

Danish Saleheen

List of Publications by Citations

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

98
papers

31,508
citations

55
h-index

107
g-index

107
ext. papers

41,598
ext. citations

23.4
avg, IF

5.18
L-index

#	Paper	IF	Citations
98	Analysis of protein-coding genetic variation in 60,706 humans. <i>Nature</i> , 2016 , 536, 285-91	50.4	6940
97	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015 , 518, 197-206	50.4	2687
96	The mutational constraint spectrum quantified from variation in 141,456 humans. <i>Nature</i> , 2020 , 581, 434-443	50.4	2278
95	Discovery and refinement of loci associated with lipid levels. <i>Nature Genetics</i> , 2013 , 45, 1274-1283	36.3	1904
94	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. <i>Nature Genetics</i> , 2012 , 44, 981-90	36.3	1482
93	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
92	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
91	Large-scale association analysis identifies new risk loci for coronary artery disease. <i>Nature Genetics</i> , 2013 , 45, 25-33	36.3	1172
90	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015 , 518, 187-196	50.4	920
89	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. <i>Nature Genetics</i> , 2014 , 46, 234-44	36.3	784
88	The genetic architecture of type 2 diabetes. <i>Nature</i> , 2016 , 536, 41-47	50.4	704
87	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. <i>Nature Genetics</i> , 2018 , 50, 524-537	36.3	536
86	Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction. <i>Nature</i> , 2015 , 518, 102-6	50.4	463
85	Diagnostic Yield and Clinical Utility of Sequencing Familial Hypercholesterolemia Genes in Patients With Severe Hypercholesterolemia. <i>Journal of the American College of Cardiology</i> , 2016 , 67, 2578-89	15.1	458
84	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017 , 542, 186-190	50.4	412
83	Genome-wide association study in individuals of South Asian ancestry identifies six new type 2 diabetes susceptibility loci. <i>Nature Genetics</i> , 2011 , 43, 984-9	36.3	406
82	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. <i>Science</i> , 2016 , 351, 1166-71	33.3	325

81	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
80	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. <i>Nature Genetics</i> , 2017 , 49, 403-415	36.3	313
79	Exome-wide association study of plasma lipids in >300,000 individuals. <i>Nature Genetics</i> , 2017 , 49, 1758-1766	36.3	310
78	Inactivating mutations in NPC1L1 and protection from coronary heart disease. <i>New England Journal of Medicine</i> , 2014 , 371, 2072-82	59.2	307
77	Association of HDL cholesterol efflux capacity with incident coronary heart disease events: a prospective case-control study. <i>Lancet Diabetes and Endocrinology</i> , 2015 , 3, 507-13	18.1	300
76	Epigenome-wide association of DNA methylation markers in peripheral blood from Indian Asians and Europeans with incident type 2 diabetes: a nested case-control study. <i>Lancet Diabetes and Endocrinology</i> , 2015 , 3, 526-534	18.1	277
75	Genetics of blood lipids among ~300,000 multi-ethnic participants of the Million Veteran Program. <i>Nature Genetics</i> , 2018 , 50, 1514-1523	36.3	260
74	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
73	Association of LPA Variants With Risk of Coronary Disease and the Implications for Lipoprotein(a)-Lowering Therapies: A Mendelian Randomization Analysis. <i>JAMA Cardiology</i> , 2018 , 3, 619-627	16.2	235
72	ANGPTL3 Deficiency and Protection Against Coronary Artery Disease. <i>Journal of the American College of Cardiology</i> , 2017 , 69, 2054-2063	15.1	226
71	Trans-ancestry genome-wide association study identifies 12 genetic loci influencing blood pressure and implicates a role for DNA methylation. <i>Nature Genetics</i> , 2015 , 47, 1282-1293	36.3	223
70	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
69	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. <i>Nature Genetics</i> , 2018 , 50, 559-571	36.3	221
68	Human knockouts and phenotypic analysis in a cohort with a high rate of consanguinity. <i>Nature</i> , 2017 , 544, 235-239	50.4	208
67	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. <i>Nature Genetics</i> , 2018 , 50, 26-41	36.3	186
66	Fifteen new risk loci for coronary artery disease highlight arterial-wall-specific mechanisms. <i>Nature Genetics</i> , 2017 , 49, 1113-1119	36.3	184
65	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. <i>Nature Genetics</i> , 2016 , 48, 1151-1161	36.3	181
64	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. <i>Molecular Psychiatry</i> , 2015 , 20, 647-656	15.1	167

