Kenneth M Rice

List of Publications by Citations

138 papers	18,189 citations	64 h-index	134 g-index
147 ext. papers	21,793 ext. citations	12.7 avg, IF	5.02 L-index

#	Paper	IF	Citations
138	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. *Nature Genetics*, **2010**, 42, 105-16	36.3	1673
137	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. *Nature* , **2011**, 478, 103-9	50.4	1564
136	Genome-wide association study of blood pressure and hypertension. *Nature Genetics*, **2009**, 41, 677-87	36.3	1065
135	Genome-wide analysis of genetic loci associated with Alzheimer disease. *JAMA - Journal of the American Medical Association*, **2010**, 303, 1832-40	27.4	888
134	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. *Nature Genetics*, **2018**, 50, 524-537	36.3	536
133	Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. *Nature Genetics*, **2010**, 42, 142-8	36.3	527
132	Meta-analysis identifies six new susceptibility loci for atrial fibrillation. *Nature Genetics*, **2012**, 44, 670-5	36.3	429
131	Detectable clonal mosaicism from birth to old age and its relationship to cancer. *Nature Genetics*, **2012**, 44, 642-50	36.3	409
130	Meta-analysis of genome-wide association studies in >80 000 subjects identifies multiple loci for C-reactive protein levels. *Circulation*, **2011**, 123, 731-8	16.7	395
129	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. *Nature Genetics*, **2018**, 50, 1412-1425	36.3	386
128	Genomewide association studies of stroke. *New England Journal of Medicine*, **2009**, 360, 1718-28	59.2	376
127	Common variants in KCNN3 are associated with lone atrial fibrillation. *Nature Genetics*, **2010**, 42, 240-4	36.3	362
126	Genome-wide association study of PR interval. *Nature Genetics*, **2010**, 42, 153-9	36.3	340
125	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. *Nature Genetics*, **2011**, 43, 1005-11	36.3	338
124	Common variants at ten loci influence QT interval duration in the QTGEN Study. *Nature Genetics*, **2009**, 41, 399-406	36.3	330
123	Variants in ZFHX3 are associated with atrial fibrillation in individuals of European ancestry. *Nature Genetics*, **2009**, 41, 879-81	36.3	307
122	Quality control and quality assurance in genotypic data for genome-wide association studies. *Genetic Epidemiology*, **2010**, 34, 591-602	2.6	303

121	Multiple loci influence erythrocyte phenotypes in the CHARGE Consortium. *Nature Genetics*, **2009**, 41, 1191-8	36.3	285
120	Genetic loci associated with plasma phospholipid n-3 fatty acids: a meta-analysis of genome-wide association studies from the CHARGE Consortium. *PLoS Genetics*, **2011**, 7, e1002193	6	257
119	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. *Nature Genetics*, **2016**, 48, 1171-1184	36.3	251
118	Common variants in 22 loci are associated with QRS duration and cardiac ventricular conduction. *Nature Genetics*, **2010**, 42, 1068-76	36.3	249
117	Incidence and mechanisms of cerebral ischemia in early clinical head injury. *Journal of Cerebral Blood Flow and Metabolism*, **2004**, 24, 202-11	7.3	241
116	Association Between Telomere Length and Risk of Cancer and Non-Neoplastic Diseases: A Mendelian Randomization Study. *JAMA Oncology*, **2017**, 3, 636-651	13.4	236
115	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, 223-32	11	233
114	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. *Nature Genetics*, **2018**, 50, 559-571	36.3	221
113	Control for Population Structure and Relatedness for Binary Traits in Genetic Association Studies via Logistic Mixed Models. *American Journal of Human Genetics*, **2016**, 98, 653-66	11	207
112	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, 940-7	36.3	168
111	Genetic variants associated with cardiac structure and function: a meta-analysis and replication of genome-wide association data. *JAMA - Journal of the American Medical Association*, **2009**, 302, 168-78	27.4	164
110	Association of hypertension drug target genes with blood pressure and hypertension in 86,588 individuals. *Hypertension*, **2011**, 57, 903-10	8.5	154
109	Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. *Nature Genetics*, **2016**, 48, 1162-70	36.3	152
108	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	6	151
107	Defining ischemic burden after traumatic brain injury using 15O PET imaging of cerebral physiology. *Journal of Cerebral Blood Flow and Metabolism*, **2004**, 24, 191-201	7.3	151
106	Association of genome-wide variation with the risk of incident heart failure in adults of European and African ancestry: a prospective meta-analysis from the cohorts for heart and aging research in genomic epidemiology (CHARGE) consortium. *Circulation: Cardiovascular Genetics*, **2010**, 3, 256-66		147
105	Genome-wide association studies of cerebral white matter lesion burden: the CHARGE consortium. *Annals of Neurology*, **2011**, 69, 928-39	9.4	146
104	Association of genetic variation with systolic and diastolic blood pressure among African Americans: the Candidate Gene Association Resource study. *Human Molecular Genetics*, **2011**, 20, 2273-84	5.6	146

