
64	Tobacco use, body mass index and the risk of malignantlymphomasâ€"A nationwide cohort study in Sweden. International Journal of Cancer, 2006, 118, 2298-2302.	2.3	37
65	Events in the cardiac arrhythmia suppression trial: Baseline predictors of mortality in placebo-treated patients. Journal of the American College of Cardiology, 1991, 18, 1434-1438.	1.2	35
66	Robust smooth segmentation approach for array CGH data analysis. Bioinformatics, 2007, 23, 2463-2469.	1.8	35
67	Super-sparse principal component analyses for high-throughput genomic data. BMC Bioinformatics, 2010, 11, 296.	1.2	35
68	Gene discovery in familial cancer syndromes by exome sequencing: prospects for the elucidation of familial colorectal cancer type X. Modern Pathology, 2012, 25, 1055-1068.	2.9	35
69	Quasi-likelihood Estimation of Non-invertible Moving Average Processes. Scandinavian Journal of Statistics, 2000, 27, 689-702.	0.9	34
70	Molecular differences in transition zone and peripheral zone prostate tumors. Carcinogenesis, 2015, 36, 632-638.	1.3	34
71	Cell-level somatic mutation detection from single-cell RNA sequencing. Bioinformatics, 2019, 35, 4679-4687.	1.8	34
72	Estimation of false discovery proportion under general dependence. Bioinformatics, 2006, 22, 3025-3031.	1.8	33

#	Article	IF	Citations
73	Doubly robust methods for handling confounding by cluster. Biostatistics, 2016, 17, 264-276.	0.9	32
74	A Reminder of the Fallibility of the Wald Statistic: Likelihood Explanation. American Statistician, 2000, 54, 54-56.	0.9	29
75	Large-scale non-targeted metabolomic profiling in three human population-based studies. Metabolomics, 2016, 12, 1.	1.4	29
76	Rediscovery rate estimation for assessing the validation of significant findings in high-throughput studies. Briefings in Bioinformatics, 2015, 16, 563-575.	3.2	27
77	Accumulation of potential driver genes with genomic alterations predicts survival of high-risk neuroblastoma patients. Biology Direct, 2018, 13, 14.	1.9	27
78	Variable selection in random calibration of near-infrared instruments: ridge regression and partial least squares regression settings. Journal of Chemometrics, 2003, 17, 174-185.	0.7	26
79	Genomic copy number variations in three Southeast Asian populations. Human Mutation, 2010, 31, 851-857.	1.1	26
80	Generalized survival models for correlated timeâ€toâ€event data. Statistics in Medicine, 2017, 36, 4743-4762.	0.8	25
81	Disease trajectories and mortality among women diagnosed with breast cancer. Breast Cancer Research, 2019, 21, 95.	2.2	23
82	Proteomic Data Analysis Workflow for Discovery of Candidate Biomarker Peaks Predictive of Clinical Outcome for Patients with Acute Myeloid Leukemia. Journal of Proteome Research, 2008, 7, 2332-2341.	1.8	22
83	Modified least-variant set normalization for miRNA microarray. Rna, 2010, 16, 2293-2303.	1.6	22
84	Advancing paternal age and offspring violent offending: A sibling-comparison study. Development and Psychopathology, 2012, 24, 739-753.	1.4	22
85	A simplified interventional mapping system (SIMS) for the selection of combinations of targeted treatments in non-small cell lung cancer. Oncotarget, 2015, 6, 14139-14152.	0.8	22
86	Creatinine and C-reactive protein in amyotrophic lateral sclerosis, multiple sclerosis and Parkinsonâ€™s disease. Brain Communications, 2020, 2, fcaa152.	1.5	21
87	A fast detection of fusion genes from paired-end RNA-seq data. BMC Genomics, 2018, 19, 786.	1.2	20
88	Genetic Landscape of the ACE2 Coronavirus Receptor. Circulation, 2022, 145, 1398-1411.	1.6	20
89	Testing a Multigene Signature of Prostate Cancer Death in the Swedish Watchful Waiting Cohort. Cancer Epidemiology Biomarkers and Prevention, 2008, 17, 1682-1688.	1.1	19
90	Comprehensive landscape of subtype-specific coding and non-coding RNA transcripts in breast cancer. Oncotarget, 2016, 7, 68851-68863.	0.8	19

#	Article	IF	Citations
91	Association Between Ease of Suppression of Ventricular Arrhythmia and Survival. Circulation, 1995, 91, 79-83.	1.6	19
