Kerrin S Small

List of Publications by Year
in descending order

107 papers	21,011 citations	23565 58 h-index	22161 113 g-index
141 all docs	141 docs citations	141 times ranked	34810 citing authors

#	Article	IF	Citations
1	A reference panel of 64,976 haplotypes for genotype imputation. Nature Genetics, 2016, 48, 1279-1283.	21.4	2,421
2	The UK10K project identifies rare variants in health and disease. Nature, 2015, 526, 82-90.	27.8	1,014
3	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. Nature Genetics, 2014, 46, 234-244.	21.4	959
4	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	27.8	952
5	Human metabolic individuality in biomedical and pharmaceutical research. Nature, 2011, 477, 54-60.	27.8	916
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.	21.4	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.	21.4	746
8	Mapping cis- and trans-regulatory effects across multiple tissues in twins. Nature Genetics, 2012, 44, 1084-1089.	21.4	701
9	Epigenome-Wide Scans Identify Differentially Methylated Regions for Age and Age-Related Phenotypes in a Healthy Ageing Population. PLoS Genetics, 2012, 8, e1002629.	3.5	620
10	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	27.8	544
11	The fecal metabolome as a functional readout of the gut microbiome. Nature Genetics, 2018, 50, 790-795.	21.4	482
12	Genome-wide association study in individuals of South Asian ancestry identifies six new type 2 diabetes susceptibility loci. Nature Genetics, 2011, 43, 984-989.	21.4	481
13	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	21.4	470
14	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.	3.5	419
15	The Architecture of Gene Regulatory Variation across Multiple Human Tissues: The MuTHER Study. PLoS Genetics, 2011, 7, e1002003.	3.5	392
16	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. Nature Genetics, 2018, 50, 559-571.	21.4	356
17	Genome-wide and fine-resolution association analysis of malaria in West Africa. Nature Genetics, 2009, 41, 657-665.	21.4	345
18	Whole-genome sequencing identifies common-to-rare variants associated with human blood metabolites. Nature Genetics, 2017, 49, 568-578.	21.4	341

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19	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341
20	Genome-wide association analyses identifies a susceptibility locus for tuberculosis on chromosome 18q11.2. Nature Genetics, 2010, 42, 739-741.	21.4	332
21	Global Analysis of DNA Methylation Variation in Adipose Tissue from Twins Reveals Links to Disease-Associated Variants in Distal Regulatory Elements. American Journal of Human Genetics, 2013, 93, 876-890.	6.2	330
22	Identification of an imprinted master trans regulator at the KLF14 locus related to multiple metabolic phenotypes. Nature Genetics, 2011, 43, 561-564.	21.4	289
23	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	21.4	286
24	Gene expression changes with age in skin, adipose tissue, blood and brain. Genome Biology, 2013, 14, R75.	9.6	263
25	Exome sequencing of 20,791Âcases of type 2 diabetes and 24,440Âcontrols. Nature, 2019, 570, 71-76.	27.8	248
26	Gene-gene and gene-environment interactions detected by transcriptome sequence analysis in twins. Nature Genetics, 2015, 47, 88-91.	21.4	215
27	Genome-wide analysis of multi-ancestry cohorts identifies new loci influencing intraocular pressure and susceptibility to glaucoma. Nature Genetics, 2014, 46, 1126-1130.	21.4	212
28	Genome-wide association analysis identifies TXNRD2, ATXN2 and FOXC1 as susceptibility loci for primary open-angle glaucoma. Nature Genetics, 2016, 48, 189-194.	21.4	211
29	Cell typeâ€“specific genetic regulation of gene expression across human tissues. Science, 2020, 369, .	12.6	210
30	A genotype calling algorithm for the Illumina BeadArray platform. Bioinformatics, 2007, 23, 2741-2746.	4.1	209
31	The Role of Adiposity in Cardiometabolic Traits: A Mendelian Randomization Analysis. PLoS Medicine, 2013, 10, e1001474.	8.4	178
32	The Genetic Architecture of Gene Expression in Peripheral Blood. American Journal of Human Genetics, 2017, 100, 228-237.	6.2	178
33	Methodological challenges of genome-wide association analysis in Africa. Nature Reviews Genetics, 2010, 11, 149-160.	16.3	167
34	Rare variants in PPARG with decreased activity in adipocyte differentiation are associated with increased risk of type 2 diabetes. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 13127-13132.	7.1	152
35	A global network for investigating the genomic epidemiology of malaria. Nature, 2008, 456, 732-737.	27.8	148
36	Singapore Genome Variation Project: A haplotype map of three Southeast Asian populations. Genome Research, 2009, 19, 2154-2162.	5.5	146

