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	Rare coding variants in RCN3 are associated with blood pressure. BMC Genomics, 2022, 23, 148.	2.8	2
2	Nasal airway transcriptome-wide association study of asthma reveals genetically driven mucus pathobiology. Nature Communications, 2022, 13, 1632.	12.8	24
3	Monogenic and Polygenic Contributions to QTc Prolongation in the Population. Circulation, 2022, 145, 1524-1533.	1.6	14
4	Bayesian Approaches to Fixed Effects <scp>Metaâ€Analysis</scp>. Research Synthesis Methods, 2022, , .	8.7	2
5	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
6	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
7	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. Communications Biology, 2022, 5, .	4.4	17
8	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
9	Meta-analysis uncovers genome-wide significant variants for rapid kidney function decline. Kidney International, 2021, 99, 926-939.	5.2	42
10	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	27.8	1,069
11	Multi-ancestry genome-wide geneâ€“sleep interactions identify novel loci for blood pressure. Molecular Psychiatry, 2021, 26, 6293-6304.	7.9	13
12	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
13	Variant-specific inflation factors for assessing population stratification at the phenotypic variance level. Nature Communications, 2021, 12, 3506.	12.8	1
14	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
15	The genomics of heart failure: design and rationale of the HERMES consortium. ESC Heart Failure, 2021, 8, 5531-5541.	3.1	11
16	Exact inference for fixedâ€effects metaâ€analysis of proportions. Research Synthesis Methods, 2021, , .	8.7	3
17	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. Nature Communications, 2020, 11, 163.	12.8	466
18	Type 2 and interferon inflammation regulate SARS-CoV-2 entry factor expression in the airway epithelium. Nature Communications, 2020, 11, 5139.	12.8	131

#	Article	IF	Citations
19	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
20	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	12.8	59
21	Improved inference for fixedâ€effects metaâ€analysis of 2 Ã—â€‰2 tables. Research Synthesis Methods, 2020, 11, 387-396.	8.7	6
22	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
23	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
24	Coagulation factor VIII, white matter hyperintensities and cognitive function: Results from the Cardiovascular Health Study. PLoS ONE, 2020, 15, e0242062.	2.5	1
25	A genome-wide association study identifies genetic loci associated with specific lobar brain volumes. Communications Biology, 2019, 2, 285.	4.4	27
26	Genetic association testing using the GENESIS R/Bioconductor package. Bioinformatics, 2019, 35, 5346-5348.	4.1	260
27	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
28	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. Nature Communications, 2019, 10, 4130.	12.8	133
29	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	21.4	251
30	A fully adjusted twoâ€stage procedure for rankâ€normalization in genetic association studies. Genetic Epidemiology, 2019, 43, 263-275.	1.3	60
31	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	12.8	64
32	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	21.4	549
33	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
34	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
35	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
36	Addressing the estimation of standard errors in fixed effects metaâ€analysis. Statistics in Medicine, 2018, 37, 1788-1809.	1.6	15

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37	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
38	Selecting Shrinkage Parameters for Effect Estimation. American Journal of Epidemiology, 2018, 187, 358-365.	3.4	0
39	GWAS and colocalization analyses implicate carotid intima-media thickness and carotid plaque loci in cardiovascular outcomes. Nature Communications, 2018, 9, 5141.	12.8	119
40	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
41	Common and Rare Coding Genetic Variation Underlying the Electrocardiographic PR Interval. Circulation Genomic and Precision Medicine, 2018, 11, e002037.	3.6	19
42	FastSKAT: Sequence kernel association tests for very large sets of markers. Genetic Epidemiology, 2018, 42, 516-527.	1.3	26
43	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
44	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
45	Multiancestry Study of Geneâ€“Lifestyle Interactions for Cardiovascular Traits in 610 475 Individuals From 124 Cohorts. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	55
46	Analysis commons, a team approach to discovery in a big-data environment for genetic epidemiology. Nature Genetics, 2017, 49, 1560-1563.	21.4	93
47	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
48	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
49	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
50	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
51	Medicareâ€“VHA dual use is associated with poorer chronic wound healing. Wound Repair and Regeneration, 2016, 24, 913-922.	3.0	2
52	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
53	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
54	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

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55	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
56	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
57	Rapid evaluation of phenotypes, SNPs and results through the dbGaP CHARGE Summary Results site. Nature Genetics, 2016, 48, 702-703.	21.4	13
58	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
59	Rare Exome Sequence Variants in CLCN6 Reduce Blood Pressure Levels and Hypertension Risk. Circulation: Cardiovascular Genetics, 2016, 9, 64-70.	5.1	44
60	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
61	Chronic Lower Limb Wound Outcomes Among Rural and Urban Veterans. Journal of Rural Health, 2015, 31, 410-420.	2.9	5
62	Multiethnic Genome-Wide Association Study of Cerebral White Matter Hyperintensities on MRI. Circulation: Cardiovascular Genetics, 2015, 8, 398-409.	5.1	162
63	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
64	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
65	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
66	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
67	Strategies to Design and Analyze Targeted Sequencing Data. Circulation: Cardiovascular Genetics, 2014, 7, 335-343.	5.1	18
68	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
69	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
70	Whole-genome sequenceâ€"based analysis of high-density lipoprotein cholesterol. Nature Genetics, 2013, 45, 899-901.	21.4	132
71	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
72	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. Nature, 2011, 478, 103-109.	27.8	1,855

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73	Behavior of QQ-Plots and Genomic Control in Studies of Gene-Environment Interaction. PLoS ONE, 2011, 6, e19416.	2.5	93
74	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
75	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
76	Model-robust regression and a Bayesian â€œsandwichâ€•estimator. Annals of Applied Statistics, 2010, 4, .	1.1	39
77	Genome-wide association study of PR interval. Nature Genetics, 2010, 42, 153-159.	21.4	400
78	Potential for Revealing Individual-Level Information in Genome-wide Association Studies. JAMA - Journal of the American Medical Association, 2010, 303, 659.	7.4	32
79	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
80	A Decision-Theoretic Formulation of Fisherâ€™s Approach to Testing. American Statistician, 2010, 64, 345-349.	1.6	16
81	Genome-wide association study of blood pressure and hypertension. Nature Genetics, 2009, 41, 677-687.	21.4	1,224
82	Bayesian statistics. Scholarpedia Journal, 2009, 4, 5230.	0.3	55
83	A Simple Diagnostic Plot Connecting Robust Estimation, Outlier Detection, and False Discovery Rates. Journal of Applied Statistics, 2006, 33, 1131-1147.	1.3	8
84	Expressing Regret: A Unified View of Credible Intervals. American Statistician, 0, , 1-9.	1.6	5
85	Coherent Tests for Interval Null Hypotheses. American Statistician, 0, , 1-9.	1.6	3
86	Bayesian optimality and intervals for Steinâ€type estimates. Stat, 0, , .	0.4	1