92	Correlation between leukocyte phenotypes and prognosis of amyotrophic lateral sclerosis. ELife, 2022, 11, .	2.8	18
93	Robust ascertainment-adjusted parameter estimation. Genetic Epidemiology, 2005, 29, 68-75.	0.6	17
94	Gene expression in 16q is associated with survival and differs between SÃ¸rlie breast cancer subtypes. Genes Chromosomes and Cancer, 2007, 46, 87-97.	1.5	16
95	Technological advances in DNA sequence enrichment and sequencing for germline genetic diagnosis. Expert Review of Molecular Diagnostics, 2012, 12, 159-173.	1.5	16
96	Associations between autoimmune diseases and amyotrophic lateral sclerosis: a register-based study. Amyotrophic Lateral Sclerosis and Frontotemporal Degeneration, 2021, 22, 211-219.	1.1	16
97	Etiology of Familial Aggregation in Melanoma and Squamous Cell Carcinoma of the Skin. Cancer Epidemiology Biomarkers and Prevention, 2007, 16, 1639-1643.	1.1	15
98	Isoform-level gene expression patterns in single-cell RNA-sequencing data. Bioinformatics, 2018, 34, 2392-2400.	1.8	15
99	Caseâ€“cohort methods for survival data on families from routine registers. Statistics in Medicine, 2008, 27, 1062-1074.	0.8	14
100	Normalization of Gene-Expression Microarray Data. Methods in Molecular Biology, 2010, 673, 37-52.	0.4	14
101	Correlating gene and protein expression data using Correlated Factor Analysis. BMC Bioinformatics, 2009, 10, 272.	1.2	13
102	Identification of recurrent regions of copy-number variants across multiple individuals. BMC Bioinformatics, 2010, 11, 147.	1.2	12
103	Bandwidth Selection for Indirect Density Estimation Based on Corrupted Histogram Data. Journal of the American Statistical Association, 1996, 91, 610-626.	1.8	11
104	Importance of familial factors in associations between offspring birth weight and parental risk of type-2 diabetes. International Journal of Epidemiology, 2008, 37, 185-192.	0.9	11
105	A population-based study of copy number variants and regions of homozygosity in healthy Swedish individuals. Journal of Human Genetics, 2011, 56, 524-533.	1.1	11
106	Extensions of the Bartlett-Lewis model for rainfall processes. Statistical Modelling, 2003, 3, 79-98.	0.5	10
107	Annotated regions of significance of SELDI-TOF-MS spectra for detecting protein biomarkers. Proteomics, 2006, 6, 6124-6133.	1.3	10
108	Operator Dependent Choice of Prostate Cancer Biopsy Has Limited Impact on a Gene Signature Analysis for the Highly Expressed Genes IGFBP3 and F3 in Prostate Cancer Epithelial Cells. PLoS ONE, 2014, 9, e109610.	1.1	10

#	Article	IF	Citations
109	Genetic Mixed Linear Models for Twin Survival Data. Behavior Genetics, 2007, 37, 621-630.	1.4	9
110	Covariance component models for multivariate binary traits in family data analysis. Statistics in Medicine, 2008, 27, 1086-1105.	0.8	9
111	A Selection Operator for Summary Association Statistics Reveals Allelic Heterogeneity of Complex Traits. American Journal of Human Genetics, 2017, 101, 903-912.	2.6	9
112	Regression standardization and attributable fraction estimation with between-within frailty models for clustered survival data. Statistical Methods in Medical Research, 2019, 28, 462-485.	0.7	9
113	The transcriptomeâ€wide landscape of molecular subtypeâ€specific <scp>mRNA</scp> expression profiles in acute myeloid leukemia. American Journal of Hematology, 2021, 96, 580-588.	2.0	9
114	Profiles of histidine-rich glycoprotein associate with age and risk of all-cause mortality. Life Science Alliance, 2020, 3, e202000817.	1.3	9
115	Biomarkers and Disease Trajectories Influencing Womenâ€™s Health: Results from the UK Biobank Cohort. Phenomics, 2022, 2, 184-193.	0.9	9
116	Constrained clustering of irregularly sampled spatial data. Journal of Statistical Computation and Simulation, 2003, 73, 853-865.	0.7	8
117	Multi-platform segmentation for joint detection of copy number variants. Bioinformatics, 2011, 27, 1555-1561.	1.8	8
