

Danish Saleheen

List of Publications by Year in descending order

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Version: 2024-02-01

92
papers

47,808
citations

17405

63
h-index

39575

94
g-index

107
all docs

107
docs citations

107
times ranked

64405
citing authors

#	ARTICLE	IF	CITATIONS
1	Analyzing human knockouts to validate GPR151 as a therapeutic target for reduction of body mass index. <i>PLoS Genetics</i> , 2022, 18, e1010093.	1.5	1
2	Identification of genetic effects underlying type 2 diabetes in South Asian and European populations. <i>Communications Biology</i> , 2022, 5, 329.	2.0	21
3	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. <i>Nature Genetics</i> , 2022, 54, 560-572.	9.4	250
4	A multi-ancestry 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> , 2022, 54, 761-771.	9.4	68
5	Deficiency of macrophage PHACTR1 impairs efferocytosis and promotes atherosclerotic plaque necrosis. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	31
6	Genetic analysis in European ancestry individuals identifies 517 loci associated with liver enzymes. <i>Nature Communications</i> , 2021, 12, 2579.	5.8	51
7	Determinants of penetrance and variable expressivity in monogenic metabolic conditions across 77,184 exomes. <i>Nature Communications</i> , 2021, 12, 3505.	5.8	49
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.	2.3	25
9	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. <i>Molecular Psychiatry</i> , 2020, 25, 2392-2409.	4.1	83
10	Genetic Interleukin 6 Signaling Deficiency Attenuates Cardiovascular Risk in Clonal Hematopoiesis. <i>Circulation</i> , 2020, 141, 124-131.	1.6	270
11	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.	9.4	91
12	Heterozygous <i>ABCG5</i> Gene Deficiency and Risk of Coronary Artery Disease. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, 417-423.	1.6	45
13	Validating a non-invasive, ALT-based non-alcoholic fatty liver phenotype in the million veteran program. <i>PLoS ONE</i> , 2020, 15, e0237430.	1.1	15
14	Genetic Predisposition to Coronary Artery Disease in Type 2 Diabetes Mellitus. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, e002769.	1.6	5
15	Evaluating drug targets through human loss-of-function genetic variation. <i>Nature</i> , 2020, 581, 459-464.	13.7	115
16	The mutational constraint spectrum quantified from variation in 141,456 humans. <i>Nature</i> , 2020, 581, 434-443.	13.7	6,140
17	The effect of <i>LRRK2</i> loss-of-function variants in humans. <i>Nature Medicine</i> , 2020, 26, 869-877.	15.2	79
18	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.	9.4	445

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19	A missense variant in Mitochondrial Amidoxime Reducing Component 1 gene and protection against liver disease. PLoS Genetics, 2020, 16, e1008629.	1.5	101
20	Genome-wide association study of peripheral artery disease in the Million Veteran Program. Nature Medicine, 2019, 25, 1274-1279.	15.2	177
21	Exome sequencing of 20,791 cases of type 2 diabetes and 24,440 controls. Nature, 2019, 570, 71-76.	13.7	248
22	Rare Protein-Truncating Variants in <i>APOB</i> , Lower Low-Density Lipoprotein Cholesterol, and Protection Against Coronary Heart Disease. Circulation Genomic and Precision Medicine, 2019, 12, e002376.	1.6	57
23	CXCL12 Derived From Endothelial Cells Promotes Atherosclerosis to Drive Coronary Artery Disease. Circulation, 2019, 139, 1338-1340.	1.6	62
24	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	9.4	89
25	DNA Sequence Variation in <i>ACVR1C</i> Encoding the Activin Receptor-Like Kinase 7 Influences Body Fat Distribution and Protects Against Type 2 Diabetes. Diabetes, 2019, 68, 226-234.	0.3	31
26	Analysis of predicted loss-of-function variants in UK Biobank identifies variants protective for disease. Nature Communications, 2018, 9, 1613.	5.8	78
27	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. Nature Genetics, 2018, 50, 559-571.	9.4	356
28	Phenotypic Consequences of a Genetic Predisposition to Enhanced Nitric Oxide Signaling. Circulation, 2018, 137, 222-232.	1.6	87
29	FP526VASCULAR CXCR4 LIMITS ATHEROSCLEROSIS BY MAINTAINING ARTERIAL INTEGRITY. Nephrology Dialysis Transplantation, 2018, 33, i216-i216.	0.4	1
30	Genetics of blood lipids among ~300,000 multi-ethnic participants of the Million Veteran Program. Nature Genetics, 2018, 50, 1514-1523.	9.4	497
31	Association of <i>LPA</i> Variants With Risk of Coronary Disease and the Implications for Lipoprotein(a)-Lowering Therapies. JAMA Cardiology, 2018, 3, 619.	3.0	428
32	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	9.4	286
33	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. Nature Genetics, 2018, 50, 524-537.	9.4	1,124
34	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. Nature Genetics, 2017, 49, 403-415.	9.4	492
35	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	13.7	544
36	Association of Rare and Common Variation in the Lipoprotein Lipase Gene With Coronary Artery Disease. JAMA - Journal of the American Medical Association, 2017, 317, 937.	3.8	148

