

Robert A Scott

List of Publications by Year in Descending Order

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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.

110
papers

18,178
citations

61
h-index

118
g-index

118
ext. papers

24,005
ext. citations

18.4
avg, IF

4.73
L-index

#	Paper	IF	Citations
110	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
109	Mapping the proteo-genomic convergence of human diseases. <i>Science</i> , 2021 , 374, eabj1541	33.3	11
108	The trans-ancestral genomic architecture of glycemic traits. <i>Nature Genetics</i> , 2021 , 53, 840-860	36.3	44
107	A cross-platform approach identifies genetic regulators of human metabolism and health. <i>Nature Genetics</i> , 2021 , 53, 54-64	36.3	18
106	Mendelian randomization for studying the effects of perturbing drug targets. <i>Wellcome Open Research</i> , 2021 , 6, 16	4.8	11
105	Identification of rare loss of function genetic variation regulating body fat distribution. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2021 ,	5.6	1
104	Genome-wide Association Analysis in Humans Links Nucleotide Metabolism to Leukocyte Telomere Length. <i>American Journal of Human Genetics</i> , 2020 , 106, 389-404	11	40
103	Exome sequencing and characterization of 49,960 individuals in the UK Biobank. <i>Nature</i> , 2020 , 586, 749-756	35.4	122
102	Phenome-wide Mendelian randomization mapping the influence of the plasma proteome on complex diseases. <i>Nature Genetics</i> , 2020 , 52, 1122-1131	36.3	75
101	Genetic Studies of Leptin Concentrations Implicate Leptin in the Regulation of Early Adiposity. <i>Diabetes</i> , 2020 , 69, 2806-2818	0.9	10
100	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
99	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
98	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. <i>Nature Communications</i> , 2019 , 10, 376	17.4	41
97	Regional fat depot masses are influenced by protein-coding gene variants. <i>PLoS ONE</i> , 2019 , 14, e0217644	4.7	0
96	Assessing the causal association of glycine with risk of cardio-metabolic diseases. <i>Nature Communications</i> , 2019 , 10, 1060	17.4	38
95	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
94	Genome-wide meta-analysis of macronutrient intake of 91,114 European ancestry participants from the cohorts for heart and aging research in genomic epidemiology consortium. <i>Molecular Psychiatry</i> , 2019 , 24, 1920-1932	15.1	30

93	Phenome-wide association analysis of LDL-cholesterol lowering genetic variants in PCSK9. <i>BMC Cardiovascular Disorders</i> , 2019 , 19, 240	2.3	8
92	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
91	Genetic predisposition to mosaic Y chromosome loss in blood. <i>Nature</i> , 2019 , 575, 652-657	50.4	83
90	Epigenome-Wide Association Study of Incident Type 2 Diabetes in a British Population: EPIC-Norfolk Study. <i>Diabetes</i> , 2019 , 68, 2315-2326	0.9	40
89	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
88	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
87	Re-analysis of public genetic data reveals a rare X-chromosomal variant associated with type 2 diabetes. <i>Nature Communications</i> , 2018 , 9, 321	17.4	50
86	Multiancestry association study identifies new asthma risk loci that colocalize with immune-cell enhancer marks. <i>Nature Genetics</i> , 2018 , 50, 42-53	36.3	246
85	Life-Course Genome-wide Association Study Meta-analysis of Total Body BMD and Assessment of Age-Specific Effects. <i>American Journal of Human Genetics</i> , 2018 , 102, 88-102	11	119
84	Interplay between genetic predisposition, macronutrient intake and type 2 diabetes incidence: analysis within EPIC-InterAct across eight European countries. <i>Diabetologia</i> , 2018 , 61, 1325-1332	10.3	14
83	Genetic inactivation of ANGPTL4 improves glucose homeostasis and is associated with reduced risk of diabetes. <i>Nature Communications</i> , 2018 , 9, 2252	17.4	71
82	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
81	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
80	Association of Genetic Variants Related to Gluteofemoral vs Abdominal Fat Distribution With Type 2 Diabetes, Coronary Disease, and Cardiovascular Risk Factors. <i>JAMA - Journal of the American Medical Association</i> , 2018 , 320, 2553-2563	27.4	78
79	Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. <i>Nature Genetics</i> , 2018 , 50, 1505-1513	36.3	675
78	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. <i>American Journal of Human Genetics</i> , 2018 , 103, 691-706	11	151
77	Association of Genetically Enhanced Lipoprotein Lipase-Mediated Lipolysis and Low-Density Lipoprotein Cholesterol-Lowering Alleles With Risk of Coronary Disease and Type 2 Diabetes. <i>JAMA Cardiology</i> , 2018 , 3, 957-966	16.2	30
76	Genome-wide analyses identify 68 new loci associated with intraocular pressure and improve risk prediction for primary open-angle glaucoma. <i>Nature Genetics</i> , 2018 , 50, 778-782	36.3	122

