

Anuj Goel

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/8285718/anuj-goel-publications-by-year.pdf>

Version: 2024-04-25

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

76
papers

21,861
citations

44
h-index

86
g-index

86
ext. papers

26,946
ext. citations

16.5
avg, IF

4.2
L-index

#	Paper	IF	Citations
76	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021 ,	50.4	24
75	Robust estimates of heritable coronary disease risk in individuals with type 2 diabetes. <i>Genetic Epidemiology</i> , 2021 ,	2.6	1
74	The trans-ancestral genomic architecture of glycemic traits. <i>Nature Genetics</i> , 2021 , 53, 840-860	36.3	44
73	Common genetic variants and modifiable risk factors underpin hypertrophic cardiomyopathy susceptibility and expressivity. <i>Nature Genetics</i> , 2021 , 53, 135-142	36.3	33
72	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. <i>Nature Communications</i> , 2021 , 12, 24	17.4	30
71	Reevaluation of the South Asian Intronic Deletion in Hypertrophic Cardiomyopathy. <i>Circulation Genomic and Precision Medicine</i> , 2020 , 13, e002783	5.2	14
70	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	7.2	
69	Genetic Predisposition to Coronary Artery Disease in Type 2 Diabetes Mellitus. <i>Circulation Genomic and Precision Medicine</i> , 2020 , 13, e002769	5.2	1
68	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	9.9	7
67	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. <i>American Journal of Epidemiology</i> , 2019 , 188, 1033-1054	3.8	39
66	Genetic variation in CADM2 as a link between psychological traits and obesity. <i>Scientific Reports</i> , 2019 , 9, 7339	4.9	18
65	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	5.6	14
64	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	36.3	59
63	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019 , 10, 4957	17.4	40
62	Manhattan++: displaying genome-wide association summary statistics with multiple annotation layers. <i>BMC Bioinformatics</i> , 2019 , 20, 610	3.6	3
61	Network analysis of coronary artery disease risk genes elucidates disease mechanisms and druggable targets. <i>Scientific Reports</i> , 2018 , 8, 3434	4.9	31
60	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	11	59

59	Mutant Muscle LIM Protein C58G causes cardiomyopathy through protein depletion. <i>Journal of Molecular and Cellular Cardiology</i> , 2018 , 121, 287-296	5.8	6
58	Lack of genetic support for shared aetiology of Coronary Artery Disease and Late-onset Alzheimer's disease. <i>Scientific Reports</i> , 2018 , 8, 7102	4.9	5
57	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	3.7	31
56	Neonatal Micro-RNA Profile Determines Endothelial Function in Offspring of Hypertensive Pregnancies. <i>Hypertension</i> , 2018 , 72, 937-945	8.5	16
55	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	9.4	14
54	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. <i>Nature Genetics</i> , 2018 , 50, 1412-1425	36.3	386
53	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	15.1	146
52	Loss of Cardioprotective Effects at the Locus as a Result of Gene-Smoking Interactions. <i>Circulation</i> , 2017 , 135, 2336-2353	16.7	36
51	A mouse-to-man candidate gene study identifies association of chronic otitis media with the loci TGIF1 and FBXO11. <i>Scientific Reports</i> , 2017 , 7, 12496	4.9	12
50	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	11.6	223
49	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 ,	8.5	85
48	Association analyses based on false discovery rate implicate new loci for coronary artery disease. <i>Nature Genetics</i> , 2017 , 49, 1385-1391	36.3	361
47	Identifying systematic heterogeneity patterns in genetic association meta-analysis studies. <i>PLoS Genetics</i> , 2017 , 13, e1006755	6	12
46	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	3.1	2
45	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. <i>Nature Communications</i> , 2016 , 7, 13357	17.4	46
44	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	36.3	251
43	No Association of Coronary Artery Disease with X-Chromosomal Variants in Comprehensive International Meta-Analysis. <i>Scientific Reports</i> , 2016 , 6, 35278	4.9	18
42	Adult height, coronary heart disease and stroke: a multi-locus Mendelian randomization meta-analysis. <i>International Journal of Epidemiology</i> , 2016 , 45, 1927-1937	7.8	65