63	Loci associated with ischaemic stroke and its subtypes (SiGN): a genome-wide association study. <i>Lancet Neurology, The</i> , 2016 , 15, 174-184	24.1	159
62	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
61	Discovery of 318 new risk loci for type 2 diabetes and related vascular outcomes among 1.4 million participants in a multi-ancestry meta-analysis. <i>Nature Genetics</i> , 2020 , 52, 680-691	36.3	140
60	Cholesterol ester transfer protein inhibition by TA-8995 in patients with mild dyslipidaemia (TULIP): a randomised, double-blind, placebo-controlled phase 2 trial. <i>Lancet, The</i> , 2015 , 386, 452-60	40	140
59	Identification of new susceptibility loci for type 2 diabetes and shared etiological pathways with coronary heart disease. <i>Nature Genetics</i> , 2017 , 49, 1450-1457	36.3	136
58	Exome sequencing of 20,791 cases of type 2 diabetes and 24,440 controls. <i>Nature</i> , 2019 , 570, 71-76	50.4	129
57	Genome-wide association study identifies a novel locus contributing to type 2 diabetes susceptibility in Sikhs of Punjabi origin from India. <i>Diabetes</i> , 2013 , 62, 1746-55	0.9	129
56	Phenotypic Characterization of Genetically Lowered Human Lipoprotein(a) Levels. <i>Journal of the American College of Cardiology</i> , 2016 , 68, 2761-2772	15.1	127
55	Genetic Interleukin 6 Signaling Deficiency Attenuates Cardiovascular Risk in Clonal Hematopoiesis. <i>Circulation</i> , 2020 , 141, 124-131	16.7	120
54	Apolipoprotein(a) isoform size, lipoprotein(a) concentration, and coronary artery disease: a mendelian randomisation analysis. <i>Lancet Diabetes and Endocrinology, the</i> , 2017 , 5, 524-533	18.1	111
53	Association of Rare and Common Variation in the Lipoprotein Lipase Gene With Coronary Artery Disease. <i>JAMA - Journal of the American Medical Association</i> , 2017 , 317, 937-946	27.4	109
52	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
51	Genome-wide association studies in the Japanese population identify seven novel loci for type 2 diabetes. <i>Nature Communications</i> , 2016 , 7, 10531	17.4	99
50	Low-frequency and common genetic variation in ischemic stroke: The METASTROKE collaboration. <i>Neurology</i> , 2016 , 86, 1217-26	6.5	98
49	Loss of Function of GALNT2 Lowers High-Density Lipoproteins in Humans, Nonhuman Primates, and Rodents. <i>Cell Metabolism</i> , 2016 , 24, 234-45	24.6	78
48	A genomic approach to therapeutic target validation identifies a glucose-lowering GLP1R variant protective for coronary heart disease. <i>Science Translational Medicine</i> , 2016 , 8, 341ra76	17.5	77
47	Genome-wide association study of peripheral artery disease in the Million Veteran Program. <i>Nature Medicine</i> , 2019 , 25, 1274-1279	50.5	73
46	The Pakistan Risk of Myocardial Infarction Study: a resource for the study of genetic, lifestyle and other determinants of myocardial infarction in South Asia. <i>European Journal of Epidemiology</i> , 2009 , 24, 329-38	12.1	67

45	A novel MMP12 locus is associated with large artery atherosclerotic stroke using a genome-wide age-at-onset informed approach. <i>PLoS Genetics</i> , 2014 , 10, e1004469	6	63
44	Analysis of predicted loss-of-function variants in UK Biobank identifies variants protective for disease. <i>Nature Communications</i> , 2018 , 9, 1613	17.4	55
43	Evaluating drug targets through human loss-of-function genetic variation. <i>Nature</i> , 2020 , 581, 459-464	50.4	53
42	Phenotypic Consequences of a Genetic Predisposition to Enhanced Nitric Oxide Signaling. <i>Circulation</i> , 2018 , 137, 222-232	16.7	53
41	Genetic variation at 16q24.2 is associated with small vessel stroke. <i>Annals of Neurology</i> , 2017 , 81, 383-394	9.4	51
40	A missense variant in Mitochondrial Amidoxime Reducing Component 1 gene and protection against liver disease. <i>PLoS Genetics</i> , 2020 , 16, e1008629	6	49
39	The effect of LRRK2 loss-of-function variants in humans. <i>Nature Medicine</i> , 2020 , 26, 869-877	50.5	47
38	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. <i>Molecular Psychiatry</i> , 2020 , 25, 2392-2409	15.1	45
37	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. <i>Nature Genetics</i> , 2019 , 51, 452-469	36.3	44
36	Loss of Cardioprotective Effects at the Locus as a Result of Gene-Smoking Interactions. <i>Circulation</i> , 2017 , 135, 2336-2353	16.7	36
35	From Loci to Biology: Functional Genomics of Genome-Wide Association for Coronary Disease. <i>Circulation Research</i> , 2016 , 118, 586-606	15.7	36
34	CXCL12 Derived From Endothelial Cells Promotes Atherosclerosis to Drive Coronary Artery Disease. <i>Circulation</i> , 2019 , 139, 1338-1340	16.7	35
33	New Blood Pressure-Associated Loci Identified in Meta-Analyses of 475 000 Individuals. <i>Circulation: Cardiovascular Genetics</i> , 2017 , 10,		33
32	Lipoprotein(a) and Risk of Myocardial Infarction and Death in Chronic Kidney Disease: Findings From the CRIC Study (Chronic Renal Insufficiency Cohort). <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2017 , 37, 1971-1978	9.4	31
31	Rare Protein-Truncating Variants in APOB, Lower Low-Density Lipoprotein Cholesterol, and Protection Against Coronary Heart Disease. <i>Circulation Genomic and Precision Medicine</i> , 2019 , 12, e002376	5.2	30
30	Common coding variant in increases the risk for large artery stroke. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 3613-3618	11.5	28
29	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. <i>Nature Genetics</i> , 2020 , 52, 1314-1332	36.3	26
28	Systolic Blood Pressure and Risk of Type 2 Diabetes: A Mendelian Randomization Study. <i>Diabetes</i> , 2017 , 66, 543-550	0.9	22