75	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017 , 542, 186-190	50.4	412
74	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
73	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. <i>Nature Genetics</i> , 2017 , 49, 834-841	36.3	257
72	Loss of Cardioprotective Effects at the Locus as a Result of Gene-Smoking Interactions. <i>Circulation</i> , 2017 , 135, 2336-2353	16.7	36
71	Genome-wide association study meta-analysis for quantitative ultrasound parameters of bone identifies five novel loci for broadband ultrasound attenuation. <i>Human Molecular Genetics</i> , 2017 , 26, 2791-2802	5.6	20
70	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. <i>Nature Communications</i> , 2017 , 8, 14977	17.4	105
69	PCSK9 genetic variants and risk of type 2 diabetes: a mendelian randomisation study. <i>Lancet Diabetes and Endocrinology</i> , 2017 , 5, 97-105	18.1	225
68	Interaction between genes and macronutrient intake on the risk of developing type 2 diabetes: systematic review and findings from European Prospective Investigation into Cancer (EPIC)-InterAct. <i>American Journal of Clinical Nutrition</i> , 2017 , 106, 263-275	7	36
67	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. <i>Diabetes</i> , 2017 , 66, 2888-2902	29.0	414
66	Genetic variants associated with mosaic Y chromosome loss highlight cell cycle genes and overlap with cancer susceptibility. <i>Nature Genetics</i> , 2017 , 49, 674-679	36.3	70
65	A Low-Frequency Inactivating Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. <i>Diabetes</i> , 2017 , 66, 2019-2032	0.9	29
64	Exome-wide association study of plasma lipids in >300,000 individuals. <i>Nature Genetics</i> , 2017 , 49, 1758-1766	36.6	310
63	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
62	Novel genetic loci associated with long-term deterioration in blood lipid concentrations and coronary artery disease in European adults. <i>International Journal of Epidemiology</i> , 2017 , 46, 1211-1222	7.8	12
61	Genome-wide analysis of health-related biomarkers in the UK Household Longitudinal Study reveals novel associations. <i>Scientific Reports</i> , 2017 , 7, 11008	4.9	49
60	Type 2 diabetes, glucose, insulin, BMI, and ischemic stroke subtypes: Mendelian randomization study. <i>Neurology</i> , 2017 , 89, 454-460	6.5	53
59	Rare Variant Analysis of Human and Rodent Obesity Genes in Individuals with Severe Childhood Obesity. <i>Scientific Reports</i> , 2017 , 7, 4394	4.9	31
58	Integrative genomic analysis implicates limited peripheral adipose storage capacity in the pathogenesis of human insulin resistance. <i>Nature Genetics</i> , 2017 , 49, 17-26	36.3	312