41	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	15.1	101
40	A meta-analysis of 120 246 individuals identifies 18 new loci for fibrinogen concentration. <i>Human Molecular Genetics</i> , 2016 , 25, 358-70	5.6	54
39	Coding Variation in ANGPTL4, LPL, and SVEP1 and the Risk of Coronary Disease. <i>New England Journal of Medicine</i> , 2016 , 374, 1134-44	59.2	325
38	A comprehensive 1,000 Genomes-based genome-wide association meta-analysis of coronary artery disease. <i>Nature Genetics</i> , 2015 , 47, 1121-1130	36.3	1290
37	Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction. <i>Nature</i> , 2015 , 518, 102-6	50.4	463
36	Rare and low-frequency variants and their association with plasma levels of fibrinogen, FVII, FVIII, and vWF. <i>Blood</i> , 2015 , 126, e19-29	2.2	45
35	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	6	220
34	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015 , 518, 187-196	50.4	920
33	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015 , 518, 197-206	50.4	2687
32	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. <i>Nature Communications</i> , 2015 , 6, 5897	17.4	147
31	Modulation of genetic associations with serum urate levels by body-mass-index in humans. <i>PLoS ONE</i> , 2015 , 10, e0119752	3.7	31
30	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	3.7	17
29	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, 223-32	11	233
28	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, 2095-9	9.4	33
27	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	11	80
26	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014 , 46, 1173-86	36.3	1339
25	Meta-analysis of gene-level tests for rare variant association. <i>Nature Genetics</i> , 2014 , 46, 200-4	36.3	142
24	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	3.7	5

23	Human genetic evidence for involvement of CD137 in atherosclerosis. <i>Molecular Medicine</i> , 2014 , 20, 456-65	8	
22	Distribution and medical impact of loss-of-function variants in the Finnish founder population. <i>PLoS Genetics</i> , 2014 , 10, e1004494	6	243
21	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, 349-60	11	131
20	Excluded calyx following percutaneous nephrolithotomy: a rare complication. <i>Indian Journal of Surgery</i> , 2013 , 75, 56-8	0.3	3
19	Meta-analysis of gene-level associations for rare variants based on single-variant statistics. <i>American Journal of Human Genetics</i> , 2013 , 93, 236-48	11	49
18	Secretory phospholipase A(2)-IIA and cardiovascular disease: a mendelian randomization study. <i>Journal of the American College of Cardiology</i> , 2013 , 62, 1966-1976	15.1	91
17	Large-scale association analysis identifies new risk loci for coronary artery disease. <i>Nature Genetics</i> , 2013 , 45, 25-33	36.3	1172
16	Association between the chromosome 9p21 locus and angiographic coronary artery disease burden: a collaborative meta-analysis. <i>Journal of the American College of Cardiology</i> , 2013 , 61, 957-70	15.1	56
15	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	6	277
14	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, 2909-14	9.4	76
13	Genome-wide association study identifies a variant in HDAC9 associated with large vessel ischemic stroke. <i>Nature Genetics</i> , 2012 , 44, 328-33	36.3	314
12	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, 659-69	36.3	615
11	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	36.3	621
10	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. <i>Nature</i> , 2011 , 478, 103-9	50.4	1564
9	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, 2624-34	0.9	285
8	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. <i>Nature Genetics</i> , 2011 , 43, 1005-11	36.3	338
7	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. <i>Nature Genetics</i> , 2010 , 42, 937-48	36.3	2267
6	Common variants at 10 genomic loci influence hemoglobin A1C levels via glycemic and nonglycemic pathways. <i>Diabetes</i> , 2010 , 59, 3229-39	0.9	314

5	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. <i>Nature Genetics</i> , 2010 , 42, 105-16	36.3	1673
4	Genetic variants associated with Lp(a) lipoprotein level and coronary disease. <i>New England Journal of Medicine</i> , 2009 , 361, 2518-28	59.2	935
3	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	3.7	125
2	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, 806-14	5.6	420
1	Discovery and systematic characterization of risk variants and genes for coronary artery disease in over a million participants		5