Kenneth M Rice

List of Publications by Year
in descending order

86	14,376	66343	58581
papers	citations	42 h-index	82 g-index

95	95	95	21415
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. Nature, 2011, 478, 103-109.	27.8	1,855
2	Genome-wide association study of blood pressure and hypertension. Nature Genetics, 2009, 41, 677-687.	21.4	1,224
3	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. Nature Genetics, 2018, 50, 524-537.	21.4	1,124
4	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	27.8	1,069
5	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	21.4	924
6	A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. Nature Genetics, 2012, 44, 659-669.	21.4	762
7	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	21.4	549
8	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. Nature Communications, 2020, 11, 163.	12.8	466
9	Genome-wide association study of PR interval. Nature Genetics, 2010, 42, 153-159.	21.4	400
10	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. Nature Genetics, 2016, 48, 1171-1184.	21.4	362
11	Control for Population Structure and Relatedness for Binary Traits in Genetic Association Studies via Logistic Mixed Models. American Journal of Human Genetics, 2016, 98, 653-666.	6.2	347
12	Association of Low-Frequency and Rare Coding-Sequence Variants with Blood Lipids and Coronary Heart Disease in 56,000 Whites and Blacks. American Journal of Human Genetics, 2014, 94, 223-232.	6.2	287
13	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
14	Genetic association testing using the GENESIS R/Bioconductor package. Bioinformatics, 2019, 35, 5346-5348.	4.1	260
15	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	21.4	251
16	Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. Nature Genetics, 2016, 48, 1162-1170.	21.4	223
17	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. American Journal of Human Genetics, 2014, 94, 233-245.	6.2	193
18	Meta-analysis of genome-wide association studies from the CHARGE consortium identifies common variants associated with carotid intima media thickness and plaque. Nature Genetics, 2011, 43, 940-947.	21.4	191

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19	Meta-Analysis of Genome-Wide Association Studies in African Americans Provides Insights into the Genetic Architecture of Type 2 Diabetes. PLoS Genetics, 2014, 10, e1004517.	3.5	191
20	Genome-wide Association Analysis of Blood-Pressure Traits in African-Ancestry Individuals Reveals Common Associated Genes in African and Non-African Populations. American Journal of Human Genetics, 2013, 93, 545-554.	6.2	189
21	Association of Genome-Wide Variation With the Risk of Incident Heart Failure in Adults of European and African Ancestry. Circulation: Cardiovascular Genetics, 2010, 3, 256-266.	5.1	176
22	Multiethnic Genome-Wide Association Study of Cerebral White Matter Hyperintensities on MRI. Circulation: Cardiovascular Genetics, 2015, 8, 398-409.	5.1	162
23	A Re-Evaluation of Fixed Effect(s) Meta-Analysis. Journal of the Royal Statistical Society Series A: Statistics in Society, 2018, 181, 205-227.	1.1	159
24	Meta-analysis of gene-environment interaction: joint estimation of SNP and SNP Ã— environment regression coefficients. Genetic Epidemiology, 2011, 35, 11-18.	1.3	158
25	Dynamic incorporation of multiple in silico functional annotations empowers rare variant association analysis of large whole-genome sequencing studies at scale. Nature Genetics, 2020, 52, 969-983.	21.4	146
26	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. Nature Communications, 2019, 10, 4130.	12.8	133
27	Whole-genome sequenceâ€“based analysis of high-density lipoprotein cholesterol. Nature Genetics, 2013, 45, 899-901.	21.4	132
28	Type 2 and interferon inflammation regulate SARS-CoV-2 entry factor expression in the airway epithelium. Nature Communications, 2020, 11, 5139.	12.8	131
29	GWAS and colocalization analyses implicate carotid intima-media thickness and carotid plaque loci in cardiovascular outcomes. Nature Communications, 2018, 9, 5141.	12.8	119
30	Multi-ancestry genome-wide geneâ€“smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. Nature Genetics, 2019, 51, 636-648.	21.4	112
31	Large-scale genome-wide analysis identifies genetic variants associated with cardiac structure and function. Journal of Clinical Investigation, 2017, 127, 1798-1812.	8.2	106
32	Efficient Variant Set Mixed Model Association Tests for Continuous and Binary Traits in Large-Scale Whole-Genome Sequencing Studies. American Journal of Human Genetics, 2019, 104, 260-274.	6.2	103
33	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. PLoS ONE, 2018, 13, e0198166.	2.5	94
34	Behavior of QQ-Plots and Genomic Control in Studies of Gene-Environment Interaction. PLoS ONE, 2011, 6, e19416.	2.5	93
35	Analysis commons, a team approach to discovery in a big-data environment for genetic epidemiology. Nature Genetics, 2017, 49, 1560-1563.	21.4	93
36	Single-trait and multi-trait genome-wide association analyses identify novel loci for blood pressure in African-ancestry populations. PLoS Genetics, 2017, 13, e1006728.	3.5	88

