Kathleen F Kerr

List of Publications by Year
in descending order

107	8,033	81900 39	51608 86
papers	citations	h-index	g-index

126	126	126	14298
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Analysis of Variance for Gene Expression Microarray Data. Journal of Computational Biology, 2000, 7, 819-837.	1.6	1,158
2	Genetic Associations with Valvular Calcification and Aortic Stenosis. New England Journal of Medicine, 2013, 368, 503-512.	27.0	767
3	Standardizing global gene expression analysis between laboratories and across platforms. Nature Methods, 2005, 2, 351-356.	19.0	416
4	Assessing the Clinical Impact of Risk Prediction Models With Decision Curves: Guidance for Correct Interpretation and Appropriate Use. Journal of Clinical Oncology, 2016, 34, 2534-2540.	1.6	392
5	Transient rapamycin treatment can increase lifespan and healthspan in middle-aged mice. ELife, 2016, 5, .	6.0	315
6	Net Reclassification Indices for Evaluating Risk Prediction Instruments. Epidemiology, 2014, 25, 114-121.	2.7	304
7	Identification of heart rateâ€“associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	21.4	282
8	Genetic Diversity and Association Studies in US Hispanic/Latino Populations: Applications in the Hispanic Community Health Study/Study of Latinos. American Journal of Human Genetics, 2016, 98, 165-184.	6.2	266
9	European Ancestry as a Risk Factor for Atrial Fibrillation in African Americans. Circulation, 2010, 122, 2009-2015.	1.6	219
10	Testing for improvement in prediction model performance. Statistics in Medicine, 2013, 32, 1467-1482.	1.6	191
11	Association of Low-Density Lipoprotein Cholesterolâ€“Related Genetic Variants With Aortic Valve Calcium and Incident Aortic Stenosis. JAMA - Journal of the American Medical Association, 2014, 312, 1764.	7.4	184
12	Design Considerations for Efficient and Effective Microarray Studies. Biometrics, 2003, 59, 822-828.	1.4	172
13	CNS tau efflux via exosomes is likely increased in Parkinson's disease but not in Alzheimer's disease. Alzheimer's and Dementia, 2016, 12, 1125-1131.	0.8	154
14	Evaluating the Incremental Value of New Biomarkers With Integrated Discrimination Improvement. American Journal of Epidemiology, 2011, 174, 364-374.	3.4	153
15	Models estimating risk of hepatocellular carcinoma in patients with alcohol or NAFLD-related cirrhosis for risk stratification. Journal of Hepatology, 2019, 71, 523-533.	3.7	124
16	The Arabidopsis thaliana Transcriptome in Response to Agrobacterium tumefaciens. Molecular Plant-Microbe Interactions, 2006, 19, 665-681.	2.6	120
17	Development of models estimating the risk of hepatocellular carcinoma after antiviral treatment for hepatitis C. Journal of Hepatology, 2018, 69, 1088-1098.	3.7	119
18	52 Genetic Loci Influencing MyocardialÂMass. Journal of the American College of Cardiology, 2016, 68, 1435-1448.	2.8	113