57	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. <i>Scientific Data</i> , 2017 , 4, 170179	8.2	22
56	Genome-wide physical activity interactions in adiposity - A meta-analysis of 200,452 adults. <i>PLoS Genetics</i> , 2017 , 13, e1006528	6	103
55	Ranking and characterization of established BMI and lipid associated loci as candidates for gene-environment interactions. <i>PLoS Genetics</i> , 2017 , 13, e1006812	6	13
54	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
53	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
52	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
51	A null mutation in ANGPTL8 does not associate with either plasma glucose or type 2 diabetes in humans. <i>BMC Endocrine Disorders</i> , 2016 , 16, 7	3.3	8
50	Unraveling the role for genetics in enabling precision prescription for weight loss-scaling up for success. <i>Obesity</i> , 2016 , 24, 12-3	8	
49	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. <i>Nature Communications</i> , 2016 , 7, 10495	17.4	180
48	Testing the role of predicted gene knockouts in human anthropometric trait variation. <i>Human Molecular Genetics</i> , 2016 , 25, 2082-2092	5.6	7
47	A Robust Example of Collider Bias in a Genetic Association Study. <i>American Journal of Human Genetics</i> , 2016 , 98, 392-3	11	60
46	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. <i>Nature Communications</i> , 2016 , 7, 10494	17.4	107
45	Association of Multiple Biomarkers of Iron Metabolism and Type 2 Diabetes: The EPIC-InterAct Study. <i>Diabetes Care</i> , 2016 , 39, 572-81	14.6	48
44	Genetic Predisposition to an Impaired Metabolism of the Branched-Chain Amino Acids and Risk of Type 2 Diabetes: A Mendelian Randomisation Analysis. <i>PLoS Medicine</i> , 2016 , 13, e1002179	11.6	214
43	A Systematic Review of Biomarkers and Risk of Incident Type 2 Diabetes: An Overview of Epidemiological, Prediction and Aetiological Research Literature. <i>PLoS ONE</i> , 2016 , 11, e0163721	3.7	39
42	No Evidence of a Common DNA Variant Profile Specific to World Class Endurance Athletes. <i>PLoS ONE</i> , 2016 , 11, e0147330	3.7	74
41	The genetic architecture of type 2 diabetes. <i>Nature</i> , 2016 , 536, 41-47	50.4	704
40	Physical and neurobehavioral determinants of reproductive onset and success. <i>Nature Genetics</i> , 2016 , 48, 617-623	36.3	118

39	A Deletion in the Canine POMC Gene Is Associated with Weight and Appetite in Obesity-Prone Labrador Retriever Dogs. <i>Cell Metabolism</i> , 2016 , 23, 893-900	24.6	79
38	Genetic Evidence for a Link Between Favorable Adiposity and Lower Risk of Type 2 Diabetes, Hypertension, and Heart Disease. <i>Diabetes</i> , 2016 , 65, 2448-60	0.9	86
37	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. <i>Nature Genetics</i> , 2016 , 48, 1303-1312	36.3	51
36	Association Between Low-Density Lipoprotein Cholesterol-Lowering Genetic Variants and Risk of Type 2 Diabetes: A Meta-analysis. <i>JAMA - Journal of the American Medical Association</i> , 2016 , 316, 1383-1391	27.4	225
35	Analysis with the exome array identifies multiple new independent variants in lipid loci. <i>Human Molecular Genetics</i> , 2016 , 25, 4094-4106	5.6	14
34	General Framework for Meta-Analysis of Haplotype Association Tests. <i>Genetic Epidemiology</i> , 2016 , 40, 244-52	2.6	
33	Dietary Intake, FTO Genetic Variants, and Adiposity: A Combined Analysis of Over 16,000 Children and Adolescents. <i>Diabetes</i> , 2015 , 64, 2467-76	0.9	66
32	Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , 2015 , 523, 459-463	60.4	119
31	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. <i>Nature Genetics</i> , 2015 , 47, 1294-1303	36.3	226
30	Causal mechanisms and balancing selection inferred from genetic associations with polycystic ovary syndrome. <i>Nature Communications</i> , 2015 , 6, 8464	17.4	203
29	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
28	Definitions of Metabolic Health and Risk of Future Type 2 Diabetes in BMI Categories: A Systematic Review and Network Meta-analysis. <i>Diabetes Care</i> , 2015 , 38, 2177-87	14.6	45
27	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. <i>Nature Genetics</i> , 2015 , 47, 1415-25	36.3	292
26	HMG-coenzyme A reductase inhibition, type 2 diabetes, and bodyweight: evidence from genetic analysis and randomised trials. <i>Lancet, The</i> , 2015 , 385, 351-61	40	409
25	Evidence of a Causal Association Between Insulinemia and Endometrial Cancer: A Mendelian Randomization Analysis. <i>Journal of the National Cancer Institute</i> , 2015 , 107,	9.7	96
24	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
23	Associations between Potentially Modifiable Risk Factors and Alzheimer Disease: A Mendelian Randomization Study. <i>PLoS Medicine</i> , 2015 , 12, e1001841; discussion e1001841	11.6	115
22	A Mendelian Randomization Study of Circulating Uric Acid and Type 2 Diabetes. <i>Diabetes</i> , 2015 , 64, 3028-36	36	79

