

Anuj Goel

List of Articles by Year in descending order

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93

peer-reviewed
articles

26,724

peer-reviewed
citations

45905

50

peer-reviewed
h-index

137648

6.28

score

96

documents

29674

doc citations

51994

52

h-index

84440

citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic therapies for cardiomyopathy: survey of attitudes of the patient community for the CureHeart project. <i>European Journal of Human Genetics</i> , 2024, 32, 1045-1052.	3.0	8
2	Genome-Wide Analysis of Left Ventricular Maximum Wall Thickness in the UK Biobank Cohort Reveals a Shared Genetic Background With Hypertrophic Cardiomyopathy. <i>Circulation Genomic and Precision Medicine</i> , 2023, 16, .	2.9	18
3	Genetic architecture of spatial electrical biomarkers for cardiac arrhythmia and relationship with cardiovascular disease. <i>Nature Communications</i> , 2023, 14, .	13.7	15
4	Genetic Determinants of the Interventricular Septum Are Linked to Ventricular Septal Defects and Hypertrophic Cardiomyopathy. <i>Circulation Genomic and Precision Medicine</i> , 2023, 16, 207-215.	2.9	8
5	CWAS of random glucose in 476,326 individuals provide insights into diabetes pathophysiology, complications and treatment stratification. <i>Nature Genetics</i> , 2023, 55, 1448-1461.	25.2	87
6	Robust estimates of heritable coronary disease risk in individuals with type 2 diabetes. <i>Genetic Epidemiology</i> , 2022, 46, 51-62.	3.1	8
7	Discovery and systematic characterization of risk variants and genes for coronary artery disease in over a million participants. <i>Nature Genetics</i> , 2022, 54, 1803-1815.	25.2	646
8	Common genetic variants and modifiable risk factors underpin hypertrophic cardiomyopathy susceptibility and expressivity. <i>Nature Genetics</i> , 2021, 53, 135-142.	25.2	316
9	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. <i>Nature Communications</i> , 2021, 12, .	13.7	134
10	The trans-ancestral genomic architecture of glycemic traits. <i>Nature Genetics</i> , 2021, 53, 840-860.	25.2	671
11	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021, 600, 675-679.	37.9	891
12	Identifying small-effect genetic associations overlooked by the conventional fixed-effect model in a large-scale meta-analysis of coronary artery disease. <i>Bioinformatics</i> , 2020, 36, 552-557.	4.7	3
13	A key role for the novel coronary artery disease gene JCAD in atherosclerosis via shear stress mechanotransduction. <i>Cardiovascular Research</i> , 2020, 116, 1863-1874.	5.5	38
14	Genetic Predisposition to Coronary Artery Disease in Type 2 Diabetes Mellitus. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, .	2.9	10
15	Reevaluation of the South Asian MYBPC3 1725bp Intronic Deletion in Hypertrophic Cardiomyopathy. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, .	2.9	39
16	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019, 10, .	13.7	118
17	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. <i>American Journal of Epidemiology</i> , 2019, 188, 1033-1054.	3.3	113
18	Genetic variation in CADM2 as a link between psychological traits and obesity. <i>Scientific Reports</i> , 2019, 9, .	3.4	64