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37	Genome-Wide Association Study for Incident Myocardial Infarction and Coronary Heart Disease in Prospective Cohort Studies: The CHARGE Consortium. PLoS ONE, 2016, 11, e0144997.	2.5	69
38	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	12.8	64
39	Multi-ancestry sleep-by-SNP interaction analysis in 126,926 individuals reveals lipid loci stratified by sleep duration. Nature Communications, 2019, 10, 5121.	12.8	62
40	A fully adjusted twoâ€stage procedure for rankâ€normalization in genetic association studies. Genetic Epidemiology, 2019, 43, 263-275.	1.3	60
41	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	12.8	59
42	Trans-ethnic Meta-analysis and Functional Annotation Illuminates theÂGenetic Architecture of Fasting Glucose and Insulin. American Journal of Human Genetics, 2016, 99, 56-75.	6.2	55
43	Multiancestry Study of Geneâ€“Lifestyle Interactions for Cardiovascular Traits in 610 475 Individuals From 124 Cohorts. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	55
44	Bayesian statistics. Scholarpedia Journal, 2009, 4, 5230.	0.3	55
45	Whole-Exome Sequencing Identifies Loci Associated with Blood Cell Traits and Reveals a Role for Alternative GFI1B Splice Variants in Human Hematopoiesis. American Journal of Human Genetics, 2016, 99, 481-488.	6.2	45
46	Rare Exome Sequence Variants in CLCN6 Reduce Blood Pressure Levels and Hypertension Risk. Circulation: Cardiovascular Genetics, 2016, 9, 64-70.	5.1	44
47	Meta-analysis uncovers genome-wide significant variants for rapid kidney function decline. Kidney International, 2021, 99, 926-939.	5.2	42
48	Model-robust regression and a Bayesian â€œsandwichâ€•estimator. Annals of Applied Statistics, 2010, 4, .	1.1	39
49	Meta-analysis of 49â€…549 individuals imputed with the 1000 Genomes Project reveals an exonic damaging variant inANGPTL4determining fasting TG levels. Journal of Medical Genetics, 2016, 53, 441-449.	3.2	34
50	Potential for Revealing Individual-Level Information in Genome-wide Association Studies. JAMA - Journal of the American Medical Association, 2010, 303, 659.	7.4	32
51	A multi-ancestry genome-wide study incorporating geneâ€“smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. Human Molecular Genetics, 2019, 28, 2615-2633.	2.9	31
52	Blood Pressure and Heart Rate Measures Associated With Increased Risk of Covert Brain Infarction and Worsening Leukoaraiosis in Older Adults. Arteriosclerosis, Thrombosis, and Vascular Biology, 2017, 37, 1579-1586.	2.4	28
53	A genome-wide association study identifies genetic loci associated with specific lobar brain volumes. Communications Biology, 2019, 2, 285.	4.4	27
54	FastSKAT: Sequence kernel association tests for very large sets of markers. Genetic Epidemiology, 2018, 42, 516-527.	1.3	26