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37	Common coding variant in <i>SERPINA1</i> increases the risk for large artery stroke. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 3613-3618.	3.3	46
38	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated With Coronary Artery Disease. Journal of the American College of Cardiology, 2017, 69, 823-836.	1.2	214
39	Apolipoprotein(a) isoform size, lipoprotein(a) concentration, and coronary artery disease: a mendelian randomisation analysis. Lancet Diabetes and Endocrinology, 2017, 5, 524-533.	5.5	165
40	Human knockouts and phenotypic analysis in a cohort with a high rate of consanguinity. Nature, 2017, 544, 235-239.	13.7	292
41	Loss of Cardioprotective Effects at the <i>ADAMTS7</i> Locus as a Result of Gene-Smoking Interactions. Circulation, 2017, 135, 2336-2353.	1.6	51
42	Fifteen new risk loci for coronary artery disease highlight arterial-wall-specific mechanisms. Nature Genetics, 2017, 49, 1113-1119.	9.4	260
43	ANGPTL3 Deficiency and Protection Against Coronary Artery Disease. Journal of the American College of Cardiology, 2017, 69, 2054-2063.	1.2	348
44	Genetic variation at 16q24.2 is associated with small vessel stroke. Annals of Neurology, 2017, 81, 383-394.	2.8	73
45	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	9.4	470
46	New Blood Pressure-Associated Loci Identified in Meta-Analyses of 475,000 Individuals. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	48
47	Lipoprotein(a) and Risk of Myocardial Infarction and Death in Chronic Kidney Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2017, 37, 1971-1978.	1.1	44
48	Systolic Blood Pressure and Risk of Type 2 Diabetes: A Mendelian Randomization Study. Diabetes, 2017, 66, 543-550.	0.3	45
49	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	2.4	31
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. PLoS Medicine, 2017, 14, e1002383.	3.9	341
51	Identification of new susceptibility loci for type 2 diabetes and shared etiological pathways with coronary heart disease. Nature Genetics, 2017, 49, 1450-1457.	9.4	218
52	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	13.7	952
53	Phenotypic Characterization of Genetically Lowered Human Lipoprotein(a) Levels. Journal of the American College of Cardiology, 2016, 68, 2761-2772.	1.2	186
54	Diagnostic Yield and Clinical Utility of Sequencing Familial Hypercholesterolemia Genes in Patients With Severe Hypercholesterolemia. Journal of the American College of Cardiology, 2016, 67, 2578-2589.	1.2	723

