

Anuj Goel

List of Publications by Citations

Source: <https://exaly.com/author-pdf/8285718/anuj-goel-publications-by-citations.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	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015 , 518, 197-206	50.4	2687
75	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
74	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
73	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. <i>Nature</i> , 2011 , 478, 103-9	50.4	1564
72	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
71	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
70	Large-scale association analysis identifies new risk loci for coronary artery disease. <i>Nature Genetics</i> , 2013 , 45, 25-33	36.3	1172
69	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
68	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015 , 518, 187-196	50.4	920
67	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
66	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
65	Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction. <i>Nature</i> , 2015 , 518, 102-6	50.4	463
64	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
63	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
62	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
61	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
60	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

59	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
58	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
57	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
56	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
55	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
54	Distribution and medical impact of loss-of-function variants in the Finnish founder population. <i>PLoS Genetics</i> , 2014 , 10, e1004494	6	243
53	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
52	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
51	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
50	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
49	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
48	Meta-analysis of gene-level tests for rare variant association. <i>Nature Genetics</i> , 2014 , 46, 200-4	36.3	142
47	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
46	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
45	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
44	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
43	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
42	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

41	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
40	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
39	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
38	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
37	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
36	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
35	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
34	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
33	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
32	The trans-ancestral genomic architecture of glycemic traits. <i>Nature Genetics</i> , 2021 , 53, 840-860	36.3	44
31	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019 , 10, 4957	17.4	40
30	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
29	Loss of Cardioprotective Effects at the Locus as a Result of Gene-Smoking Interactions. <i>Circulation</i> , 2017 , 135, 2336-2353	16.7	36
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	Common genetic variants and modifiable risk factors underpin hypertrophic cardiomyopathy susceptibility and expressivity. <i>Nature Genetics</i> , 2021 , 53, 135-142	36.3	33
26	Network analysis of coronary artery disease risk genes elucidates disease mechanisms and druggable targets. <i>Scientific Reports</i> , 2018 , 8, 3434	4.9	31
25	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
24	Modulation of genetic associations with serum urate levels by body-mass-index in humans. <i>PLoS ONE</i> , 2015 , 10, e0119752	3.7	31

23	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. <i>Nature Communications</i> , 2021 , 12, 24	17.4	30
22	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021 ,	50.4	24
21	Genetic variation in CADM2 as a link between psychological traits and obesity. <i>Scientific Reports</i> , 2019 , 9, 7339	4.9	18
20	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
19	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
18	Neonatal Micro-RNA Profile Determines Endothelial Function in Offspring of Hypertensive Pregnancies. <i>Hypertension</i> , 2018 , 72, 937-945	8.5	16
17	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
16	Reevaluation of the South Asian Intronic Deletion in Hypertrophic Cardiomyopathy. <i>Circulation Genomic and Precision Medicine</i> , 2020 , 13, e002783	5.2	14
15	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
14	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
13	Identifying systematic heterogeneity patterns in genetic association meta-analysis studies. <i>PLoS Genetics</i> , 2017 , 13, e1006755	6	12
12	Human genetic evidence for involvement of CD137 in atherosclerosis. <i>Molecular Medicine</i> , 2014 , 20, 456-465	6.5	8
11	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
10	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
9	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
8	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
7	Discovery and systematic characterization of risk variants and genes for coronary artery disease in over a million participants		5
6	Excluded calyx following percutaneous nephrolithotomy: a rare complication. <i>Indian Journal of Surgery</i> , 2013 , 75, 56-8	0.3	3

5	Manhattan++: displaying genome-wide association summary statistics with multiple annotation layers. <i>BMC Bioinformatics</i> , 2019 , 20, 610	3.6	3
4	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
3	Robust estimates of heritable coronary disease risk in individuals with type 2 diabetes. <i>Genetic Epidemiology</i> , 2021 ,	2.6	1
2	Genetic Predisposition to Coronary Artery Disease in Type 2 Diabetes Mellitus. <i>Circulation Genomic and Precision Medicine</i> , 2020 , 13, e002769	5.2	1
1	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	