103	Association of genetic variations with nonfatal venous thrombosis in postmenopausal women. *JAMA - Journal of the American Medical Association*, **2007**, 297, 489-98	27.4	144
102	Association of gene variants with incident myocardial infarction in the Cardiovascular Health Study. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2008**, 28, 173-9	9.4	140
101	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. *Nature Communications*, **2020**, 11, 163	17.4	140
100	A genome-wide association study of depressive symptoms. *Biological Psychiatry*, **2013**, 73, 667-78	7.9	135
99	Meta-analysis of gene-environment interaction: joint estimation of SNP and SNP environment regression coefficients. *Genetic Epidemiology*, **2011**, 35, 11-8	2.6	121
98	Multiethnic genome-wide association study of cerebral white matter hyperintensities on MRI. *Circulation: Cardiovascular Genetics*, **2015**, 8, 398-409		119
97	Whole-genome sequence-based analysis of high-density lipoprotein cholesterol. *Nature Genetics*, **2013**, 45, 899-901	36.3	117
96	Interactions of dietary whole-grain intake with fasting glucose- and insulin-related genetic loci in individuals of European descent: a meta-analysis of 14 cohort studies. *Diabetes Care*, **2010**, 33, 2684-91	14.6	112
95	GWASTools: an R/Bioconductor package for quality control and analysis of genome-wide association studies. *Bioinformatics*, **2012**, 28, 3329-31	7.2	111
94	Genome-wide association analysis identifies multiple loci related to resting heart rate. *Human Molecular Genetics*, **2010**, 19, 3885-94	5.6	106
93	Identification of additional risk loci for stroke and small vessel disease: a meta-analysis of genome-wide association studies. *Lancet Neurology, The*, **2016**, 15, 695-707	24.1	100
92	A re-evaluation of fixed effect(s) meta-analysis. *Journal of the Royal Statistical Society Series A: Statistics in Society*, **2018**, 181, 205-227	2.1	97
91	Type 2 Diabetes Variants Disrupt Function of SLC16A11 through Two Distinct Mechanisms. *Cell*, **2017**, 170, 199-212.e20	56.2	94
90	Genetic association testing using the GENESIS R/Bioconductor package. *Bioinformatics*, **2019**, 35, 5346-5348	7.2	92
89	Genetic variation associated with plasma von Willebrand factor levels and the risk of incident venous thrombosis. *Blood*, **2011**, 117, 6007-11	2.2	87
88	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. *Hypertension*, **2017**,	8.5	85
87	Gene-age interactions in blood pressure regulation: a large-scale investigation with the CHARGE, Global BPgen, and ICBP Consortia. *American Journal of Human Genetics*, **2014**, 95, 24-38	11	80
86	A genome-wide association study for venous thromboembolism: the extended cohorts for heart and aging research in genomic epidemiology (CHARGE) consortium. *Genetic Epidemiology*, **2013**, 37, 512-521	2.6	80