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19	A multi-ancestry genome-wide study incorporating gene-smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. <i>Human Molecular Genetics</i> , 2019, 28, 2615-2633.	2.9	44
20	Multi-ancestry genome-wide gene-smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. <i>Nature Genetics</i> , 2019, 51, 636-648.	25.2	134
21	Network analysis of coronary artery disease risk genes elucidates disease mechanisms and druggable targets. <i>Scientific Reports</i> , 2018, 8, .	3.4	46
22	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. <i>American Journal of Human Genetics</i> , 2018, 102, 375-400.	6.5	157
23	Neonatal MicroRNA Profile Determines Endothelial Function in Offspring of Hypertensive Pregnancies. <i>Hypertension</i> , 2018, 72, 937-945.	6.6	37
24	Differential Gene Expression in Macrophages From Human Atherosclerotic Plaques Shows Convergence on Pathways Implicated by Genome-Wide Association Study Risk Variants. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2018, 38, 2718-2730.	6.0	28
25	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. <i>Nature Genetics</i> , 2018, 50, 1412-1425.	25.2	1,327
26	Mutant Muscle LIM Protein C58G causes cardiomyopathy through protein depletion. <i>Journal of Molecular and Cellular Cardiology</i> , 2018, 121, 287-296.	3.8	33
27	Lack of genetic support for shared aetiology of Coronary Artery Disease and Late-onset Alzheimer's disease. <i>Scientific Reports</i> , 2018, 8, .	3.4	19
28	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. <i>PLoS ONE</i> , 2018, 13, e0198166.	2.3	117
29	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated With Coronary Artery Disease. <i>Journal of the American College of Cardiology</i> , 2017, 69, 823-836.	2.3	247
30	Loss of Cardioprotective Effects at the ADAMTS7 Locus as a Result of Gene-Smoking Interactions. <i>Circulation</i> , 2017, 135, 2336-2353.	18.1	60
31	A mouse-to-man candidate gene study identifies association of chronic otitis media with the loci TCIF1 and FBXO11. <i>Scientific Reports</i> , 2017, 7, .	3.4	24
32	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. <i>Hypertension</i> , 2017, 70, .	6.6	145
33	Association analyses based on false discovery rate implicate new loci for coronary artery disease. <i>Nature Genetics</i> , 2017, 49, 1385-1391.	25.2	695
34	Impact of common genetic determinants of Hemoglobin A1c on type 2 diabetes risk and diagnosis in ancestrally diverse populations: A transethnic genome-wide meta-analysis. <i>PLoS Medicine</i> , 2017, 14, e1002383.	8.0	408
35	Identification of a novel proinsulin-associated SNP and demonstration that proinsulin is unlikely to be a causal factor in subclinical vascular remodelling using Mendelian randomisation. <i>Atherosclerosis</i> , 2017, 266, 196-204.	1.5	3
36	Identifying systematic heterogeneity patterns in genetic association meta-analysis studies. <i>PLoS Genetics</i> , 2017, 13, e1006755.	3.2	22

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37	Coding Variation in ANGPTL4, LPL, and SVEP1 and the Risk of Coronary Disease. <i>New England Journal of Medicine</i> , 2016, 374, 1134-1144.	34.5	487
38	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. <i>Nature Communications</i> , 2016, 7, .	13.7	91
39	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. <i>Nature Genetics</i> , 2016, 48, 1171-1184.	25.2	415
40	No Association of Coronary Artery Disease with X-Chromosomal Variants in Comprehensive International Meta-Analysis. <i>Scientific Reports</i> , 2016, 6, .	3.4	31
41	Adult height, coronary heart disease and stroke: a multi-locus Mendelian randomization meta-analysis. <i>International Journal of Epidemiology</i> , 2016, 45, 1927-1937.	4.9	113
42	Causal Assessment of Serum Urate Levels in Cardiometabolic Diseases Through a Mendelian Randomization Study. <i>Journal of the American College of Cardiology</i> , 2016, 67, 407-416.	2.3	166
43	A meta-analysis of 120 246 individuals identifies 18 new loci for fibrinogen concentration. <i>Human Molecular Genetics</i> , 2016, 25, 358-370.	2.9	90
44	Rare and low-frequency variants and their association with plasma levels of fibrinogen, FVII, FVIII, and vWF. <i>Blood</i> , 2015, 126, e19-e29.	4.5	77
45	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. <i>PLoS Genetics</i> , 2015, 11, e1005378.	3.2	398
46	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015, 518, 187-196.	37.9	1,582
47	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206.	37.9	4,495
48	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. <i>Nature Communications</i> , 2015, 6, .	13.7	191
49	A comprehensive 1000 Genomes-based genome-wide association meta-analysis of coronary artery disease. <i>Nature Genetics</i> , 2015, 47, 1121-1130.	25.2	2,502
50	Modulation of Genetic Associations with Serum Urate Levels by Body-Mass-Index in Humans. <i>PLoS ONE</i> , 2015, 10, e0119752.	2.3	71
51	Analysis of the Role of Interleukin 6 Receptor Haplotypes in the Regulation of Circulating Levels of Inflammatory Biomarkers and Risk of Coronary Heart Disease. <i>PLoS ONE</i> , 2015, 10, e0119980.	2.3	23
52	No Evidence for Genome-Wide Interactions on Plasma Fibrinogen by Smoking, Alcohol Consumption and Body Mass Index: Results from Meta-Analyses of 80,607 Subjects. <i>PLoS ONE</i> , 2014, 9, e111156.	2.3	9
53	Human Genetic Evidence for Involvement of CD137 in Atherosclerosis. <i>Molecular Medicine</i> , 2014, 20, 456-465.	5.6	10
54	Distribution and Medical Impact of Loss-of-Function Variants in the Finnish Founder Population. <i>PLoS Genetics</i> , 2014, 10, e1004494.	3.2	392

