Robert A Scott

List of Publications by Year
in descending order

111 papers	27,859 citations	11639 70 h-index	22147 113 g-index
118 all docs	118 docs citations	118 times ranked	35090 citing authors

#	Article	IF	Citations
1	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	13.7	3,823
2	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	9.4	1,818
3	Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. Nature Genetics, 2018, 50, 1505-1513.	9.4	1,331
4	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	13.7	1,328
5	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	13.7	952
6	A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. Nature Genetics, 2012, 44, 659-669.	9.4	762
7	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. Nature Genetics, 2012, 44, 991-1005.	9.4	746
8	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.3	615
9	HMG-coenzyme A reductase inhibition, type 2 diabetes, and bodyweight: evidence from genetic analysis and randomised trials. Lancet, The, 2015, 385, 351-361.	6.3	562
10	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	13.7	544
11	Association between alcohol and cardiovascular disease: Mendelian randomisation analysis based on individual participant data. BMJ, The, 2014, 349, g4164-g4164.	3.0	528
12	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	9.4	470
13	Integrative genomic analysis implicates limited peripheral adipose storage capacity in the pathogenesis of human insulin resistance. Nature Genetics, 2017, 49, 17-26.	9.4	452
14	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. Nature Genetics, 2017, 49, 834-841.	9.4	426
15	Multiancestry association study identifies new asthma risk loci that colocalize with immune-cell enhancer marks. Nature Genetics, 2018, 50, 42-53.	9.4	426
16	Association of HDL cholesterol efflux capacity with incident coronary heart disease events: a prospective case-control study. Lancet Diabetes and Endocrinology,the, 2015, 3, 507-513.	5.5	389
17	Exome sequencing and characterization of 49,960 individuals in the UK Biobank. Nature, 2020, 586, 749-756.	13.7	369
18	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. Nature Genetics, 2015, 47, 1415-1425.	9.4	365

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19	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. Nature Genetics, 2015, 47, 1294-1303.	9.4	357
20	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
21	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
22	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	9.4	341
23	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. PLoS Genetics, 2015, 11, e1005378.	1.5	331
24	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. American Journal of Human Genetics, 2018, 103, 691-706.	2.6	326
25	Genetic Predisposition to an Impaired Metabolism of the Branched-Chain Amino Acids and Risk of Type 2 Diabetes: A Mendelian Randomisation Analysis. PLoS Medicine, 2016, 13, e1002179.	3.9	324
26	Association Between Low-Density Lipoprotein Cholesterolâ€“Lowering Genetic Variants and Risk of Type 2 Diabetes. JAMA - Journal of the American Medical Association, 2016, 316, 1383.	3.8	310
27	Causal mechanisms and balancing selection inferred from genetic associations with polycystic ovary syndrome. Nature Communications, 2015, 6, 8464.	5.8	304
28	PCSK9 genetic variants and risk of type 2 diabetes: a mendelian randomisation study. Lancet Diabetes and Endocrinology,the, 2017, 5, 97-105.	5.5	298
29	Phenome-wide Mendelian randomization mapping the influence of the plasma proteome on complex diseases. Nature Genetics, 2020, 52, 1122-1131.	9.4	298
30	Trans-ancestry genome-wide association study identifies 12 genetic loci influencing blood pressure and implicates a role for DNA methylation. Nature Genetics, 2015, 47, 1282-1293.	9.4	294
31	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
32	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	9.4	261
33	Life-Course Genome-wide Association Study Meta-analysis of Total Body BMD and Assessment of Age-Specific Effects. American Journal of Human Genetics, 2018, 102, 88-102.	2.6	252
34	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nature Genetics, 2022, 54, 560-572.	9.4	250
35	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. Nature Communications, 2016, 7, 10495.	5.8	245
36	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated WithÂCoronary ArteryÂDisease. Journal of the American College of Cardiology, 2017, 69, 823-836.	1.2	214

