

Kerrin S Small

List of Publications by Citations

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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.

115
papers

14,827
citations

53
h-index

121
g-index

141
ext. papers

18,672
ext. citations

16.9
avg, IF

5.33
L-index

#	Paper	IF	Citations
115	A reference panel of 64,976 haplotypes for genotype imputation. <i>Nature Genetics</i> , 2016 , 48, 1279-83	36.3	1447
114	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. <i>Nature Genetics</i> , 2014 , 46, 234-44	36.3	784
113	The UK10K project identifies rare variants in health and disease. <i>Nature</i> , 2015 , 526, 82-90	50.4	776
112	Human metabolic individuality in biomedical and pharmaceutical research. <i>Nature</i> , 2011 , 477, 54-60	50.4	728
111	The genetic architecture of type 2 diabetes. <i>Nature</i> , 2016 , 536, 41-47	50.4	704
110	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
109	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
108	Mapping cis- and trans-regulatory effects across multiple tissues in twins. <i>Nature Genetics</i> , 2012 , 44, 1084-93	36.3	572
107	Epigenome-wide scans identify differentially methylated regions for age and age-related phenotypes in a healthy ageing population. <i>PLoS Genetics</i> , 2012 , 8, e1002629	6	501
106	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017 , 542, 186-190	50.4	412
105	Genome-wide association study in individuals of South Asian ancestry identifies six new type 2 diabetes susceptibility loci. <i>Nature Genetics</i> , 2011 , 43, 984-9	36.3	406
104	The architecture of gene regulatory variation across multiple human tissues: the MuTHER study. <i>PLoS Genetics</i> , 2011 , 7, e1002003	6	336
103	Novel loci for adiponectin levels and their influence on type 2 diabetes and metabolic traits: a multi-ethnic meta-analysis of 45,891 individuals. <i>PLoS Genetics</i> , 2012 , 8, e1002607	6	326
102	Exome-wide association study of plasma lipids in >300,000 individuals. <i>Nature Genetics</i> , 2017 , 49, 1758-1766	36.3	310
101	Genome-wide and fine-resolution association analysis of malaria in West Africa. <i>Nature Genetics</i> , 2009 , 41, 657-65	36.3	297
100	Genome-wide association analyses identifies a susceptibility locus for tuberculosis on chromosome 18q11.2. <i>Nature Genetics</i> , 2010 , 42, 739-741	36.3	276
99	Global analysis of DNA methylation variation in adipose tissue from twins reveals links to disease-associated variants in distal regulatory elements. <i>American Journal of Human Genetics</i> , 2013 , 93, 876-90	11	269

98	The fecal metabolome as a functional readout of the gut microbiome. <i>Nature Genetics</i> , 2018 , 50, 790-795	36.3	262
97	Identification of an imprinted master trans regulator at the KLF14 locus related to multiple metabolic phenotypes. <i>Nature Genetics</i> , 2011 , 43, 561-4	36.3	253
96	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
95	Whole-genome sequencing identifies common-to-rare variants associated with human blood metabolites. <i>Nature Genetics</i> , 2017 , 49, 568-578	36.3	210
94	A genotype calling algorithm for the Illumina BeadArray platform. <i>Bioinformatics</i> , 2007 , 23, 2741-6	7.2	194
93	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
92	Gene expression changes with age in skin, adipose tissue, blood and brain. <i>Genome Biology</i> , 2013 , 14, R75	18.3	185
91	Genome-wide analysis of multi-ancestry cohorts identifies new loci influencing intraocular pressure and susceptibility to glaucoma. <i>Nature Genetics</i> , 2014 , 46, 1126-1130	36.3	171
90	Genome-wide association analysis identifies TXNRD2, ATXN2 and FOXC1 as susceptibility loci for primary open-angle glaucoma. <i>Nature Genetics</i> , 2016 , 48, 189-94	36.3	159
89	The role of adiposity in cardiometabolic traits: a Mendelian randomization analysis. <i>PLoS Medicine</i> , 2013 , 10, e1001474	11.6	144
88	Methodological challenges of genome-wide association analysis in Africa. <i>Nature Reviews Genetics</i> , 2010 , 11, 149-60	30.1	143
87	Gene-gene and gene-environment interactions detected by transcriptome sequence analysis in twins. <i>Nature Genetics</i> , 2015 , 47, 88-91	36.3	140
86	Exome sequencing of 20,791 cases of type 2 diabetes and 24,440 controls. <i>Nature</i> , 2019 , 570, 71-76	50.4	129
85	Singapore Genome Variation Project: a haplotype map of three Southeast Asian populations. <i>Genome Research</i> , 2009 , 19, 2154-62	9.7	129
84	A global network for investigating the genomic epidemiology of malaria. <i>Nature</i> , 2008 , 456, 732-7	50.4	123
83	Rare variants in PPARG with decreased activity in adipocyte differentiation are associated with increased risk of type 2 diabetes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 13127-32	11.5	121
82	The Genetic Architecture of Gene Expression in Peripheral Blood. <i>American Journal of Human Genetics</i> , 2017 , 100, 228-237	11	98
81	Extreme genomic variation in a natural population. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 5698-703	11.5	97