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55	Gene-centric Meta-analysis in 87,736 Individuals of European Ancestry Identifies Multiple Blood-Pressure-Related Loci. <i>American Journal of Human Genetics</i> , 2014, 94, 349-360.	6.5	167
56	Association of Low-Frequency and Rare Coding-Sequence Variants with Blood Lipids and Coronary Heart Disease in 56,000 Whites and Blacks. <i>American Journal of Human Genetics</i> , 2014, 94, 223-232.	6.5	309
57	A Common LPA Null Allele Associates With Lower Lipoprotein(a) Levels and Coronary Artery Disease Risk. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2014, 34, 2095-2099.	6.0	58
58	Gene-Age Interactions in Blood Pressure Regulation: A Large-Scale Investigation with the CHARGE, Global BPgen, and ICBP Consortia. <i>American Journal of Human Genetics</i> , 2014, 95, 24-38.	6.5	126
59	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014, 46, 1173-1186.	25.2	1,972
60	LPA null mutation genotyping and qPCR analysis refine kringle isoform analysis of Lp(a) levels. <i>Atherosclerosis</i> , 2014, 232, e5.	1.5	1
61	Use of encode data to identify putative functional variants in coronary artery disease GWAS. <i>Atherosclerosis</i> , 2014, 237, e8.	1.5	0
62	Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction. <i>Nature</i> , 2014, 518, 102-106.	37.9	632
63	Meta-analysis of Gene-Level Associations for Rare Variants Based on Single-Variant Statistics. <i>American Journal of Human Genetics</i> , 2013, 93, 236-248.	6.5	65
64	Re: Rourke et al.: Clinical Spectrum of Presenting Signs and Symptoms of Anterior Urethral Stricture: Detailed Analysis of Single-institutional Cohort (<i>Urology</i> 2012;79:1163-1167). <i>Urology</i> , 2013, 81, 216.	1.4	0
65	Secretory Phospholipase A2-IIA and Cardiovascular Disease. <i>Journal of the American College of Cardiology</i> , 2013, 62, 1966-1976.	2.3	122
66	Association Between the Chromosome 9p21 Locus and Angiographic Coronary Artery Disease Burden. <i>Journal of the American College of Cardiology</i> , 2013, 61, 957-970.	2.3	59
67	Re: Elkoushy et al.: Pulsed Fluoroscopy in Ureteroscopy and Percutaneous Nephrolithotomy (<i>Urology</i>) Tj ETQq1 1 0.784314 μ gBT /Ov	1.4	1
68	Re: Hoy et al.: Expanded Use of Dorsal Onlay Augmented Anastomotic Urethroplasty With Buccal Mucosa for Long Segment Bulbar Urethral Strictures: Analysis of Outcomes and Complications (<i>Urology</i> 2013;81:1357-1361). <i>Urology</i> , 2013, 82, 1193.	1.4	1
69	Re: Palminteri et al.: Contemporary Urethral Stricture Characteristics in the Developed World (<i>Urology</i> 2013;81:191-197). <i>Urology</i> , 2013, 82, 495.	1.4	3
70	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. <i>PLoS Genetics</i> , 2013, 9, e1003500.	3.2	421
71	Exome Sequencing and Directed Clinical Phenotyping Diagnose Cholesterol Ester Storage Disease Presenting as Autosomal Recessive Hypercholesterolemia. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2013, 33, 2909-2914.	6.0	96
72	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. <i>Nature Genetics</i> , 2012, 44, 991-1005.	25.2	806

