Kerrin S Small

List of Publications by Year in Descending Order

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	Genetic variation influencing DNA methylation provides insights into molecular mechanisms regulating genomic function.. *Nature Genetics*, **2022**,	36.3	6
114	The trans-ancestral genomic architecture of glycemic traits. *Nature Genetics*, **2021**, 53, 840-860	36.3	44
113	Determinants of penetrance and variable expressivity in monogenic metabolic conditions across 77,184 exomes. *Nature Communications*, **2021**, 12, 3505	17.4	5
112	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	3	41
111	Further evidence supporting a potential role for ADH1B in obesity. *Scientific Reports*, **2021**, 11, 1932	4.9	1
110	Current smoking and COVID-19 risk: results from a population symptom app in over 2.4 million people. *Thorax*, **2021**, 76, 714-722	7.3	47
109	Identification of rare loss of function genetic variation regulating body fat distribution. *Journal of Clinical Endocrinology and Metabolism*, **2021**,	5.6	1
108	RSPO3 impacts body fat distribution and regulates adipose cell biology in vitro. *Nature Communications*, **2020**, 11, 2797	17.4	15
107	Regulatory sites for splicing in human basal ganglia are enriched for disease-relevant information. *Nature Communications*, **2020**, 11, 1041	17.4	6
106	X chromosome dosage of histone demethylase KDM5C determines sex differences in adiposity. *Journal of Clinical Investigation*, **2020**, 130, 5688-5702	15.9	17
105	ACE2 expression in adipose tissue is associated with COVID-19 cardio-metabolic risk factors and cell type composition **2020**,		4
104	Estrogen receptor □controls metabolism in white and brown adipocytes by regulating and mitochondrial remodeling. *Science Translational Medicine*, **2020**, 12,	17.5	32
103	Cell type-specific genetic regulation of gene expression across human tissues. *Science*, **2020**, 369,	33.3	68
102	Common variants in SOX-2 and congenital cataract genes contribute to age-related nuclear cataract. *Communications Biology*, **2020**, 3, 755	6.7	3
101	Concordance for clonal hematopoiesis is limited in elderly twins. *Blood*, **2020**, 135, 269-273	2.2	18
100	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	11	37
99	Exome sequencing of 20,791□cases of type 2 diabetes and 24,440□controls. *Nature*, **2019**, 570, 71-76	50.4	129

98	Interferon inducible X-linked gene CXorf21 may contribute to sexual dimorphism in Systemic Lupus Erythematosus. *Nature Communications*, **2019**, 10, 2164	17.4	35
97	Epigenetic findings in periodontitis in UK twins: a cross-sectional study. *Clinical Epigenetics*, **2019**, 11, 27	7.7	17
96	TwinsUK: The UK Adult Twin Registry Update. *Twin Research and Human Genetics*, **2019**, 22, 523-529	2.2	51
95	Nuclear genetic regulation of the human mitochondrial transcriptome. *ELife*, **2019**, 8,	8.9	32
94	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. *Nature Genetics*, **2019**, 51, 452-469	36.3	44
93	Heritability of skewed X-inactivation in female twins is tissue-specific and associated with age. *Nature Communications*, **2019**, 10, 5339	17.4	19
92	Integration of human adipocyte chromosomal interactions with adipose gene expression prioritizes obesity-related genes from GWAS. *Nature Communications*, **2018**, 9, 1512	17.4	41
91	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. *Nature Genetics*, **2018**, 50, 559-571	36.3	221
90	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	36.3	82
89	Age-dependent changes in mean and variance of gene expression across tissues in a twin cohort. *Human Molecular Genetics*, **2018**, 27, 732-741	5.6	43
88	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. *Nature Genetics*, **2018**, 50, 26-41	36.3	186
87	Smoking induces coordinated DNA methylation and gene expression changes in adipose tissue with consequences for metabolic health. *Clinical Epigenetics*, **2018**, 10, 126	7.7	56
86	Fasting and time of day independently modulate circadian rhythm relevant gene expression in adipose and skin tissue. *BMC Genomics*, **2018**, 19, 659	4.5	4
85	The fecal metabolome as a functional readout of the gut microbiome. *Nature Genetics*, **2018**, 50, 790-795	36.3	262
84	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, 1003-1017	5.6	28
83	Rare and low-frequency coding variants alter human adult height. *Nature*, **2017**, 542, 186-190	50.4	412
82	Genetic Regulation of Adipose Gene Expression and Cardio-Metabolic Traits. *American Journal of Human Genetics*, **2017**, 100, 428-443	11	87
81	Whole-genome sequencing identifies common-to-rare variants associated with human blood metabolites. *Nature Genetics*, **2017**, 49, 568-578	36.3	210

