Laura J Scott

List of Publications by Year
in descending order

72 papers	31,854 citations	50170 46 h-index	76769 74 g-index
81 all docs	81 docs citations	81 times ranked	38151 citing authors

#	Article	IF	Citations
1	Sex-Dependent Shared and Nonshared Genetic Architecture Across Mood and Psychotic Disorders. Biological Psychiatry, 2022, 91, 102-117.	0.7	61
2	Dissecting the Shared Genetic Architecture of Suicide Attempt, Psychiatric Disorders, and Known Risk Factors. Biological Psychiatry, 2022, 91, 313-327.	0.7	114
3	Genome-wide association studies of metabolites in Finnish men identify disease-relevant loci. Nature Communications, 2022, 13, 1644.	5.8	63
4	Rare coding variants in ten genes confer substantial risk for schizophrenia. Nature, 2022, 604, 509-516.	13.7	326
5	Exome sequencing in bipolar disorder identifies AKAP11 as a risk gene shared with schizophrenia. Nature Genetics, 2022, 54, 541-547.	9.4	65
6	ACE2 expression in adipose tissue is associated with cardio-metabolic risk factors and cell type compositionâ€"implications for COVID-19. International Journal of Obesity, 2022, 46, 1478-1486.	1.6	18
7	Robust, flexible, and scalable tests for Hardyâ€"Weinberg equilibrium across diverse ancestries. Genetics, 2021, 218, .	1.2	6
8	A powerful subset-based method identifies gene set associations and improves interpretation in UK Biobank. American Journal of Human Genetics, 2021, 108, 669-681.	2.6	8
9	Genome-wide association study of more than 40,000 bipolar disorder cases provides new insights into the underlying biology. Nature Genetics, 2021, 53, 817-829.	9.4	629
10	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	9.4	341
11	Genetic effects on liver chromatin accessibility identify disease regulatory variants. American Journal of Human Genetics, 2021, 108, 1169-1189.	2.6	22
12	Investigating rare pathogenic/likely pathogenic exonic variation in bipolar disorder. Molecular Psychiatry, 2021, 26, 5239-5250.	4.1	15
13	Cabbage and Sauerkraut Consumption in Adolescence and Adulthood and Breast Cancer Risk among US-Resident Polish Migrant Women. International Journal of Environmental Research and Public Health, 2021, 18, 10795.	1.2	8
14	Prediction of suicidal ideation risk in a prospective cohort study of medical interns. PLoS ONE, 2021, 16, e0260620.	1.1	10
15	Heritability of the Fibromyalgia Phenotype Varies by Age. Arthritis and Rheumatology, 2020, 72, 815-823.	2.9	15
16	Genomic prediction of depression risk and resilience under stress. Nature Human Behaviour, 2020, 4, 111-118.	6.2	28
17	Adiponectin GWAS loci harboring extensive allelic heterogeneity exhibit distinct molecular consequences. PLoS Genetics, 2020, 16, e1009019.	1.5	11
18	Ancestry-agnostic estimation of DNA sample contamination from sequence reads. Genome Research, 2020, 30, 185-194.	2.4	51

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19	Genetic variant effects on gene expression in human pancreatic islets and their implications for T2D. Nature Communications, 2020, 11, 4912.	5.8	89
20	New alcohol-related genes suggest shared genetic mechanisms with neuropsychiatric disorders. Nature Human Behaviour, 2019, 3, 950-961.	6.2	75
21	Exome sequencing of Finnish isolates enhances rare-variant association power. Nature, 2019, 572, 323-328.	13.7	161
22	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	5.8	84
23	Colocalization of GWAS and eQTL signals at loci with multiple signals identifies additional candidate genes for body fat distribution. Human Molecular Genetics, 2019, 28, 4161-4172.	1.4	41
24	Adipose Tissue Gene Expression Associations Reveal Hundreds of Candidate Genes for Cardiometabolic Traits. American Journal of Human Genetics, 2019, 105, 773-787.	2.6	45
25	Exome sequencing of 20,791Âcases of type 2 diabetes and 24,440Âcontrols. Nature, 2019, 570, 71-76.	13.7	248
26	Integrative analysis of gene expression, DNA methylation, physiological traits, and genetic variation in human skeletal muscle. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 10883-10888.	3.3	114
27	Genome-wide association study identifies 30 loci associated with bipolar disorder. Nature Genetics, 2019, 51, 793-803.	9.4	1,191
28	Trans-ethnic association study of blood pressure determinants in over 750,000 individuals. Nature Genetics, 2019, 51, 51-62.	9.4	328
29	A Partial Loss-of-Function Variant in AKT2 Is Associated With Reduced Insulin-Mediated Glucose Uptake in Multiple Insulin-Sensitive Tissues: A Genotype-Based Callback Positron Emission Tomography Study. Diabetes, 2018, 67, 334-342.	0.3	37
30	Extremely rare variants reveal patterns of germline mutation rate heterogeneity in humans. Nature Communications, 2018, 9, 3753.	5.8	121
31	Interactions between genetic variation and cellular environment in skeletal muscle gene expression. PLoS ONE, 2018, 13, e0195788.	1.1	18
32	Genetic Regulation of Adipose Gene Expression and Cardio-Metabolic Traits. American Journal of Human Genetics, 2017, 100, 428-443.	2.6	141
33	Genetic regulatory signatures underlying islet gene expression and type 2 diabetes. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 2301-2306.	3.3	189
34	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.3	615
35	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
36	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. Nature Communications, 2017, 8, 80.	5.8	147