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37	Regulatory variants at KLF14 influence type 2 diabetes risk via a female-specific effect on adipocyte size and body composition. Nature Genetics, 2018, 50, 572-580.	21.4	143
38	Tensor decomposition for multiple-tissue gene expression experiments. Nature Genetics, 2016, 48, 1094-1100.	21.4	142
39	Genetic Regulation of Adipose Gene Expression and Cardio-Metabolic Traits. American Journal of Human Genetics, 2017, 100, 428-443.	6.2	141
40	Genetic interactions affecting human gene expression identified by variance association mapping. ELife, 2014, 3, e01381.	6.0	137
41	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. American Journal of Human Genetics, 2017, 100, 865-884.	6.2	131
42	TwinsUK: The UK Adult Twin Registry Update. Twin Research and Human Genetics, 2019, 22, 523-529.	0.6	116
43	Smoking induces coordinated DNA methylation and gene expression changes in adipose tissue with consequences for metabolic health. Clinical Epigenetics, 2018, 10, 126.	4.1	110
44	Allelic heterogeneity of G6PD deficiency in West Africa and severe malaria susceptibility. European Journal of Human Genetics, 2009, 17, 1080-1085.	2.8	109
45	Extreme genomic variation in a natural population. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 5698-5703.	7.1	105
46	Current smoking and COVID-19 risk: results from a population symptom app in over 2.4 million people. Thorax, 2021, 76, 714-722.	5.6	105
47	An integrated epigenomic analysis for type 2 diabetes susceptibility loci in monozygotic twins. Nature Communications, 2014, 5, 5719.	12.8	100
48	Imputation-Based Meta-Analysis of Severe Malaria in Three African Populations. PLoS Genetics, 2013, 9, e1003509.	3.5	95
49	Identification and Functional Characterization of G6PC2 Coding Variants Influencing Glycemic Traits Define an Effector Transcript at the G6PC2-ABCB11 Locus. PLoS Genetics, 2015, 11, e1004876.	3.5	95
50	A haplome alignment and reference sequence of the highly polymorphic Ciona savignyi genome. Genome Biology, 2007, 8, R41.	9.6	90
51	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	21.4	89
52	Predicting causal variants affecting expression by using whole-genome sequencing and RNA-seq from multiple human tissues. Nature Genetics, 2017, 49, 1747-1751.	21.4	88
53	Interferon inducible X-linked gene CXorf21 may contribute to sexual dimorphism in Systemic Lupus Erythematosus. Nature Communications, 2019, 10, 2164.	12.8	88
54	Eight Common Genetic Variants Associated with Serum DHEAS Levels Suggest a Key Role in Ageing Mechanisms. PLoS Genetics, 2011, 7, e1002025.	3.5	87