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19	Comparative transcriptome analysis ofAgrobacterium tumefaciensin response to plant signal salicylic acid, indole-3-acetic acid and Î³-amino butyric acid reveals signalling cross-talk andAgrobacterium-plant co-evolution. Cellular Microbiology, 2008, 10, 2339-2354.	2.1	102
20	Genetic loci associated with heart rate variability and their effects on cardiac disease risk. Nature Communications, 2017, 8, 15805.	12.8	95
21	Evaluation of methods for oligonucleotide array data via quantitative real-time PCR. BMC Bioinformatics, 2006, 7, 23.	2.6	89
22	Genome-Wide Association Studies of the PR Interval in African Americans. PLoS Genetics, 2011, 7, e1001304.	3.5	88
23	Multicenter Study of Acetaminophen Hepatotoxicity Reveals the Importance of Biological Endpoints in Genomic Analyses. Toxicological Sciences, 2007, 99, 326-337.	3.1	79
24	Population Structure of Hispanics in the United States: The Multi-Ethnic Study of Atherosclerosis. PLoS Genetics, 2012, 8, e1002640.	3.5	79
25	Large-Scale Candidate Gene Analysis in Whites and African Americans Identifies IL6R Polymorphism in Relation to Atrial Fibrillation. Circulation: Cardiovascular Genetics, 2011, 4, 557-564.	5.1	74
26	Linear Models for Microarray Data Analysis: Hidden Similarities and Differences. Journal of Computational Biology, 2003, 10, 891-901.	1.6	73
27	Genetics of coronary artery calcification among African Americans, a meta-analysis. BMC Medical Genetics, 2013, 14, 75.	2.1	73
28	Empirical evaluation of data transformations and ranking statistics for microarray analysis. Nucleic Acids Research, 2004, 32, 5471-5479.	14.5	71
29	Genome-wide Association Study of Platelet Count Identifies Ancestry-Specific Loci in Hispanic/Latino Americans. American Journal of Human Genetics, 2016, 98, 229-242.	6.2	71
30	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. Nature Communications, 2018, 9, 2904.	12.8	71
31	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	12.8	59
32	African Ancestryâ€“Specific Alleles and Kidney Disease Risk in Hispanics/Latinos. Journal of the American Society of Nephrology: JASN, 2017, 28, 915-922.	6.1	57
33	Meta-analysis of loci associated with age at natural menopause in African-American women. Human Molecular Genetics, 2014, 23, 3327-3342.	2.9	54
34	Genome-wide association study of age at menarche in African-American women. Human Molecular Genetics, 2013, 22, 3329-3346.	2.9	52
35	Comments on the analysis of unbalanced microarray data. Bioinformatics, 2009, 25, 2035-2041.	4.1	50
36	Interleukin-8 and Tumor Necrosis Factor Predict Acute Kidney Injury After Pediatric Cardiac Surgery. Annals of Thoracic Surgery, 2017, 104, 2072-2079.	1.3	49

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37	Novel Loci Associated With PR Interval in a Genome-Wide Association Study of 10 African American Cohorts. Circulation: Cardiovascular Genetics, 2012, 5, 639-646.	5.1	48
38	Admixture Mapping of Coronary Artery Calcified Plaque in African Americans With Type 2 Diabetes Mellitus. Circulation: Cardiovascular Genetics, 2013, 6, 97-105.	5.1	43
39	An open science study of ageing in companion dogs. Nature, 2022, 602, 51-57.	27.8	43
40	Harborview Burns â€“ 1974 to 2009. PLoS ONE, 2012, 7, e40086.	2.5	42
41	A powerful statistical framework for generalization testing in GWAS, with application to the HCHS/SOL. Genetic Epidemiology, 2017, 41, 251-258.	1.3	41
42	Impact of Ancestry and Common Genetic Variants on QT Interval in African Americans. Circulation: Cardiovascular Genetics, 2012, 5, 647-655.	5.1	38
43	Fifteen Genetic Loci Associated With the Electrocardiographic P Wave. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	38
44	Fine-mapping, novel loci identification, and SNP association transferability in a genome-wide association study of QRS duration in African Americans. Human Molecular Genetics, 2016, 25, 4350-4368.	2.9	37
45	Genomeâ€wide association study of generalized anxiety symptoms in the Hispanic Community Health Study/Study of Latinos. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2017, 174, 132-143.	1.7	37
46	Further Insight Into the Incremental Value of New Markers: The Interpretation of Performance Measures and the Importance of Clinical Context. American Journal of Epidemiology, 2012, 176, 482-487.	3.4	32
47	Genome-wide association study of dental caries in the Hispanic Communities Health Study/Study of Latinos (HCHS/SOL). Human Molecular Genetics, 2016, 25, 807-816.	2.9	29
48	Plasma Î±-synuclein and cognitive impairment in the Parkinson's Associated Risk Syndrome: A pilot study. Neurobiology of Disease, 2018, 116, 53-59.	4.4	29
49	Developing Risk Prediction Models for Kidney Injury and Assessing Incremental Value for Novel Biomarkers. Clinical Journal of the American Society of Nephrology: CJASN, 2014, 9, 1488-1496.	4.5	28
50	Evaluating biomarkers for prognostic enrichment of clinical trials. Clinical Trials, 2017, 14, 629-638.	1.6	28
51	Efficient 2^kFactorial Designs for Blocks of Size 2 with Microarray Applications. Journal of Quality Technology, 2006, 38, 309-318.	2.5	26
52	Assessment of Second-Opinion Strategies for Diagnoses of Cutaneous Melanocytic Lesions. JAMA Network Open, 2019, 2, e1912597.	5.9	26
53	Association of Triglyceride-Related Genetic Variants With MitralÂAnnularÂCalcification. Journal of the American College of Cardiology, 2017, 69, 2941-2948.	2.8	25
54	Genome-Wide Association Study of Blood Pressure Traits by Hispanic/Latino Background: the Hispanic Community Health Study/Study of Latinos. Scientific Reports, 2017, 7, 10348.	3.3	24