80	Allelic heterogeneity of G6PD deficiency in West Africa and severe malaria susceptibility. <i>European Journal of Human Genetics</i> , 2009 , 17, 1080-5	5.3	92
79	Genetic Regulation of Adipose Gene Expression and Cardio-Metabolic Traits. <i>American Journal of Human Genetics</i> , 2017 , 100, 428-443	11	87
78	Tensor decomposition for multiple-tissue gene expression experiments. <i>Nature Genetics</i> , 2016 , 48, 1094-1100	36.3	87
77	Genetic interactions affecting human gene expression identified by variance association mapping. <i>ELife</i> , 2014 , 3, e01381	8.9	86
76	An integrated epigenomic analysis for type 2 diabetes susceptibility loci in monozygotic twins. <i>Nature Communications</i> , 2014 , 5, 5719	17.4	85
75	Regulatory variants at KLF14 influence type 2 diabetes risk via a female-specific effect on adipocyte size and body composition. <i>Nature Genetics</i> , 2018 , 50, 572-580	36.3	82
74	A haplome alignment and reference sequence of the highly polymorphic <i>Ciona savignyi</i> genome. <i>Genome Biology</i> , 2007 , 8, R41	18.3	82
73	Identification and functional characterization of G6PC2 coding variants influencing glycemc traits define an effector transcript at the G6PC2-ABCB11 locus. <i>PLoS Genetics</i> , 2015 , 11, e1004876	6	76
72	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. <i>American Journal of Human Genetics</i> , 2017 , 100, 865-884	11	74
71	Imputation-based meta-analysis of severe malaria in three African populations. <i>PLoS Genetics</i> , 2013 , 9, e1003509	6	74
70	The presence of methylation quantitative trait loci indicates a direct genetic influence on the level of DNA methylation in adipose tissue. <i>PLoS ONE</i> , 2013 , 8, e55923	3.7	71
69	Eight common genetic variants associated with serum DHEAS levels suggest a key role in ageing mechanisms. <i>PLoS Genetics</i> , 2011 , 7, e1002025	6	69
68	Cell type-specific genetic regulation of gene expression across human tissues. <i>Science</i> , 2020 , 369,	33.3	68
67	Detecting and characterizing genomic signatures of positive selection in global populations. <i>American Journal of Human Genetics</i> , 2013 , 92, 866-81	11	56
66	Smoking induces coordinated DNA methylation and gene expression changes in adipose tissue with consequences for metabolic health. <i>Clinical Epigenetics</i> , 2018 , 10, 126	7.7	56
65	Predicting causal variants affecting expression by using whole-genome sequencing and RNA-seq from multiple human tissues. <i>Nature Genetics</i> , 2017 , 49, 1747-1751	36.3	55
64	Positive selection of a CD36 nonsense variant in sub-Saharan Africa, but no association with severe malaria phenotypes. <i>Human Molecular Genetics</i> , 2009 , 18, 2683-92	5.6	53
63	Genome-wide comparisons of variation in linkage disequilibrium. <i>Genome Research</i> , 2009 , 19, 1849-60	9.7	53