80	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. *American Journal of Human Genetics*, **2017**, 100, 865-884	11	74
79	A Low-Frequency Inactivating Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. *Diabetes*, **2017**, 66, 2019-2032	0.9	29
78	Time-dependent genetic effects on gene expression implicate aging processes. *Genome Research*, **2017**, 27, 545-552	9.7	18
77	The Genetic Architecture of Gene Expression in Peripheral Blood. *American Journal of Human Genetics*, **2017**, 100, 228-237	11	98
76	Exome-wide association study of plasma lipids in >300,000 individuals. *Nature Genetics*, **2017**, 49, 1758-1766	36.3	310
75	Predicting causal variants affecting expression by using whole-genome sequencing and RNA-seq from multiple human tissues. *Nature Genetics*, **2017**, 49, 1747-1751	36.3	55
74	Genetic correlations reveal the shared genetic architecture of transcription in human peripheral blood. *Nature Communications*, **2017**, 8, 483	17.4	10
73	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. *Scientific Data*, **2017**, 4, 170179	8.2	22
72	A reference panel of 64,976 haplotypes for genotype imputation. *Nature Genetics*, **2016**, 48, 1279-83	36.3	1447
71	Autosomal genetic control of human gene expression does not differ across the sexes. *Genome Biology*, **2016**, 17, 248	18.3	10
70	Genome-wide association analysis identifies TXNRD2, ATXN2 and FOXC1 as susceptibility loci for primary open-angle glaucoma. *Nature Genetics*, **2016**, 48, 189-94	36.3	159
69	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	1.9	14
68	The genetic architecture of type 2 diabetes. *Nature*, **2016**, 536, 41-47	50.4	704
67	Adiposity-Dependent Regulatory Effects on Multi-tissue Transcriptomes. *American Journal of Human Genetics*, **2016**, 99, 567-579	11	17
66	Tensor decomposition for multiple-tissue gene expression experiments. *Nature Genetics*, **2016**, 48, 1094-1100	36.3	87
65	Metabolomic profiling to dissect the role of visceral fat in cardiometabolic health. *Obesity*, **2016**, 24, 1380-8	8	30
64	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	6	76
63	The UK10K project identifies rare variants in health and disease. *Nature*, **2015**, 526, 82-90	50.4	776

62	Gene-gene and gene-environment interactions detected by transcriptome sequence analysis in twins. *Nature Genetics*, **2015**, 47, 88-91	36.3	140
61	Genome-wide analysis of multi-ancestry cohorts identifies new loci influencing intraocular pressure and susceptibility to glaucoma. *Nature Genetics*, **2014**, 46, 1126-1130	36.3	171
60	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. *Nature Genetics*, **2014**, 46, 234-44	36.3	784
59	Expression of phosphofructokinase in skeletal muscle is influenced by genetic variation and associated with insulin sensitivity. *Diabetes*, **2014**, 63, 1154-65	0.9	25
58	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, 710-20	11	19
57	An integrated epigenomic analysis for type 2 diabetes susceptibility loci in monozygotic twins. *Nature Communications*, **2014**, 5, 5719	17.4	85
56	The rate of nonallelic homologous recombination in males is highly variable, correlated between monozygotic twins and independent of age. *PLoS Genetics*, **2014**, 10, e1004195	6	12
55	ABCC5 transporter is a novel type 2 diabetes susceptibility gene in European and African American populations. *Annals of Human Genetics*, **2014**, 78, 333-44	2.2	11
54	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, 13127-32	11.5	121
53	Interrogating causal pathways linking genetic variants, small molecule metabolites, and circulating lipids. *Genome Medicine*, **2014**, 6, 25	14.4	14
52	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, 3343-8	5.6	32
51	Genetic interactions affecting human gene expression identified by variance association mapping. *ELife*, **2014**, 3, e01381	8.9	86
50	Detecting and characterizing genomic signatures of positive selection in global populations. *American Journal of Human Genetics*, **2013**, 92, 866-81	11	56
49	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, 876-90	11	269
48	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	11	6
47	Imputation-based meta-analysis of severe malaria in three African populations. *PLoS Genetics*, **2013**, 9, e1003509	6	74
46	The role of adiposity in cardiometabolic traits: a Mendelian randomization analysis. *PLoS Medicine*, **2013**, 10, e1001474	11.6	144
45	Gene expression changes with age in skin, adipose tissue, blood and brain. *Genome Biology*, **2013**, 14, R75	18.3	185