118	Sparse partial leastâ€squares regression for highâ€throughput survival data analysis. Statistics in Medicine, 2013, 32, 5340-5352.	0.8	8
119	Bounds on sufficient-cause interaction. European Journal of Epidemiology, 2014, 29, 813-820.	2.5	8
120	Distinct effects of anti-inflammatory and anti-thrombotic drugs on cancer characteristics at diagnosis. European Journal of Cancer, 2015, 51, 751-757.	1.3	8
121	Improving the Prediction of Prostate Cancer Overall Survival by Supplementing Readily Available Clinical Data with Gene Expression Levels of IGFBP3 and F3 in Formalin-Fixed Paraffin Embedded Core Needle Biopsy Material. PLoS ONE, 2016, 11, e0145545.	1.1	8
122	Alternating EM algorithm for a bilinear model in isoform quantification from RNA-seq data. Bioinformatics, 2020, 36, 805-812.	1.8	8
123	Circall: fast and accurate methodology for discovery of circular RNAs from paired-end RNA-sequencing data. BMC Bioinformatics, 2021, 22, 495.	1.2	8
124	Model-based maximum covariance analysis for irregularly observed climatological data. Journal of Agricultural, Biological, and Environmental Statistics, 2007, 12, 1-24.	0.7	7
125	Classification of array CGH data using smoothed logistic regression model. Statistics in Medicine, 2009, 28, 3798-3810.	0.8	7
126	Wallet Game: Probability, Likelihood, and Extended Likelihood. American Statistician, 2017, 71, 120-122.	0.9	7

#	Article	IF	Citations
127	Gastrointestinal biopsies and amyotrophic lateral sclerosis â€“ results from a cohort study of 1.1 million individuals. Amyotrophic Lateral Sclerosis and Frontotemporal Degeneration, 2021, 22, 410-418.	1.1	7
128	The frequency of misattributed paternity in Sweden is low and decreasing: A nationwide cohort study. Journal of Internal Medicine, 2022, 291, 95-100.	2.7	7
129	The ABC model of prostate cancer: A conceptual framework for the design and interpretation of prognostic studies. Cancer, 2017, 123, 1490-1496.	2.0	6
130	Confidence as Likelihood. Statistical Science, 2021, 36, .	1.6	6
131	Isoform-level quantification for single-cell RNA sequencing. Bioinformatics, 2022, 38, 1287-1294.	1.8	6
132	Computing empirical likelihood from the bootstrap. Statistics and Probability Letters, 2000, 47, 337-345.	0.4	5
133	Analysis and prediction of the BSE incidence in Ireland. Preventive Veterinary Medicine, 2004, 62, 267-283.	0.7	5
134	Regions of homozygosity in three Southeast Asian populations. Journal of Human Genetics, 2012, 57, 101-108.	1.1	5
135	Direct Calculation of the Variance of Maximum Penalized Likelihood Estimates via EM Algorithm. American Statistician, 2014, 68, 93-97.	0.9	5
136	A Critical Look at Entropyâ€Based Geneâ€Gene Interaction Measures. Genetic Epidemiology, 2016, 40, 416-424.	0.6	5
137	On the relationship between the heritability and the attributable fraction. Human Genetics, 2019, 138, 425-435.	1.8	5
138	Two-staged estimation of variance components in generalized linear mixed models. Journal of Statistical Computation and Simulation, 2001, 69, 1-17.	0.7	4
139	Nontrivial Replication of Loci Detected by Multi-Trait Methods. Frontiers in Genetics, 2021, 12, 627989.	1.1	4
140	Consistent Estimation for Non-Gaussian Non-Causal Autoregessive Processes. Journal of Time Series Analysis, 1999, 20, 417-423.	0.7	3
141	Estimating the number of true discoveries in genomeâ€wide association studies. Statistics in Medicine, 2012, 31, 1177-1189.	0.8	3
142	Identifying and Assessing Interesting Subgroups in a Heterogeneous Population. BioMed Research International, 2015, 2015, 1-13.	0.9	3
143	Patterns of acute inflammatory symptoms prior to cancer diagnosis. Scientific Reports, 2017, 7, 67.	1.6	3
144	CREDO: Highly confident disease-relevant A-to-I RNA-editing discovery in breast cancer. Scientific Reports, 2019, 9, 5064.	1.6	3

#	Article	IF	Citations
145	Fusion Gene Detection Using Whole-Exome Sequencing Data in Cancer Patients. Frontiers in Genetics, 2022, 13, 820493.	1.1	3