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37	Genome-wide analyses identify 68 new loci associated with intraocular pressure and improve risk prediction for primary open-angle glaucoma. Nature Genetics, 2018, 50, 778-782.	9.4	214
38	Genetic predisposition to mosaic Y chromosome loss in blood. Nature, 2019, 575, 652-657.	13.7	198
39	Novel loci affecting iron homeostasis and their effects in individuals at risk for hemochromatosis. Nature Communications, 2014, 5, 4926.	5.8	192
40	Mapping the proteo-genomic convergence of human diseases. Science, 2021, 374, eabj1541.	6.0	192
41	Genetic Evidence for a Normal-Weight â€œMetabolically Obeseâ€•Phenotype Linking Insulin Resistance, Hypertension, Coronary Artery Disease, and Type 2 Diabetes. Diabetes, 2014, 63, 4369-4377.	0.3	185
42	Gene-Lifestyle Interaction and Type 2 Diabetes: The EPIC InterAct Case-Cohort Study. PLoS Medicine, 2014, 11, e1001647.	3.9	180
43	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. Nature Communications, 2015, 6, 5897.	5.8	173
44	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	13.7	173
45	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. Nature Communications, 2017, 8, 14977.	5.8	169
46	Association between circulating 25-hydroxyvitamin D and incident type 2 diabetes: a mendelian randomisation study. Lancet Diabetes and Endocrinology,the, 2015, 3, 35-42.	5.5	164
47	Physical and neurobehavioral determinants of reproductive onset and success. Nature Genetics, 2016, 48, 617-623.	9.4	158
48	Genome-wide physical activity interactions in adiposity â€• A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	1.5	158
49	Common Genetic Variants Highlight the Role of Insulin Resistance and Body Fat Distribution in Type 2 Diabetes, Independent of Obesity. Diabetes, 2014, 63, 4378-4387.	0.3	153
50	Associations between Potentially Modifiable Risk Factors and Alzheimer Disease: A Mendelian Randomization Study. PLoS Medicine, 2015, 12, e1001841.	3.9	153
51	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. Nature Communications, 2016, 7, 10494.	5.8	153
52	Association of Genetic Variants Related to Gluteofemoral vs Abdominal Fat Distribution With Type 2 Diabetes, Coronary Disease, and Cardiovascular Risk Factors. JAMA - Journal of the American Medical Association, 2018, 320, 2553.	3.8	152
53	Genome-wide association analysis identifies six new loci associated with forced vital capacity. Nature Genetics, 2014, 46, 669-677.	9.4	131
54	Evidence of a Causal Association Between Insulinemia and Endometrial Cancer: A Mendelian Randomization Analysis. Journal of the National Cancer Institute, 2015, 107, .	3.0	129