85	Characterization of large structural genetic mosaicism in human autosomes. *American Journal of Human Genetics*, **2015**, 96, 487-97	11	77
84	Intersubject variability and reproducibility of 15O PET studies. *Journal of Cerebral Blood Flow and Metabolism*, **2006**, 26, 48-57	7.3	77
83	Genome-wide association studies of MRI-defined brain infarcts: meta-analysis from the CHARGE Consortium. *Stroke*, **2010**, 41, 210-7	6.7	74
82	Behavior of QQ-plots and genomic control in studies of gene-environment interaction. *PLoS ONE*, **2011**, 6, e19416	3.7	73
81	Blood pressure variability and the risk of all-cause mortality, incident myocardial infarction, and incident stroke in the cardiovascular health study. *American Journal of Hypertension*, **2013**, 26, 1210-7	2.3	71
80	Does induced hypertension reduce cerebral ischaemia within the traumatized human brain?. *Brain*, **2004**, 127, 2479-90	11.2	71
79	Large-scale genome-wide analysis identifies genetic variants associated with cardiac structure and function. *Journal of Clinical Investigation*, **2017**, 127, 1798-1812	15.9	68
78	Genomic variation associated with mortality among adults of European and African ancestry with heart failure: the cohorts for heart and aging research in genomic epidemiology consortium. *Circulation: Cardiovascular Genetics*, **2010**, 3, 248-55		66
77	Causal Effect of Plasminogen Activator Inhibitor Type 1 on Coronary Heart Disease. *Journal of the American Heart Association*, **2017**, 6,	6	65
76	Variation in inflammation-related genes and risk of incident nonfatal myocardial infarction or ischemic stroke. *Atherosclerosis*, **2008**, 198, 166-73	3.1	65
75	GWAS and colocalization analyses implicate carotid intima-media thickness and carotid plaque loci in cardiovascular outcomes. *Nature Communications*, **2018**, 9, 5141	17.4	64
74	A genome-wide association study identifies novel loci associated with circulating IGF-I and IGFBP-3. *Human Molecular Genetics*, **2011**, 20, 1241-51	5.6	60
73	Multi-ancestry genome-wide gene-smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. *Nature Genetics*, **2019**, 51, 636-648	36.3	59
72	Variation in eicosanoid genes, non-fatal myocardial infarction and ischemic stroke. *Atherosclerosis*, **2009**, 204, e58-63	3.1	59
71	Single-trait and multi-trait genome-wide association analyses identify novel loci for blood pressure in African-ancestry populations. *PLoS Genetics*, **2017**, 13, e1006728	6	58
70	Matrix metalloproteinase-3 (MMP3) and MMP9 genes and risk of myocardial infarction, ischemic stroke, and hemorrhagic stroke. *Atherosclerosis*, **2008**, 201, 130-7	3.1	55
69	Effects of long-term averaging of quantitative blood pressure traits on the detection of genetic associations. *American Journal of Human Genetics*, **2014**, 95, 49-65	11	52
68	Consumption of meat is associated with higher fasting glucose and insulin concentrations regardless of glucose and insulin genetic risk scores: a meta-analysis of 50,345 Caucasians. *American Journal of Clinical Nutrition*, **2015**, 102, 1266-78	7	51

67	Common genetic variation near the phospholamban gene is associated with cardiac repolarisation: meta-analysis of three genome-wide association studies. *PLoS ONE*, **2009**, 4, e6138	3.7	50
66	Common variation in cytochrome P450 epoxygenase genes and the risk of incident nonfatal myocardial infarction and ischemic stroke. *Pharmacogenetics and Genomics*, **2008**, 18, 535-43	1.9	47
65	Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. *American Journal of Human Genetics*, **2016**, 99, 8-21	11	47
64	Predicting stroke through genetic risk functions: the CHARGE Risk Score Project. *Stroke*, **2014**, 45, 403-12	6.7	46
63	Cholesterol ester transfer protein, interleukin-8, peroxisome proliferator activator receptor alpha, and Toll-like receptor 4 genetic variations and risk of incident nonfatal myocardial infarction and ischemic stroke. *American Journal of Cardiology*, **2008**, 101, 1683-8	3	46
62	Simple estimates of haplotype relative risks in case-control data. *Genetic Epidemiology*, **2006**, 30, 485-94	2.6	42
61	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. *Nature Communications*, **2019**, 10, 376	17.4	41
60	Trans-ethnic Meta-analysis and Functional Annotation Illuminates the Genetic Architecture of Fasting Glucose and Insulin. *American Journal of Human Genetics*, **2016**, 99, 56-75	11	41
59	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. *American Journal of Epidemiology*, **2019**, 188, 1033-1054	3.8	39
58	Gene variants associated with ischemic stroke: the cardiovascular health study. *Stroke*, **2009**, 40, 363-8	6.7	38
57	A meta-analysis of genome-wide association studies of asthma in Puerto Ricans. *European Respiratory Journal*, **2017**, 49,	13.6	36
56	Endogenous red blood cell membrane fatty acids and sudden cardiac arrest. *Metabolism: Clinical and Experimental*, **2010**, 59, 1029-34	12.7	36
55	Model-robust regression and a Bayesian sandwich estimator. *Annals of Applied Statistics*, **2010**, 4,	2.1	33
54	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. *PLoS ONE*, **2018**, 13, e0198166	3.7	31
53	Multi-ancestry sleep-by-SNP interaction analysis in 126,926 individuals reveals lipid loci stratified by sleep duration. *Nature Communications*, **2019**, 10, 5121	17.4	31
52	Generalized estimating equations for genome-wide association studies using longitudinal phenotype data. *Statistics in Medicine*, **2015**, 34, 118-30	2.3	31
51	Red blood cell membrane alpha-linolenic acid and the risk of sudden cardiac arrest. *Metabolism: Clinical and Experimental*, **2009**, 58, 534-40	12.7	31
50	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, 481-8	11	31