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55	Common and Rare Genetic Variation in <i>CCR2</i> , <i>CCR5</i> , or <i>CX3CR1</i> and Risk of Atherosclerotic Coronary Heart Disease and Glucometabolic Traits. <i>Circulation: Cardiovascular Genetics</i> , 2016, 9, 250-258.	5.1	20
56	Coding Variation in <i>ANGPTL4</i> , <i>LPL</i> and <i>SVEP1</i> and the Risk of Coronary Disease. <i>New England Journal of Medicine</i> , 2016, 374, 1134-1144.	13.9	427
57	Low-frequency and common genetic variation in ischemic stroke. <i>Neurology</i> , 2016, 86, 1217-1226.	1.5	141
58	Disentangling the Causal Association of Plasma Lipid Traits and Type 2 Diabetes Using Human Genetics. <i>JAMA Cardiology</i> , 2016, 1, 631.	3.0	3
59	Loss of Function of <i>GALNT2</i> Lowers High-Density Lipoproteins in Humans, Nonhuman Primates, and Rodents. <i>Cell Metabolism</i> , 2016, 24, 234-245.	7.2	103
60	Analysis of protein-coding genetic variation in 60,706 humans. <i>Nature</i> , 2016, 536, 285-291.	13.7	9,051
61	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. <i>Nature Genetics</i> , 2016, 48, 1151-1161.	9.4	261
62	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.	9.4	362
63	A genomic approach to therapeutic target validation identifies a glucose-lowering <i>GLP1R</i> variant protective for coronary heart disease. <i>Science Translational Medicine</i> , 2016, 8, 341ra76.	5.8	100
64	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.	1.9	4
65	Genome-wide association studies in the Japanese population identify seven novel loci for type 2 diabetes. <i>Nature Communications</i> , 2016, 7, 10531.	5.8	149
66	Loci associated with ischaemic stroke and its subtypes (SiGN): a genome-wide association study. <i>Lancet Neurology</i> , The, 2016, 15, 174-184.	4.9	217
67	Rare variant in scavenger receptor <i>BI</i> raises HDL cholesterol and increases risk of coronary heart disease. <i>Science</i> , 2016, 351, 1166-1171.	6.0	438
68	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.	1.2	138
69	From Loci to Biology. <i>Circulation Research</i> , 2016, 118, 586-606.	2.0	54
70	Transancestral fine-mapping of four type 2 diabetes susceptibility loci highlights potential causal regulatory mechanisms. <i>Human Molecular Genetics</i> , 2016, 25, 2070-2081.	1.4	21
71	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	27
72	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</i> , The, 2015, 386, 452-460.	6.3	173

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73	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, 507-513.	5.5	389
74	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015, 518, 187-196.	13.7	1,328
75	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206.	13.7	3,823
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.	5.5	396
77	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.	9.4	294
78	A comprehensive 1000 Genomes-based genome-wide association meta-analysis of coronary artery disease. <i>Nature Genetics</i> , 2015, 47, 1121-1130.	9.4	2,054
79	Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction. <i>Nature</i> , 2015, 518, 102-106.	13.7	581
80	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. <i>Molecular Psychiatry</i> , 2015, 20, 647-656.	4.1	235
81	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.	1.5	75
82	Inactivating Mutations in <i>NPC1L1</i> and Protection from Coronary Heart Disease. <i>New England Journal of Medicine</i> , 2014, 371, 2072-2082.	13.9	386
83	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, 1811-1819.	1.1	20
84	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014, 46, 1173-1186.	9.4	1,818
85	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. <i>Nature Genetics</i> , 2014, 46, 234-244.	9.4	959
86	Frequency and Determinants of Intracranial Atherosclerotic Stroke in Urban Pakistan. <i>Journal of Stroke and Cerebrovascular Diseases</i> , 2014, 23, 2174-2182.	0.7	6
87	Discovery and refinement of loci associated with lipid levels. <i>Nature Genetics</i> , 2013, 45, 1274-1283.	9.4	2,641
88	Large-scale association analysis identifies new risk loci for coronary artery disease. <i>Nature Genetics</i> , 2013, 45, 25-33.	9.4	1,439
89	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, 1746-1755.	0.3	167
90	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. <i>Nature Genetics</i> , 2012, 44, 981-990.	9.4	1,748

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91	Genome-wide association study in individuals of South Asian ancestry identifies six new type 2 diabetes susceptibility loci. <i>Nature Genetics</i> , 2011, 43, 984-989.	9.4	481
92	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, 329-338.	2.5	83