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37	A Type 2 Diabetesâ€“Associated Functional Regulatory Variant in a Pancreatic Islet Enhancer at the ADCY5 Locus. Diabetes, 2017, 66, 2521-2530.	0.3	54
38	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	2.4	31
39	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	13.7	952
40	The genetic regulatory signature of type 2 diabetes in human skeletal muscle. Nature Communications, 2016, 7, 11764.	5.8	114
41	Exome Sequencing of Familial Bipolar Disorder. JAMA Psychiatry, 2016, 73, 590.	6.0	97
42	Next-generation genotype imputation service and methods. Nature Genetics, 2016, 48, 1284-1287.	9.4	2,828
43	A reference panel of 64,976 haplotypes for genotype imputation. Nature Genetics, 2016, 48, 1279-1283.	9.4	2,421
44	Fine-Mapping of Type 2 Diabetes Loci. , 2016, , 127-151.		0
45	An efficient resampling method for calibrating single and gene-based rare variant association analysis in caseâ€“control studies. Biostatistics, 2016, 17, 1-15.	0.9	46
46	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	13.7	173
47	ChIP-Enrich: gene set enrichment testing for ChIP-seq data. Nucleic Acids Research, 2014, 42, e105-e105.	6.5	136
48	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. Nature Genetics, 2014, 46, 234-244.	9.4	959
49	Broad-Enrich: functional interpretation of large sets of broad genomic regions. Bioinformatics, 2014, 30, i393-i400.	1.8	21
50	Recommended Joint and Metaâ€Analysis Strategies for Caseâ€Control Association Testing of Single Lowâ€Count Variants. Genetic Epidemiology, 2013, 37, 539-550.	0.6	133
51	Stratifying Type 2 Diabetes Cases by BMI Identifies Genetic Risk Variants in LAMA1 and Enrichment for Risk Variants in Lean Compared to Obese Cases. PLoS Genetics, 2012, 8, e1002741.	1.5	190
52	Novel Loci for Adiponectin Levels and Their Influence on Type 2 Diabetes and Metabolic Traits: A Multi-Ethnic Meta-Analysis of 45,891 Individuals. PLoS Genetics, 2012, 8, e1002607.	1.5	419
53	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. Nature Genetics, 2012, 44, 981-990.	9.4	1,748
54	What Will Diabetes Genomes Tell Us?. Current Diabetes Reports, 2012, 12, 643-650.	1.7	10

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55	Identifying Plausible Genetic Models Based on Association and Linkage Results: Application to Type 2 Diabetes. Genetic Epidemiology, 2012, 36, 820-828.	0.6	6
56	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. Nature, 2011, 478, 103-109.	13.7	1,855
57	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. Nature Genetics, 2010, 42, 579-589.	9.4	1,631
58	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nature Genetics, 2010, 42, 937-948.	9.4	2,634
59	Detailed Physiologic Characterization Reveals Diverse Mechanisms for Novel Genetic Loci Regulating Glucose and Insulin Metabolism in Humans. Diabetes, 2010, 59, 1266-1275.	0.3	237
60	Global Epigenomic Analysis of Primary Human Pancreatic Islets Provides Insights into Type 2 Diabetes Susceptibility Loci. Cell Metabolism, 2010, 12, 443-455.	7.2	190
61	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. Nature Genetics, 2010, 42, 105-116.	9.4	1,982
62	Genome-wide association and meta-analysis of bipolar disorder in individuals of European ancestry. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 7501-7506.	3.3	274
63	Variants in MTNR1B influence fasting glucose levels. Nature Genetics, 2009, 41, 77-81.	9.4	662
64	Tissue-specific alternative splicing of TCF7L2. Human Molecular Genetics, 2009, 18, 3795-3804.	1.4	100
65	Newly identified loci that influence lipid concentrations and risk of coronary artery disease. Nature Genetics, 2008, 40, 161-169.	9.4	1,488
66	Meta-analysis of genome-wide association data and large-scale replication identifies additional susceptibility loci for type 2 diabetes. Nature Genetics, 2008, 40, 638-645.	9.4	1,683
67	Comprehensive Association Study of Type 2 Diabetes and Related Quantitative Traits With 222 Candidate Genes. Diabetes, 2008, 57, 3136-3144.	0.3	104
68	A Genome-Wide Association Study of Type 2 Diabetes in Finns Detects Multiple Susceptibility Variants. Science, 2007, 316, 1341-1345.	6.0	2,534
69	Association of Transcription Factor 7-Like 2 (TCF7L2) Variants With Type 2 Diabetes in a Finnish Sample. Diabetes, 2006, 55, 2649-2653.	0.3	224
70	Genetic Variation Near the Hepatocyte Nuclear Factor-4Â Gene Predicts Susceptibility to Type 2 Diabetes. Diabetes, 2004, 53, 1141-1149.	0.3	255
71	Assessing Whether an Allele Can Account in Part for a Linkage Signal: The Genotype-IBD Sharing Test (GIST). American Journal of Human Genetics, 2004, 74, 418-431.	2.6	58
72	A Large Set of Finnish Affected Sibling Pair Families With Type 2 Diabetes Suggests Susceptibility Loci on Chromosomes 6, 11, and 14. Diabetes, 2004, 53, 821-829.	0.3	73