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55	The Presence of Methylation Quantitative Trait Loci Indicates a Direct Genetic Influence on the Level of DNA Methylation in Adipose Tissue. PLoS ONE, 2013, 8, e55923.	2.5	83
56	Probable delirium is a presenting symptom of COVID-19 in frail, older adults: a cohort study of 322 hospitalised and 535 community-based older adults. Age and Ageing, 2021, 50, 40-48.	1.6	82
57	Age-dependent changes in mean and variance of gene expression across tissues in a twin cohort. Human Molecular Genetics, 2018, 27, 732-741.	2.9	77
58	Cell-Type Heterogeneity in Adipose Tissue Is Associated with Complex Traits and Reveals Disease-Relevant Cell-Specific eQTLs. American Journal of Human Genetics, 2019, 104, 1013-1024.	6.2	76
59	Integration of human adipocyte chromosomal interactions with adipose gene expression prioritizes obesity-related genes from GWAS. Nature Communications, 2018, 9, 1512.	12.8	75
60	Detecting and Characterizing Genomic Signatures of Positive Selection in Global Populations. American Journal of Human Genetics, 2013, 92, 866-881.	6.2	71
61	Estrogen receptor Î± controls metabolism in white and brown adipocytes by regulating Polg1 and mitochondrial remodeling. Science Translational Medicine, 2020, 12, .	12.4	64
62	Positive selection of a CD36 nonsense variant in sub-Saharan Africa, but no association with severe malaria phenotypes. Human Molecular Genetics, 2009, 18, 2683-2692.	2.9	63
63	X chromosome dosage of histone demethylase KDM5C determines sex differences in adiposity. Journal of Clinical Investigation, 2020, 130, 5688-5702.	8.2	62
64	Genetic variation influencing DNA methylation provides insights into molecular mechanisms regulating genomic function. Nature Genetics, 2022, 54, 18-29.	21.4	60
65	Genome-wide comparisons of variation in linkage disequilibrium. Genome Research, 2009, 19, 1849-1860.	5.5	58
66	Nuclear genetic regulation of the human mitochondrial transcriptome. ELife, 2019, 8, .	6.0	56
67	Tumor Necrosis Factor and Lymphotoxinâ€Î± Polymorphisms and Severe Malaria in African Populations. Journal of Infectious Diseases, 2009, 199, 569-575.	4.0	52
68	Determinants of penetrance and variable expressivity in monogenic metabolic conditions across 77,184 exomes. Nature Communications, 2021, 12, 3505.	12.8	49
69	Extent, Causes, and Consequences of Small RNA Expression Variation in Human Adipose Tissue. PLoS Genetics, 2012, 8, e1002704.	3.5	48
70	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.	0.6	47
71	Heritability of skewed X-inactivation in female twins is tissue-specific and associated with age. Nature Communications, 2019, 10, 5339.	12.8	47
72	Expression of Phosphofructokinase in Skeletal Muscle Is Influenced by Genetic Variation and Associated With Insulin Sensitivity. Diabetes, 2014, 63, 1154-1165.	0.6	41

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73	Metabolomic profiling to dissect the role of visceral fat in cardiometabolic health. Obesity, 2016, 24, 1380-1388.	3.0	41
74	A genome-wide association study of intra-ocular pressure suggests a novel association in the gene FAM125B in the TwinsUK cohort. Human Molecular Genetics, 2014, 23, 3343-3348.	2.9	39
75	Mapping eQTLs with RNA-seq reveals novel susceptibility genes, non-coding RNAs and alternative-splicing events in systemic lupus erythematosus. Human Molecular Genetics, 2017, 26, ddw417.	2.9	39
76	Concordance for clonal hematopoiesis is limited in elderly twins. Blood, 2020, 135, 269-273.	1.4	38
77	Epigenetic findings in periodontitis in UK twins: a cross-sectional study. Clinical Epigenetics, 2019, 11, 27.	4.1	37
78	RSPO3 impacts body fat distribution and regulates adipose cell biology in vitro. Nature Communications, 2020, 11, 2797.	12.8	34
79	Time-dependent genetic effects on gene expression implicate aging processes. Genome Research, 2017, 27, 545-552.	5.5	31
80	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	5.3	31
81	Power consequences of linkage disequilibrium variation between populations. Genetic Epidemiology, 2009, 33, 128-135.	1.3	28
82	Adiposity-Dependent Regulatory Effects on Multi-tissue Transcriptomes. American Journal of Human Genetics, 2016, 99, 567-579.	6.2	26
83	Variation in human genes encoding adhesion and proinflammatory molecules are associated with severe malaria in the Vietnamese. Genes and Immunity, 2012, 13, 503-508.	4.1	24
84	Simulation of Finnish Population History, Guided by Empirical Genetic Data, to Assess Power of Rare-Variant Tests in Finland. American Journal of Human Genetics, 2014, 94, 710-720.	6.2	24
85	Rare coding variants in 35 genes associate with circulating lipid levelsâ€"A multi-ancestry analysis of 170,000 exomes. American Journal of Human Genetics, 2022, 109, 81-96.	6.2	24
86	Genetic correlations reveal the shared genetic architecture of transcription in human peripheral blood. Nature Communications, 2017, 8, 483.	12.8	22
87	Regulatory sites for splicing in human basal ganglia are enriched for disease-relevant information. Nature Communications, 2020, 11, 1041.	12.8	22
88	Integrated multiomics approach identifies calcium and integrin-binding protein-2 as a novel gene for pulse wave velocity. Journal of Hypertension, 2016, 34, 79-87.	0.5	18
89	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.	3.4	18
90	Global Analysis of DNA Methylation Variation in Adipose Tissue from Twins Reveals Links to Disease-Associated Variants in Distal Regulatory Elements. American Journal of Human Genetics, 2013, 93, 1158.	6.2	17