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73	Genome-wide association study identifies a variant in HDAC9 associated with large vessel ischemic stroke. <i>Nature Genetics</i> , 2012, 44, 328-333.	25.2	408
74	Re: Welk et al.: The Augmented Nontransected Anastomotic Urethroplasty for the Treatment of Bulbar Urethral Stricture (<i>Urology</i> 2012;79:917-921). <i>Urology</i> , 2012, 80, 959.	1.4	0
75	Re: Penbegul et al.: Safety and Efficacy of Ultrasound-Guided Percutaneous Nephrolithotomy of Urinary Stone Disease in Children (<i>Urology</i> 2012;79:1015-1019). <i>Urology</i> , 2012, 80, 956.	1.4	0
76	TGFB1 genetic polymorphisms and coronary heart disease risk: a meta-analysis. <i>BMC Medical Genetics</i> , 2012, 13, .	1.8	34
77	A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. <i>Nature Genetics</i> , 2012, 44, 659-669.	25.2	834
78	Large-scale association analysis identifies new risk loci for coronary artery disease. <i>Nature Genetics</i> , 2012, 45, 25-33.	25.2	1,567
79	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. <i>Nature</i> , 2011, 478, 103-109.	37.9	2,000
80	Genome-Wide Association Identifies Nine Common Variants Associated With Fasting Proinsulin Levels and Provides New Insights Into the Pathophysiology of Type 2 Diabetes. <i>Diabetes</i> , 2011, 60, 2624-2634.	4.2	356
81	Buccal Mucosal Graft Urethroplasty for Penile Stricture: Only Dorsal or Combined Dorsal and Ventral Graft Placement?. <i>Urology</i> , 2011, 77, 1482-1486.	1.4	12
82	Variants at the Endocannabinoid Receptor CB1 Gene (CNR1) and Insulin Sensitivity, Type 2 Diabetes, and Coronary Heart Disease. <i>Obesity</i> , 2011, 19, 2031-2037.	4.0	17
83	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. <i>Nature Genetics</i> , 2011, 43, 1005-1011.	25.2	424
84	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. <i>Nature Genetics</i> , 2010, 42, 937-948.	25.2	2,789
85	Common Variants at 10 Genomic Loci Influence Hemoglobin A1C Levels via Glycemic and Nonglycemic Pathways. <i>Diabetes</i> , 2010, 59, 3229-3239.	4.2	426
86	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. <i>Nature Genetics</i> , 2010, 42, 105-116.	25.2	2,112
87	Meatoplasty using double buccal mucosal graft technique. <i>International Urology and Nephrology</i> , 2009, 41, 885-887.	1.4	30
88	Genetic Variants Associated with Lp(a) Lipoprotein Level and Coronary Disease. <i>New England Journal of Medicine</i> , 2009, 361, 2518-2528.	34.5	1,504
89	Relationship between CAD Risk Genotype in the Chromosome 9p21 Locus and Gene Expression. Identification of Eight New ANRIL Splice Variants. <i>PLoS ONE</i> , 2009, 4, e7677.	2.3	155
90	Susceptibility to coronary artery disease and diabetes is encoded by distinct, tightly linked SNPs in the ANRIL locus on chromosome 9p. <i>Human Molecular Genetics</i> , 2008, 17, 806-814.	2.9	491

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91	Adrenal Gland Tumorigenesis after Gonadectomy in Mice Is a Complex Genetic Trait Driven by Epistatic Loci. <i>Endocrinology</i> , 2008, 149, 651-661.	2.5	47
92	eQTL Explorer: integrated mining of combined genetic linkage and expression experiments. <i>Bioinformatics</i> , 2006, 22, 509-511.	4.7	23
93	Title is missing!. <i>International Urology and Nephrology</i> , 2001, 33, 491-492.	1.4	7