62	TwinsUK: The UK Adult Twin Registry Update. <i>Twin Research and Human Genetics</i> , 2019 , 22, 523-529	2.2	51
61	Current smoking and COVID-19 risk: results from a population symptom app in over 2.4 million people. <i>Thorax</i> , 2021 , 76, 714-722	7.3	47
60	The trans-ancestral genomic architecture of glycemic traits. <i>Nature Genetics</i> , 2021 , 53, 840-860	36.3	44
59	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
58	Age-dependent changes in mean and variance of gene expression across tissues in a twin cohort. <i>Human Molecular Genetics</i> , 2018 , 27, 732-741	5.6	43
57	Extent, causes, and consequences of small RNA expression variation in human adipose tissue. <i>PLoS Genetics</i> , 2012 , 8, e1002704	6	43
56	Tumor necrosis factor and lymphotoxin-alpha polymorphisms and severe malaria in African populations. <i>Journal of Infectious Diseases</i> , 2009 , 199, 569-75	7	42
55	Integration of human adipocyte chromosomal interactions with adipose gene expression prioritizes obesity-related genes from GWAS. <i>Nature Communications</i> , 2018 , 9, 1512	17.4	41
54	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. <i>Age and Ageing</i> , 2021 , 50, 40-48	3	41
53	Cell-Type Heterogeneity in Adipose Tissue Is Associated with Complex Traits and Reveals Disease-Relevant Cell-Specific eQTLs. <i>American Journal of Human Genetics</i> , 2019 , 104, 1013-1024	11	37
52	Interferon inducible X-linked gene CXorf21 may contribute to sexual dimorphism in Systemic Lupus Erythematosus. <i>Nature Communications</i> , 2019 , 10, 2164	17.4	35
51	A genome-wide association study of intra-ocular pressure suggests a novel association in the gene FAM125B in the TwinsUK cohort. <i>Human Molecular Genetics</i> , 2014 , 23, 3343-8	5.6	32
50	Nuclear genetic regulation of the human mitochondrial transcriptome. <i>ELife</i> , 2019 , 8,	8.9	32
49	Estrogen receptor α controls metabolism in white and brown adipocytes by regulating and mitochondrial remodeling. <i>Science Translational Medicine</i> , 2020 , 12,	17.5	32
48	Metabolomic profiling to dissect the role of visceral fat in cardiometabolic health. <i>Obesity</i> , 2016 , 24, 1380-8	8	30
47	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
46	Mapping eQTLs with RNA-seq reveals novel susceptibility genes, non-coding RNAs and alternative-splicing events in systemic lupus erythematosus. <i>Human Molecular Genetics</i> , 2017 , 26, 1003-1017	5.6	28
45	Power consequences of linkage disequilibrium variation between populations. <i>Genetic Epidemiology</i> , 2009 , 33, 128-35	2.6	27

44	Expression of phosphofructokinase in skeletal muscle is influenced by genetic variation and associated with insulin sensitivity. <i>Diabetes</i> , 2014 , 63, 1154-65	0.9	25
43	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. <i>Scientific Data</i> , 2017 , 4, 170179	8.2	22
42	Simulation of Finnish population history, guided by empirical genetic data, to assess power of rare-variant tests in Finland. <i>American Journal of Human Genetics</i> , 2014 , 94, 710-20	11	19
41	Heritability of skewed X-inactivation in female twins is tissue-specific and associated with age. <i>Nature Communications</i> , 2019 , 10, 5339	17.4	19
40	Time-dependent genetic effects on gene expression implicate aging processes. <i>Genome Research</i> , 2017 , 27, 545-552	9.7	18
39	Variation in human genes encoding adhesion and proinflammatory molecules are associated with severe malaria in the Vietnamese. <i>Genes and Immunity</i> , 2012 , 13, 503-8	4.4	18
38	Concordance for clonal hematopoiesis is limited in elderly twins. <i>Blood</i> , 2020 , 135, 269-273	2.2	18
37	Epigenetic findings in periodontitis in UK twins: a cross-sectional study. <i>Clinical Epigenetics</i> , 2019 , 11, 27	7.7	17
36	X chromosome dosage of histone demethylase KDM5C determines sex differences in adiposity. <i>Journal of Clinical Investigation</i> , 2020 , 130, 5688-5702	15.9	17
35	Adiposity-Dependent Regulatory Effects on Multi-tissue Transcriptomes. <i>American Journal of Human Genetics</i> , 2016 , 99, 567-579	11	17
34	RSPO3 impacts body fat distribution and regulates adipose cell biology in vitro. <i>Nature Communications</i> , 2020 , 11, 2797	17.4	15
33	Interrogating causal pathways linking genetic variants, small molecule metabolites, and circulating lipids. <i>Genome Medicine</i> , 2014 , 6, 25	14.4	14
32	Integrated multiomics approach identifies calcium and integrin-binding protein-2 as a novel gene for pulse wave velocity. <i>Journal of Hypertension</i> , 2016 , 34, 79-87	1.9	14
31	Whole genome-amplified DNA: insights and imputation. <i>Nature Methods</i> , 2008 , 5, 279-80	21.6	13
30	The rate of nonallelic homologous recombination in males is highly variable, correlated between monozygotic twins and independent of age. <i>PLoS Genetics</i> , 2014 , 10, e1004195	6	12
29	ABCC5 transporter is a novel type 2 diabetes susceptibility gene in European and African American populations. <i>Annals of Human Genetics</i> , 2014 , 78, 333-44	2.2	11
28	Autosomal genetic control of human gene expression does not differ across the sexes. <i>Genome Biology</i> , 2016 , 17, 248	18.3	10
27	Genetic correlations reveal the shared genetic architecture of transcription in human peripheral blood. <i>Nature Communications</i> , 2017 , 8, 483	17.4	10