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55	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. American Journal of Human Genetics, 2018, 102, 375-400.	2.6	123
56	Genetic Evidence for a Link Between Favorable Adiposity and Lower Risk of Type 2 Diabetes, Hypertension, and Heart Disease. Diabetes, 2016, 65, 2448-2460.	0.3	122
57	Genome-wide Association Analysis in Humans Links Nucleotide Metabolism to Leukocyte Telomere Length. American Journal of Human Genetics, 2020, 106, 389-404.	2.6	118
58	A Deletion in the Canine POMC Gene Is Associated with Weight and Appetite in Obesity-Prone Labrador Retriever Dogs. Cell Metabolism, 2016, 23, 893-900.	7.2	117
59	Genetic variants associated with mosaic Y chromosome loss highlight cell cycle genes and overlap with cancer susceptibility. Nature Genetics, 2017, 49, 674-679.	9.4	117
60	A cross-platform approach identifies genetic regulators of human metabolism and health. Nature Genetics, 2021, 53, 54-64.	9.4	117
61	Multi-ancestry genome-wide geneâ€“smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. Nature Genetics, 2019, 51, 636-648.	9.4	112
62	Gene-Age Interactions in Blood Pressure Regulation: A Large-Scale Investigation with the CHARGE, Global BPgen, and ICBP Consortia. American Journal of Human Genetics, 2014, 95, 24-38.	2.6	109
63	Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation. Nature Communications, 2015, 6, 8658.	5.8	108
64	A genomic approach to therapeutic target validation identifies a glucose-lowering GLP1R variant protective for coronary heart disease. Science Translational Medicine, 2016, 8, 341ra76.	5.8	100
65	Genetic inactivation of ANGPTL4 improves glucose homeostasis and is associated with reduced risk of diabetes. Nature Communications, 2018, 9, 2252.	5.8	99
66	A Mendelian Randomization Study of Circulating Uric Acid and Type 2 Diabetes. Diabetes, 2015, 64, 3028-3036.	0.3	98
67	No Evidence of a Common DNA Variant Profile Specific to World Class Endurance Athletes. PLoS ONE, 2016, 11, e0147330.	1.1	96
68	A Robust Example of Collider Bias in a Genetic Association Study. American Journal of Human Genetics, 2016, 98, 392-393.	2.6	95
69	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. PLoS ONE, 2018, 13, e0198166.	1.1	94
70	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	9.4	89
71	Genome-wide analysis of health-related biomarkers in the UK Household Longitudinal Study reveals novel associations. Scientific Reports, 2017, 7, 11008.	1.6	88
72	Re-analysis of public genetic data reveals a rare X-chromosomal variant associated with type 2 diabetes. Nature Communications, 2018, 9, 321.	5.8	85

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73	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	1.6	85
74	Assessing the causal association of glycine with risk of cardio-metabolic diseases. Nature Communications, 2019, 10, 1060.	5.8	85
75	Type 2 diabetes, glucose, insulin, BMI, and ischemic stroke subtypes. Neurology, 2017, 89, 454-460.	1.5	84
76	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. Molecular Psychiatry, 2020, 25, 2392-2409.	4.1	83
77	Novel Approach Identifies SNPs in SLC2A10 and KCNK9 with Evidence for Parent-of-Origin Effect on Body Mass Index. PLoS Genetics, 2014, 10, e1004508.	1.5	80
78	Epigenome-Wide Association Study of Incident Type 2 Diabetes in a British Population: EPIC-Norfolk Study. Diabetes, 2019, 68, 2315-2326.	0.3	77
79	Dietary Intake, FTO Genetic Variants, and Adiposity: A Combined Analysis of Over 16,000 Children and Adolescents. Diabetes, 2015, 64, 2467-2476.	0.3	74
80	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. Nature Communications, 2016, 7, 13357.	5.8	74
81	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. Nature Genetics, 2016, 48, 1303-1312.	9.4	66
82	Association of Multiple Biomarkers of Iron Metabolism and Type 2 Diabetes: The EPIC-InterAct Study. Diabetes Care, 2016, 39, 572-581.	4.3	65
83	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	5.8	64
84	Definitions of Metabolic Health and Risk of Future Type 2 Diabetes in BMI Categories: A Systematic Review and Network Meta-analysis. Diabetes Care, 2015, 38, 2177-2187.	4.3	61
85	Association of Genetically Enhanced Lipoprotein Lipaseâ€“Mediated Lipolysis and Low-Density Lipoprotein Cholesterolâ€“Lowering Alleles With Risk of Coronary Disease and Type 2 Diabetes. JAMA Cardiology, 2018, 3, 957.	3.0	55
86	Loss of Cardioprotective Effects at the ADAMTS7 Locus as a Result of Gene-Smoking Interactions. Circulation, 2017, 135, 2336-2353.	1.6	51
87	A Systematic Review of Biomarkers and Risk of Incident Type 2 Diabetes: An Overview of Epidemiological, Prediction and Aetiological Research Literature. PLoS ONE, 2016, 11, e0163721.	1.1	51
88	Rare Variant Analysis of Human and Rodent Obesity Genes in Individuals with Severe Childhood Obesity. Scientific Reports, 2017, 7, 4394.	1.6	50
89	Mendelian randomization for studying the effects of perturbing drug targets. Wellcome Open Research, 2021, 6, 16.	0.9	48
90	A Low-Frequency Inactivating AKT2 Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. Diabetes, 2017, 66, 2019-2032.	0.3	47