146	Modelling infectious disease transmission with complex exposure pattern and sparse outcome data. Statistics in Medicine, 2004, 23, 3013-3032.	0.8	2
147	Svensson et al. Respond to "Maternal Genes and Environment in Preterm Birth". American Journal of Epidemiology, 2009, 170, 1386-1387.	1.6	2
148	A random-effect model approach for group variable selection. Computational Statistics and Data Analysis, 2015, 89, 147-157.	0.7	2
149	Nonparametric estimation of the rediscovery rate. Statistics in Medicine, 2016, 35, 3203-3212.	0.8	2
150	One CNV Discordance in NRXN1 Observed Upon Genome-wide Screening in 38 Pairs of Adult Healthy Monozygotic Twins. Twin Research and Human Genetics, 2016, 19, 97-103.	0.3	2
151	Sparse estimation of geneâ€“gene interactions in prediction models. Statistical Methods in Medical Research, 2017, 26, 2319-2332.	0.7	2
152	RPASE: Individualâ€based alleleâ€specific expression detection without prior knowledge of haplotype phase. Molecular Ecology Resources, 2018, 18, 1247-1262.	2.2	2
153	Genetic and phenotypic links between obesity and extracellular vesicles. Human Molecular Genetics, 2022, 31, 3643-3651.	1.4	2
154	Matched Ascertainment of Informative Families for Complex Genetic Modelling. Behavior Genetics, 2010, 40, 404-414.	1.4	1
155	Genetic analysis of ageâ€ata€onset traits based on caseâ€“control family data. Statistics in Medicine, 2010, 29, 3258-3266.	0.8	1
156	Copy number polymorphisms in new HapMap III and Singapore populations. Journal of Human Genetics, 2011, 56, 552-560.	1.1	1
157	Likelihood ratio and score burden tests for detecting disease-associated rare variants. Statistical Applications in Genetics and Molecular Biology, 2015, 14, 481-95.	0.2	1
158	Sparse alternatives to ridge regression: a random effects approach. Journal of Applied Statistics, 2015, 42, 12-26.	0.6	1
159	Likelihoodâ€based inference for bounds of causal parameters. Statistics in Medicine, 2018, 37, 4695-4706.	0.8	1
160	Sparse pathway-based prediction models for high-throughput molecular data. Computational Statistics and Data Analysis, 2018, 126, 125-135.	0.7	1
161	LIKELIHOOD PERSPECTIVES IN THE CONSENSUS AND CONTROVERSIES OF STATISTICAL MODELLING AND INFERENCE. , 2004, , 23-52.		1
162	High-Throughput Functional Ex-Vivo Drug Testing and Multi-Omics Profiling in Patients with Acute Myeloid Leukemia. Blood, 2019, 134, 4641-4641.	0.6	1

#	Article	IF	Citations
163	Gene expression biomarkers to predict overall survival of prostate cancer patients.. Journal of Clinical Oncology, 2012, 30, 4561-4561.	0.8	1
164	Quantification of mutantâ€“allele expression at isoform level in cancer from RNA-seq data. NAR Genomics and Bioinformatics, 2022, 4, .	1.5	1
165	The Evolution of High-Throughput Sequencing Technologies: From Sanger to Single-Molecule Sequencing. , 2013, , 1-30.		0
166	Resolving Zeckhauserâ€™s paradox. Theory and Decision, 2020, 88, 595-607.	0.5	0
167	A systems genomics approach to uncover the molecular properties of cancer genes. Scientific Reports, 2020, 10, 18392.	1.6	0
168	Popperâ€™s Falsification and Corroboration from the Statistical Perspectives. , 2021, , 121-147.		0
169	A gene expression signature to predicit overall, prostate cancer, and nonâ€“prostate cancer survival.. Journal of Clinical Oncology, 2013, 31, 51-51.	0.8	0
170	Therapeutic Interventional Mapping System (TIMS): A novel strategy for the selection of tri-targeted therapy combinations for non-small cell lung cancer (NSCLC).. Journal of Clinical Oncology, 2015, 33, 7524-7524.	0.8	0
171	Validation of a 3-gene signature and development of an authentic cohort database to improve overall survival prediction and clinical treatment decision for patients with newly diagnosed prostate cancer.. Journal of Clinical Oncology, 2016, 34, 5047-5047.	0.8	0
172	Integration of Distinct Analysis Strategies Improves Tissue-Trait Association Identification. Frontiers in Genetics, 2022, 13, 798269.	1.1	0