27	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. <i>Scientific Data</i> , 2017 , 4, 170179	8.2	22
26	Physical activity, smoking, and genetic predisposition to obesity in people from Pakistan: the PROMIS study. <i>BMC Medical Genetics</i> , 2015 , 16, 114	2.1	21
25	Heterozygous Gene Deficiency and Risk of Coronary Artery Disease. <i>Circulation Genomic and Precision Medicine</i> , 2020 , 13, 417-423	5.2	21
24	Transancestral fine-mapping of four type 2 diabetes susceptibility loci highlights potential causal regulatory mechanisms. <i>Human Molecular Genetics</i> , 2016 , 25, 2070-2081	5.6	20
23	Epidemiology and public health policy of tobacco use and cardiovascular disorders in low- and middle-income countries. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2014 , 34, 1811-9	9.4	15
22	Common and Rare Genetic Variation in CCR2, CCR5, or CX3CR1 and Risk of Atherosclerotic Coronary Heart Disease and Glucometabolic Traits. <i>Circulation: Cardiovascular Genetics</i> , 2016 , 9, 250-8		14
21	Discovery of 318 novel loci for type-2 diabetes and related micro- and macrovascular outcomes among 1.4 million participants in a multi-ethnic meta-analysis		13
20	DNA Sequence Variation in Encoding the Activin Receptor-Like Kinase 7 Influences Body Fat Distribution and Protects Against Type 2 Diabetes. <i>Diabetes</i> , 2019 , 68, 226-234	0.9	12
19	Deficiency of macrophage PHACTR1 impairs efferocytosis and promotes atherosclerotic plaque necrosis. <i>Journal of Clinical Investigation</i> , 2021 , 131,	15.9	10
18	Human loss-of-function variants suggest that partial LRRK2 inhibition is a safe therapeutic strategy for Parkinson's disease		7
17	Genetic analysis in European ancestry individuals identifies 517 loci associated with liver enzymes. <i>Nature Communications</i> , 2021 , 12, 2579	17.4	7
16	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation.. <i>Nature Genetics</i> , 2022 ,	36.3	7
15	Frequency and determinants of intracranial atherosclerotic stroke in urban Pakistan. <i>Journal of Stroke and Cerebrovascular Diseases</i> , 2014 , 23, 2174-2182	2.8	6
14	Validating a non-invasive, ALT-based non-alcoholic fatty liver phenotype in the million veteran program. <i>PLoS ONE</i> , 2020 , 15, e0237430	3.7	5
13	Determinants of penetrance and variable expressivity in monogenic metabolic conditions across 77,184 exomes. <i>Nature Communications</i> , 2021 , 12, 3505	17.4	5
12	A trans-ancestry genome-wide association study of unexplained chronic ALT elevation as a proxy for nonalcoholic fatty liver disease with histological and radiological validation		5
11	Using Mendelian Randomization studies to Assess Causality and Identify New Therapeutic Targets in Cardiovascular Medicine. <i>Current Genetic Medicine Reports</i> , 2016 , 4, 207-212	2.2	4
10	A missense variant in Mitochondrial Amidoxime Reducing Component 1 gene and protection against liver disease		4

9	Tissue-Specific Alteration of Metabolic Pathways Influences Glycemic Regulation		4
8	Genome-wide analysis of blood lipid metabolites in over 5000 South Asians reveals biological insights at cardiometabolic disease loci. <i>BMC Medicine</i> , 2021 , 19, 232	11.4	3
7	Genetic discovery and translational decision support from exome sequencing of 20,791 type 2 diabetes cases and 24,440 controls from five ancestries		2
6	Identification of genetic effects underlying type 2 diabetes in South Asian and European populations.. <i>Communications Biology</i> , 2022 , 5, 329	6.7	2
5	A multiancestry genome-wide association study of unexplained chronic ALT elevation as a proxy for nonalcoholic fatty liver disease with histological and radiological validation. <i>Nature Genetics</i> ,	36.3	2
4	Genome-wide analysis of blood lipid metabolites in over 5,000 South Asians reveals biological insights at cardiometabolic disease loci		1
3	Genetic Predisposition to Coronary Artery Disease in Type 2 Diabetes Mellitus. <i>Circulation Genomic and Precision Medicine</i> , 2020 , 13, e002769	5.2	1
2	FP526VASCULAR CXCR4 LIMITS ATHEROSCLEROSIS BY MAINTAINING ARTERIAL INTEGRITY. <i>Nephrology Dialysis Transplantation</i> , 2018 , 33, i216-i216	4.3	1
1	Analyzing human knockouts to validate GPR151 as a therapeutic target for reduction of body mass index.. <i>PLoS Genetics</i> , 2022 , 18, e1010093	6	0