21	Association of HDL cholesterol efflux capacity with incident coronary heart disease events: a prospective case-control study. <i>Lancet Diabetes and Endocrinology,the</i> , 2015 , 3, 507-13	18.1	300
20	Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation. <i>Nature Communications</i> , 2015 , 6, 8658	17.4	79
19	Rare coding variants and X-linked loci associated with age at menarche. <i>Nature Communications</i> , 2015 , 6, 7756	17.4	23
18	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015 , 518, 187-196	50.4	920
17	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015 , 518, 197-206	50.4	2687
16	Association between circulating 25-hydroxyvitamin D and incident type 2 diabetes: a mendelian randomisation study. <i>Lancet Diabetes and Endocrinology,the</i> , 2015 , 3, 35-42	18.1	135
15	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
14	Novel loci affecting iron homeostasis and their effects in individuals at risk for hemochromatosis. <i>Nature Communications</i> , 2014 , 5, 4926	17.4	121
13	Genome-wide association analysis identifies six new loci associated with forced vital capacity. <i>Nature Genetics</i> , 2014 , 46, 669-77	36.3	104
12	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
11	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
10	Association between alcohol and cardiovascular disease: Mendelian randomisation analysis based on individual participant data. <i>BMJ, The</i> , 2014 , 349, g4164	5.9	406
9	Common genetic variants highlight the role of insulin resistance and body fat distribution in type 2 diabetes, independent of obesity. <i>Diabetes</i> , 2014 , 63, 4378-4387	0.9	127
8	Gene-lifestyle interaction and type 2 diabetes: the EPIC interact case-cohort study. <i>PLoS Medicine</i> , 2014 , 11, e1001647	11.6	149
7	Novel approach identifies SNPs in SLC2A10 and KCNK9 with evidence for parent-of-origin effect on body mass index. <i>PLoS Genetics</i> , 2014 , 10, e1004508	6	45
6	Genetic evidence for a normal-weight "metabolically obese" phenotype linking insulin resistance, hypertension, coronary artery disease, and type 2 diabetes. <i>Diabetes</i> , 2014 , 63, 4369-77	0.9	131
5	A low-frequency variant in MAPK14 provides mechanistic evidence of a link with myeloperoxidase: a prognostic cardiovascular risk marker. <i>Journal of the American Heart Association</i> , 2014 , 3,	6	6
4	Abstract 19753: Hdl Cholesterol Efflux Capacity is Inversely Associated With Incident Chd Events Independent of Hdl-c and Apoa-i Concentrations. <i>Circulation</i> , 2014 , 130,	16.7	2

3	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
2	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
1	No interactions between previously associated 2-hour glucose gene variants and physical activity or BMI on 2-hour glucose levels. <i>Diabetes</i> , 2012 , 61, 1291-6	0.9	21