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91	The Rate of Nonallelic Homologous Recombination in Males Is Highly Variable, Correlated between Monozygotic Twins and Independent of Age. PLoS Genetics, 2014, 10, e1004195.	3.5	17
92	Interrogating causal pathways linking genetic variants, small molecule metabolites, and circulating lipids. Genome Medicine, 2014, 6, 25.	8.2	17
93	Autosomal genetic control of human gene expression does not differ across the sexes. Genome Biology, 2016, 17, 248.	8.8	15
94	Whole genomeâ€“amplified DNA: insights and imputation. Nature Methods, 2008, 5, 279-280.	19.0	13
95	Identification of Rare Loss-of-Function Genetic Variation Regulating Body Fat Distribution. Journal of Clinical Endocrinology and Metabolism, 2022, 107, 1065-1077.	3.6	12
96	Assessing Genuine Parents-Offspring Trios for Genetic Association Studies. Human Heredity, 2009, 67, 26-37.	0.8	11
97	ABCC5 Transporter is a Novel Type 2 Diabetes Susceptibility Gene in European and African American Populations. Annals of Human Genetics, 2014, 78, 333-344.	0.8	11
98	Further evidence supporting a potential role for ADH1B in obesity. Scientific Reports, 2021, 11, 1932.	3.3	11
99	Common variants in SOX-2 and congenital cataract genes contribute to age-related nuclear cataract. Communications Biology, 2020, 3, 755.	4.4	10
100	Perturbation Analysis: A Simple Method for Filtering SNPs with Erroneous Genotyping in Genomeâ€Wide Association Studies. Annals of Human Genetics, 2008, 72, 368-374.	0.8	9
101	Fasting and time of day independently modulate circadian rhythm relevant gene expression in adipose and skin tissue. BMC Genomics, 2018, 19, 659.	2.8	9
102	A novel method for haplotype clustering and visualization. Genetic Epidemiology, 2010, 34, 34-41.	1.3	6
103	Adipose methylome integrative-omic analyses reveal genetic and dietary metabolic health drivers and insulin resistance classifiers. Genome Medicine, 2022, 14, .	8.2	6
104	A Bayesian approach using covariance of single nucleotide polymorphism data to detect differences in linkage disequilibrium patterns between groups of individuals. Bioinformatics, 2010, 26, 1999-2003.	4.1	5
105	Chaining Algorithms for Alignment of Draft Sequence. Lecture Notes in Computer Science, 2004, , 326-337.	1.3	4
106	Abstract 50: Procollagen C-endopeptidase Enhancer protein 2 (PCPE2) Deficiency Profoundly Affects Adipose Distribution in Mice and Humans and Links HDL Metabolism to Adipocyte Biology. Arteriosclerosis, Thrombosis, and Vascular Biology, 2016, 36, .	2.4	0
107	Introducing ExHiBITT â€“ Exploring Host microBIome inTeractions in Twins â€“, a colon multiomic cohort study. Wellcome Open Research, 0, 5, 30.	1.8	0