49	Multiancestry Study of Gene-Lifestyle Interactions for Cardiovascular Traits in 610 475 Individuals From 124 Cohorts: Design and Rationale. *Circulation: Cardiovascular Genetics*, **2017**, 10,		30
48	Genome-wide Trans-ethnic Meta-analysis Identifies Seven Genetic Loci Influencing Erythrocyte Traits and a Role for RBPMS in Erythropoiesis. *American Journal of Human Genetics*, **2017**, 100, 51-63	11	30
47	Equivalence Between Conditional and Random-Effects Likelihoods for Pair-Matched Case-Control Studies. *Journal of the American Statistical Association*, **2008**, 103, 385-396	2.8	29
46	Genome-wide profiling of blood pressure in adults and children. *Hypertension*, **2012**, 59, 241-7	8.5	28
45	Orthostatic hypotension and novel blood pressure-associated gene variants: Genetics of Postural Hemodynamics (GPH) Consortium. *European Heart Journal*, **2012**, 33, 2331-41	9.5	27
44	Discovery of Genetic Variation on Chromosome 5q22 Associated with Mortality in Heart Failure. *PLoS Genetics*, **2016**, 12, e1006034	6	26
43	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. *Nature Genetics*, **2020**, 52, 1314-1332	36.3	26
42	Exome-chip meta-analysis identifies novel loci associated with cardiac conduction, including ADAMTS6. *Genome Biology*, **2018**, 19, 87	18.3	25
41	Equivalence Between Conditional and Mixture Approaches to the Rasch Model and Matched Case-Control Studies, With Applications. *Journal of the American Statistical Association*, **2004**, 99, 510-522	2.8	25
40	Erythrocyte very long-chain saturated fatty acids associated with lower risk of incident sudden cardiac arrest. *Prostaglandins Leukotrienes and Essential Fatty Acids*, **2014**, 91, 149-53	2.8	23
39	Common variants in the CRP gene in relation to longevity and cause-specific mortality in older adults: the Cardiovascular Health Study. *Atherosclerosis*, **2008**, 197, 922-30	3.1	21
38	Common genetic variation in six lipid-related and statin-related genes, statin use and risk of incident nonfatal myocardial infarction and stroke. *Pharmacogenetics and Genomics*, **2008**, 18, 677-82	1.9	20
37	Full-likelihood approaches to misclassification of a binary exposure in matched case-control studies. *Statistics in Medicine*, **2003**, 22, 3177-94	2.3	19
36	Sugar-sweetened beverage intake associations with fasting glucose and insulin concentrations are not modified by selected genetic variants in a ChREBP-FGF21 pathway: a meta-analysis. *Diabetologia*, **2018**, 61, 317-330	10.3	17
35	Genetic and lifestyle risk factors for MRI-defined brain infarcts in a population-based setting. *Neurology*, **2019**,	6.5	17
34	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. *Nature Communications*, **2020**, 11, 2542	17.4	16
33	FastSKAT: Sequence kernel association tests for very large sets of markers. *Genetic Epidemiology*, **2018**, 42, 516-527	2.6	16
32	Strategies to design and analyze targeted sequencing data: cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium Targeted Sequencing Study. *Circulation: Cardiovascular Genetics*, **2014**, 7, 335-43		15