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91	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. American Journal of Clinical Nutrition, 2017, 106, 263-275.	2.2	46
92	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. Molecular Psychiatry, 2019, 24, 1920-1932.	4.1	44
93	Rare coding variants and X-linked loci associated with age at menarche. Nature Communications, 2015, 6, 7756.	5.8	32
94	Genome-wide association study meta-analysis for quantitative ultrasound parameters of bone identifies five novel loci for broadband ultrasound attenuation. Human Molecular Genetics, 2017, 26, 2791-2802.	1.4	32
95	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	2.4	31
96	Genetic Studies of Leptin Concentrations Implicate Leptin in the Regulation of Early Adiposity. Diabetes, 2020, 69, 2806-2818.	0.3	26
97	Ranking and characterization of established BMI and lipid associated loci as candidates for gene-environment interactions. PLoS Genetics, 2017, 13, e1006812.	1.5	24
98	No Interactions Between Previously Associated 2-Hour Glucose Gene Variants and Physical Activity or BMI on 2-Hour Glucose Levels. Diabetes, 2012, 61, 1291-1296.	0.3	23
99	Phenome-wide association analysis of LDL-cholesterol lowering genetic variants in PCSK9. BMC Cardiovascular Disorders, 2019, 19, 240.	0.7	22
100	Interplay between genetic predisposition, macronutrient intake and type 2 diabetes incidence: analysis within EPIC-InterAct across eight European countries. Diabetologia, 2018, 61, 1325-1332.	2.9	20
101	Analysis with the exome array identifies multiple new independent variants in lipid loci. Human Molecular Genetics, 2016, 25, 4094-4106.	1.4	19
102	Novel genetic loci associated with long-term deterioration in blood lipid concentrations and coronary artery disease in European adults. International Journal of Epidemiology, 2016, 46, dyw245.	0.9	17
103	Identification of Rare Loss-of-Function Genetic Variation Regulating Body Fat Distribution. Journal of Clinical Endocrinology and Metabolism, 2022, 107, 1065-1077.	1.8	12
104	Testing the role of predicted gene knockouts in human anthropometric trait variation. Human Molecular Genetics, 2016, 25, 2082-2092.	1.4	10
105	A null mutation in ANGPTL8 does not associate with either plasma glucose or type 2 diabetes in humans. BMC Endocrine Disorders, 2016, 16, 7.	0.9	9
106	Regional fat depot masses are influenced by protein-coding gene variants. PLoS ONE, 2019, 14, e0217644.	1.1	9
107	A Lowâ€Frequency Variant in MAPK14 Provides Mechanistic Evidence of a Link With Myeloperoxidase: A Prognostic Cardiovascular Risk Marker. Journal of the American Heart Association, 2014, 3, .	1.6	7
108	Abstract 19753: Hdl Cholesterol Efflux Capacity is Inversely Associated With Incident Chd Events Independent of Hdl-c and Apoa-i Concentrations. Circulation, 2014, 130, .	1.6	2

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109	Unraveling the role for genetics in enabling precision prescription for weight lossâ€"scaling up for success. Obesity, 2016, 24, 12-13.	1.5	1
110	General Framework for Metaâ€Analysis of Haplotype Association Tests. Genetic Epidemiology, 2016, 40, 244-252.	0.6	0
111	Abstract 49: A Genome-wide Meta-analysis of the Combined Influence of Physical Activity and Genetic Variants on Body Fat Distribution in 94,779 Individuals of European Descent. Circulation, 2014, 129, .	1.6	0