44	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	3.7	71
43	Epigenome-wide scans identify differentially methylated regions for age and age-related phenotypes in a healthy ageing population. *PLoS Genetics*, **2012**, 8, e1002629	6	501
42	Mapping cis- and trans-regulatory effects across multiple tissues in twins. *Nature Genetics*, **2012**, 44, 1084-9	36.3	572
41	A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. *Nature Genetics*, **2012**, 44, 659-69	36.3	615
40	Extent, causes, and consequences of small RNA expression variation in human adipose tissue. *PLoS Genetics*, **2012**, 8, e1002704	6	43
39	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	6	326
38	Variation in human genes encoding adhesion and proinflammatory molecules are associated with severe malaria in the Vietnamese. *Genes and Immunity*, **2012**, 13, 503-8	4.4	18
37	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. *Nature Genetics*, **2012**, 44, 991-1005	36.3	621
36	Genome-wide association study in individuals of South Asian ancestry identifies six new type 2 diabetes susceptibility loci. *Nature Genetics*, **2011**, 43, 984-9	36.3	406
35	Human metabolic individuality in biomedical and pharmaceutical research. *Nature*, **2011**, 477, 54-60	50.4	728
34	Identification of an imprinted master trans regulator at the KLF14 locus related to multiple metabolic phenotypes. *Nature Genetics*, **2011**, 43, 561-4	36.3	253
33	The architecture of gene regulatory variation across multiple human tissues: the MuTHER study. *PLoS Genetics*, **2011**, 7, e1002003	6	336
32	Eight common genetic variants associated with serum DHEAS levels suggest a key role in ageing mechanisms. *PLoS Genetics*, **2011**, 7, e1002025	6	69
31	Genome-wide association analyses identifies a susceptibility locus for tuberculosis on chromosome 18q11.2. *Nature Genetics*, **2010**, 42, 739-741	36.3	276
30	Methodological challenges of genome-wide association analysis in Africa. *Nature Reviews Genetics*, **2010**, 11, 149-60	30.1	143
29	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	7.2	5
28	A novel method for haplotype clustering and visualization. *Genetic Epidemiology*, **2010**, 34, 34-41	2.6	5
27	Tumor necrosis factor and lymphotoxin-alpha polymorphisms and severe malaria in African populations. *Journal of Infectious Diseases*, **2009**, 199, 569-75	7	42

26	Positive selection of a CD36 nonsense variant in sub-Saharan Africa, but no association with severe malaria phenotypes. *Human Molecular Genetics*, **2009**, 18, 2683-92	5.6	53
25	Assessing genuine parents-offspring trios for genetic association studies. *Human Heredity*, **2009**, 67, 26-37	1.1	10
24	Singapore Genome Variation Project: a haplotype map of three Southeast Asian populations. *Genome Research*, **2009**, 19, 2154-62	9.7	129
23	Genome-wide comparisons of variation in linkage disequilibrium. *Genome Research*, **2009**, 19, 1849-60	9.7	53
22	Power consequences of linkage disequilibrium variation between populations. *Genetic Epidemiology*, **2009**, 33, 128-35	2.6	27
21	Allelic heterogeneity of G6PD deficiency in West Africa and severe malaria susceptibility. *European Journal of Human Genetics*, **2009**, 17, 1080-5	5.3	92
20	Genome-wide and fine-resolution association analysis of malaria in West Africa. *Nature Genetics*, **2009**, 41, 657-65	36.3	297
19	A global network for investigating the genomic epidemiology of malaria. *Nature*, **2008**, 456, 732-7	50.4	123
18	Whole genome-amplified DNA: insights and imputation. *Nature Methods*, **2008**, 5, 279-80	21.6	13
17	Perturbation analysis: a simple method for filtering SNPs with erroneous genotyping in genome-wide association studies. *Annals of Human Genetics*, **2008**, 72, 368-74	2.2	6
16	Extreme genomic variation in a natural population. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 5698-703	11.5	97
15	A genotype calling algorithm for the Illumina BeadArray platform. *Bioinformatics*, **2007**, 23, 2741-6	7.2	194
14	A haplome alignment and reference sequence of the highly polymorphic Ciona savignyi genome. *Genome Biology*, **2007**, 8, R41	18.3	82
13	Chaining Algorithms for Alignment of Draft Sequence. *Lecture Notes in Computer Science*, **2004**, 326-337	0.9	3
12	Introducing ExHiBITT Exploring Host microBIome inTeractions in Twins a colon multiomic cohort study. *Wellcome Open Research*,5, 30	4.8	
11	Quantifying the degree of sharing of genetic and non-genetic causes of gene expression variability across four tissues		3
10	Age-dependent changes in mean and variance of gene expression across tissues in a twin cohort		4
9	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes		4

8	Cell-type heterogeneity in adipose tissue is associated with complex traits and reveals disease-relevant cell-specific eQTLs	4
7	Protein-Coding Variants Implicate Novel Genes Related to Lipid Homeostasis Contributing to Body Fat Distribution	1
6	Smoking induces coordinated DNA methylation and gene expression changes in adipose tissue with consequences for metabolic health	2
5	Genetic discovery and translational decision support from exome sequencing of 20,791 type 2 diabetes cases and 24,440 controls from five ancestries	2
4	Genome-wide scan and fine-mapping of rare nonsynonymous associations implicates intracellular lipolysis genes in fat distribution and cardio-metabolic risk	2
3	Tissue-Specific Alteration of Metabolic Pathways Influences Glycemic Regulation	4
2	Cell type specific genetic regulation of gene expression across human tissues	7
1	Predicting causal variants affecting expression using whole genome sequence and RNA-seq from multiple human tissues	2