31	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	3.7	15
30	An Empirical Comparison of Joint and Stratified Frameworks for Studying G E Interactions: Systolic Blood Pressure and Smoking in the CHARGE Gene-Lifestyle Interactions Working Group. *Genetic Epidemiology*, **2016**, 40, 404-15	2.6	15
29	A multi-ancestry genome-wide study incorporating gene-smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. *Human Molecular Genetics*, **2019**, 28, 2615-2633	5.6	14
28	IL1B genetic variation and plasma C-reactive protein level among young adults: the CARDIA study. *Atherosclerosis*, **2009**, 202, 513-20	3.1	14
27	A Decision-Theoretic Formulation of Fisher Approach to Testing. *American Statistician*, **2010**, 64, 345-349	3	13
26	Common and Rare Coding Genetic Variation Underlying the Electrocardiographic PR Interval. *Circulation Genomic and Precision Medicine*, **2018**, 11, e002037	5.2	11
25	Exome Chip Analysis Identifies Low-Frequency and Rare Variants in MRPL38 for White Matter Hyperintensities on Brain Magnetic Resonance Imaging. *Stroke*, **2018**, 49, 1812-1819	6.7	10
24	The role of environmental heterogeneity in meta-analysis of gene-environment interactions with quantitative traits. *Genetic Epidemiology*, **2014**, 38, 416-29	2.6	10
23	Parent-of-Origin Effects of the APOB Gene on Adiposity in Young Adults. *PLoS Genetics*, **2015**, 11, e1005573	6	9
22	Misclassification in a matched case-control study with variable matching ratio: application to a study of c-erbB-2 overexpression and breast cancer. *Statistics in Medicine*, **2003**, 22, 2459-68	2.3	6
21	Knowing the signs: a direct and generalizable motivation of two-sided tests. *Journal of the Royal Statistical Society Series A: Statistics in Society*, **2020**, 183, 411-430	2.1	4
20	Genetic analysis of over one million people identifies 535 novel loci for blood pressure		4
19	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. *Molecular Psychiatry*, **2021**, 26, 2111-2125	15.1	3
18	Bayesian mixture modeling using a hybrid sampler with application to protein subfamily identification. *Biostatistics*, **2010**, 11, 18-33	3.7	3
17	Multi-ancestry genome-wide gene-sleep interactions identify novel loci for blood pressure. *Molecular Psychiatry*, **2021**,	15.1	3
16	Screening for interaction effects in gene expression data. *PLoS ONE*, **2017**, 12, e0173847	3.7	2
15	Discovering novel risk factors for venous thrombosis: a candidate-gene approach. *Thrombosis Research*, **2009**, 123 Suppl 4, S25-9	8.2	2
14	Genome-wide association study provides new insights into the genetic architecture and pathogenesis of heart failure		2

13	Nonclassical Monocytes (CD14dimCD16+) Are Associated With Carotid Intima-Media Thickness Progression for Men but Not Women: The Multi-Ethnic Study of Atherosclerosis-Brief Report. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2021**, 41, 1810-1817	9.4	2
12	Genome-wide gene-environment interactions on quantitative traits using family data. *European Journal of Human Genetics*, **2016**, 24, 1022-8	5.3	1
11	An Efficient Markov Chain Monte Carlo Method for Mixture Models by Neighborhood Pruning. *Journal of Computational and Graphical Statistics*, **2012**, 21, 197-216	1.4	1
10	On Bayesian analysis of misclassified data from a matched case-control study with a validation sub-study by Gordon J. Prescott and Paul H. Garthwaite. *Statistics in Medicine*, **2006**, 25, 537-9; author reply 539-40	2.3	1
9	FastSKAT: Sequence kernel association tests for very large sets of markers		1
8	Novel blood pressure locus and gene discovery using GWAS and expression datasets from blood and the kidney		1
7	Multi-ancestry analysis of gene-sleep interactions in 126,926 individuals identifies multiple novel blood lipid loci that contribute to our understanding of sleep-associated adverse blood lipid profile		1
6	Cholesterol Variability and Cranial Magnetic Resonance Imaging Findings in Older Adults: The Cardiovascular Health Study. *Stroke*, **2020**, 51, 69-74	6.7	1
5	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	3.7	1
4	The genomics of heart failure: design and rationale of the HERMES consortium. *ESC Heart Failure*, **2021**,	3.7	1
3	Expressing Regret: A Unified View of Credible Intervals. *American Statistician*,1-9	5	1
2	General Framework for Meta-Analysis of Haplotype Association Tests. *Genetic Epidemiology*, **2016**, 40, 244-52	2.6	
1	Accounting for population structure in genetic studies of cystic fibrosis. *Human Genetics and Genomics Advances*, **2022**, 100117	0.8	