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55	Nasal airway transcriptome-wide association study of asthma reveals genetically driven mucus pathobiology. Nature Communications, 2022, 13, 1632.	12.8	24
56	Common and Rare Coding Genetic Variation Underlying the Electrocardiographic PR Interval. Circulation Genomic and Precision Medicine, 2018, 11, e002037.	3.6	19
57	Sequence Analysis of Six Blood Pressure Candidate Regions in 4,178 Individuals: The Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Targeted Sequencing Study. PLoS ONE, 2014, 9, e109155.	2.5	19
58	Strategies to Design and Analyze Targeted Sequencing Data. Circulation: Cardiovascular Genetics, 2014, 7, 335-343.	5.1	18
59	Genetic loci and prioritization of genes for kidney function decline derived from a meta-analysis of 62 longitudinal genome-wide association studies. Kidney International, 2022, 102, 624-639.	5.2	18
60	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. Communications Biology, 2022, 5, .	4.4	17
61	A Decision-Theoretic Formulation of Fisherâ€™s Approach to Testing. American Statistician, 2010, 64, 345-349.	1.6	16
62	Addressing the estimation of standard errors in fixed effects metaâ€analysis. Statistics in Medicine, 2018, 37, 1788-1809.	1.6	15
63	Monogenic and Polygenic Contributions to QTc Prolongation in the Population. Circulation, 2022, 145, 1524-1533.	1.6	14
64	Maternal-Fetal Disposition of Glyburide in Pregnant Mice Is Dependent on Gestational Age. Journal of Pharmacology and Experimental Therapeutics, 2014, 350, 425-434.	2.5	13
65	Rapid evaluation of phenotypes, SNPs and results through the dbGaP CHARGE Summary Results site. Nature Genetics, 2016, 48, 702-703.	21.4	13
66	Multi-ancestry genome-wide geneâ€“sleep interactions identify novel loci for blood pressure. Molecular Psychiatry, 2021, 26, 6293-6304.	7.9	13
67	Insights From a Large-Scale Whole-Genome Sequencing Study of Systolic Blood Pressure, Diastolic Blood Pressure, and Hypertension. Hypertension, 2022, 79, 1656-1667.	2.7	12
68	The genomics of heart failure: design and rationale of the HERMES consortium. ESC Heart Failure, 2021, 8, 5531-5541.	3.1	11
69	A Simple Diagnostic Plot Connecting Robust Estimation, Outlier Detection, and False Discovery Rates. Journal of Applied Statistics, 2006, 33, 1131-1147.	1.3	8
70	Knowing the signs: a direct and generalizable motivation of twoâ€sided tests. Journal of the Royal Statistical Society Series A: Statistics in Society, 2020, 183, 411-430.	1.1	7
71	Improved inference for fixedâ€effects metaâ€analysis of 2 Ã—â€‰2 tables. Research Synthesis Methods, 2020, 11, 387-396.	8.7	6
72	Chronic Lower Limb Wound Outcomes Among Rural and Urban Veterans. Journal of Rural Health, 2015, 31, 410-420.	2.9	5

#	Article	IF	Citations
73	Genetic loci associated with prevalent and incident myocardial infarction and coronary heart disease in the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium. PLoS ONE, 2020, 15, e0230035.	2.5	5
74	Expressing Regret: A Unified View of Credible Intervals. American Statistician, 0, , 1-9.	1.6	5
75	Identification of novel and rare variants associated with handgrip strength using whole genome sequence data from the NHLBI Trans-Omics in Precision Medicine (TOPMed) Program. PLoS ONE, 2021, 16, e0253611.	2.5	4
76	Chloe Krakauer and Kenneth Riceâ€™s contribution to the Discussion of â€˜Testing by betting: A strategy for statistical and scientific communicationâ€™ by Glenn Shafer. Journal of the Royal Statistical Society Series A: Statistics in Society, 2021, 184, 452-453.	1.1	3
77	Exact inference for fixedâ€effects metaâ€analysis of proportions. Research Synthesis Methods, 2021, , .	8.7	3
78	Coherent Tests for Interval Null Hypotheses. American Statistician, 0, , 1-9.	1.6	3
79	Quantifying the Excess Risk of Adverse COVID-19 Outcomes in Unvaccinated Individuals With Diabetes Mellitus, Hypertension, Ischaemic Heart Disease or Myocardial Injury: A Meta-Analysis. Frontiers in Cardiovascular Medicine, 2022, 9, 871151.	2.4	3
80	Medicareâ€VHA dual use is associated with poorer chronic wound healing. Wound Repair and Regeneration, 2016, 24, 913-922.	3.0	2
81	Rare coding variants in RCN3 are associated with blood pressure. BMC Genomics, 2022, 23, 148.	2.8	2
82	Bayesian Approaches to Fixed Effects <scp>Metaâ€Analysis</scp>. Research Synthesis Methods, 2022, , .	8.7	2
83	Variant-specific inflation factors for assessing population stratification at the phenotypic variance level. Nature Communications, 2021, 12, 3506.	12.8	1
84	Coagulation factor VIII, white matter hyperintensities and cognitive function: Results from the Cardiovascular Health Study. PLoS ONE, 2020, 15, e0242062.	2.5	1
85	Bayesian optimality and intervals for Steinâ€type estimates. Stat, 0, , .	0.4	1
86	Selecting Shrinkage Parameters for Effect Estimation. American Journal of Epidemiology, 2018, 187, 358-365.	3.4	0