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55	GWAS of the electrocardiographic QT interval in Hispanics/Latinos generalizes previously identified loci and identifies population-specific signals. Scientific Reports, 2017, 7, 17075.	3.3	23
56	Functional Genomics Unique to Week 20 Post Wounding in the Deep Cone/Fat Dome of the Duroc/Yorkshire Porcine Model of Fibroproliferative Scarring. PLoS ONE, 2011, 6, e19024.	2.5	21
57	RiGoR: reporting guidelines to address common sources of bias in risk model development. Biomarker Research, 2015, 3, 2.	6.8	21
58	What Is the Best Reference RNA? And Other Questions Regarding the Design and Analysis of Two-color Microarray Experiments. OMICS A Journal of Integrative Biology, 2007, 11, 152-165.	2.0	19
59	A Common SCN5A Variant Is Associated with PR Interval and Atrial Fibrillation Among African Americans. Journal of Cardiovascular Electrophysiology, 2014, 25, 1150-1157.	1.7	19
60	Improving risk classification of critical illness with biomarkers: A simulation study. Journal of Critical Care, 2013, 28, 541-548.	2.2	18
61	Methodological issues in current practice may leadÂto bias in the development of biomarker combinations for predicting acute kidney injury. Kidney International, 2016, 89, 429-438.	5.2	18
62	Genome-wide association study of heart rate and its variability in Hispanic/Latino cohorts. Heart Rhythm, 2017, 14, 1675-1684.	0.7	18
63	Urinalysis findings and urinary kidney injury biomarker concentrations. BMC Nephrology, 2017, 18, 218.	1.8	17
64	Extended analysis of benchmark datasets for Agilent two-color microarrays. BMC Bioinformatics, 2007, 8, 371.	2.6	16
65	Joint Modeling, Covariate Adjustment, and Interaction. Epidemiology, 2011, 22, 805-812.	2.7	15
66	Genome-wide association study of depressive symptoms in the Hispanic Community Health Study/Study of Latinos. Journal of Psychiatric Research, 2018, 99, 167-176.	3.1	15
67	Biomarker combinations for diagnosis and prognosis in multicenter studies: Principles and methods. Statistical Methods in Medical Research, 2019, 28, 969-985.	1.5	15
68	Risk prediction for complex diseases: application to Parkinson disease. Genetics in Medicine, 2013, 15, 361-367.	2.4	14
69	Assessing the Clinical Impact of Risk Models for Opting Out of Treatment. Medical Decision Making, 2019, 39, 86-90.	2.4	14
70	Excess Patient Visits for Cough and Pulmonary Disease at a Large US Health System in the Months Prior to the COVID-19 Pandemic: Time-Series Analysis. Journal of Medical Internet Research, 2020, 22, e21562.	4.3	14
71	Genome-wide association study of PR interval in Hispanics/Latinos identifies novel locus at ID2. Heart, 2018, 104, 904-911.	2.9	12
72	The Importance of Uncertainty and Opt-In v. Opt-Out: Best Practices for Decision Curve Analysis. Medical Decision Making, 2019, 39, 491-492.	2.4	11