26	Assessing genuine parents-offspring trios for genetic association studies. <i>Human Heredity</i> , 2009 , 67, 26-37	1.1	10
25	Cell type specific genetic regulation of gene expression across human tissues		7
24	Regulatory sites for splicing in human basal ganglia are enriched for disease-relevant information. <i>Nature Communications</i> , 2020 , 11, 1041	17.4	6
23	Global Analysis of DNA Methylation Variation in Adipose Tissue from Twins Reveals Links to Disease-Associated Variants in Distal Regulatory Elements. <i>American Journal of Human Genetics</i> , 2013 , 93, 1158	11	6
22	Perturbation analysis: a simple method for filtering SNPs with erroneous genotyping in genome-wide association studies. <i>Annals of Human Genetics</i> , 2008 , 72, 368-74	2.2	6
21	Genetic variation influencing DNA methylation provides insights into molecular mechanisms regulating genomic function.. <i>Nature Genetics</i> , 2022 ,	36.3	6
20	A Bayesian approach using covariance of single nucleotide polymorphism data to detect differences in linkage disequilibrium patterns between groups of individuals. <i>Bioinformatics</i> , 2010 , 26, 1999-2003	7.2	5
19	A novel method for haplotype clustering and visualization. <i>Genetic Epidemiology</i> , 2010 , 34, 34-41	2.6	5
18	Determinants of penetrance and variable expressivity in monogenic metabolic conditions across 77,184 exomes. <i>Nature Communications</i> , 2021 , 12, 3505	17.4	5
17	Age-dependent changes in mean and variance of gene expression across tissues in a twin cohort		4
16	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes		4
15	ACE2 expression in adipose tissue is associated with COVID-19 cardio-metabolic risk factors and cell type composition 2020 ,		4
14	Cell-type heterogeneity in adipose tissue is associated with complex traits and reveals disease-relevant cell-specific eQTLs		4
13	Tissue-Specific Alteration of Metabolic Pathways Influences Glycemic Regulation		4
12	Fasting and time of day independently modulate circadian rhythm relevant gene expression in adipose and skin tissue. <i>BMC Genomics</i> , 2018 , 19, 659	4.5	4
11	Chaining Algorithms for Alignment of Draft Sequence. <i>Lecture Notes in Computer Science</i> , 2004 , 326-337	0.9	3
10	Quantifying the degree of sharing of genetic and non-genetic causes of gene expression variability across four tissues		3
9	Common variants in SOX-2 and congenital cataract genes contribute to age-related nuclear cataract. <i>Communications Biology</i> , 2020 , 3, 755	6.7	3

8	Smoking induces coordinated DNA methylation and gene expression changes in adipose tissue with consequences for metabolic health		2
7	Genetic discovery and translational decision support from exome sequencing of 20,791 type 2 diabetes cases and 24,440 controls from five ancestries		2
6	Genome-wide scan and fine-mapping of rare nonsynonymous associations implicates intracellular lipolysis genes in fat distribution and cardio-metabolic risk		2
5	Predicting causal variants affecting expression using whole genome sequence and RNA-seq from multiple human tissues		2
4	Protein-Coding Variants Implicate Novel Genes Related to Lipid Homeostasis Contributing to Body Fat Distribution		1
3	Further evidence supporting a potential role for ADH1B in obesity. <i>Scientific Reports</i> , 2021, 11, 1932	4.9	1
2	Identification of rare loss of function genetic variation regulating body fat distribution. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2021,	5.6	1
1	Introducing ExHiBITT [Exploring Host microBlome inTeractions in Twins] a colon multiomic cohort study. <i>Wellcome Open Research</i> , 5, 30	4.8	