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73	Epigenome-wide analysis of long-term air pollution exposure and DNA methylation in monocytes: results from the Multi-Ethnic Study of Atherosclerosis. Epigenetics, 2022, 17, 1-17.	2.7	11
74	First things first: risk model performance metrics should reflect the clinical application. Statistics in Medicine, 2017, 36, 4503-4508.	1.6	10
75	Variants Associated with the Ankle Brachial Index Differ by Hispanic/Latino Ethnic Group: a genome-wide association study in the Hispanic Community Health Study/Study of Latinos. Scientific Reports, 2019, 9, 11410.	3.3	10
76	Age and Physical Activity Levels in Companion Dogs: Results From the Dog Aging Project. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2022, 77, 1986-1993.	3.6	10
77	Development of biomarker combinations for postoperative acute kidney injury via Bayesian model selection in a multicenter cohort study. Biomarker Research, 2018, 6, 3.	6.8	8
78	GWAS of QRS duration identifies new loci specific to Hispanic/Latino populations. PLoS ONE, 2019, 14, e0217796.	2.5	8
79	Quantifying Donor Effects on Transplant Outcomes Using Kidney Pairs from Deceased Donors. Clinical Journal of the American Society of Nephrology: CJASN, 2019, 14, 1781-1787.	4.5	8
80	Pathology Traineesâ€™ Experience and Attitudes on Use of Digital Whole Slide Images. Academic Pathology, 2020, 7, 2374289520951922.	1.1	8
81	More scanning, but not zooming, is associated with diagnostic accuracy in evaluating digital breast pathology slides. Journal of Vision, 2021, 21, 7.	0.3	7
82	Once-daily feeding is associated with better health in companion dogs: results from the Dog Aging Project. GeroScience, 2022, 44, 1779-1790.	4.6	6
83	Lifetime prevalence of malignant and benign tumours in companion dogs: Crossâ€sectional analysis of Dog Aging Project baseline survey. Veterinary and Comparative Oncology, 2022, 20, 797-804.	1.8	6
84	Optimality Criteria for the Design of 2-Color Microarray Studies. Statistical Applications in Genetics and Molecular Biology, 2012, 11, Article 10.	0.6	5
85	Histopathologic synoptic reporting of invasive melanoma: How reliable are the data?. Cancer, 2021, 127, 3125-3136.	4.1	5
86	Using ordinal outcomes to construct and select biomarker combinations for single-level prediction. Diagnostic and Prognostic Research, 2018, 2, 8.	1.8	4
87	BioPETsurv: Methodology and open source software to evaluate biomarkers for prognostic enrichment of time-to-event clinical trials. PLoS ONE, 2020, 15, e0239486.	2.5	4
88	Reply to A.J. Vickers et al. Journal of Clinical Oncology, 2017, 35, 473-475.	1.6	3
89	Reply. Annals of Thoracic Surgery, 2018, 106, 641.	1.3	3
90	Developing Biomarker Panels to Predict Progression of Acute Kidney Injury After Cardiac Surgery. Kidney International Reports, 2019, 4, 1677-1688.	0.8	3

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91	Recalibration Methods for Improved Clinical Utility of Risk Scores. Medical Decision Making, 2022, 42, 500-512.	2.4	3
92	A Comparison of Two Classes of Methods for Estimating False Discovery Rates in Microarray Studies. Scientifica, 2012, 2012, 1-9.	1.7	2
93	Tuberculosis State Is Associated with Expression of Toll-Like Receptor 2 in Sputum Macrophages. MSphere, 2017, 2, .	2.9	2
94	Empirical evaluation of data transformations and ranking statistics for microarray analysis. Nucleic Acids Research, 2004, 32, 5972-5972.	14.5	1
95	Developing biomarker combinations in multicenter studies via direct maximization and penalization. Statistics in Medicine, 2020, 39, 3412-3426.	1.6	1
96	Histopathological Diagnosis of Cutaneous Melanocytic Lesions: Blinded and <scp>Nonâ€Blinded</scp> Second Opinions Offer Similar Improvement in Diagnostic Accuracy. Clinical and Experimental Dermatology, 2022, , .	1.3	1
97	Stationary Gaussian processes on the vertices of the k-cube. Journal of Statistical Planning and Inference, 2004, 118, 1-8.	0.6	0
98	Sources of Variation in Microarray Experiments. , 2006, , 37-47.		0
99	Design Principles for Microarray Investigations. , 2007, , 39-49.		0
100	Comparisons of cancer staging systems should be based on overall performance in the population. Clinical Trials, 2017, 14, 659-660.	1.6	0
101	Gastrointestinal Cancer Survival and Radiation Exposure among Atomic Bomb Survivors: The Life Span Study. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 412-418.	2.5	0
102	Title is missing!. , 2020, 15, e0239486.		0
103	Title is missing!. , 2020, 15, e0239486.		0
104	Title is missing!. , 2020, 15, e0239486.		0
105	Title is missing!. , 2020, 15, e0239486.		0
106	Title is missing!. , 2020, 15, e0239486.		0
107	Title is missing!. , 2020, 15, e0239486.		0