Sonia Shah

List of Publications by Citations

75 papers	12,371 citations	40 h-index	83 g-index
83 ext. papers	15,062 ext. citations	10.7 avg, IF	4.52 L-index

#	Paper	IF	Citations
75	Discovery and refinement of loci associated with lipid levels. *Nature Genetics*, **2013**, 45, 1274-1283	36.3	1904
74	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. *Nature Genetics*, **2012**, 44, 981-90	36.3	1482
73	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
72	DNA methylation age of blood predicts all-cause mortality in later life. *Genome Biology*, **2015**, 16, 25	18.3	670
71	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
70	Common variants associated with plasma triglycerides and risk for coronary artery disease. *Nature Genetics*, **2013**, 45, 1345-52	36.3	597
69	DNA methylation-based measures of biological age: meta-analysis predicting time to death. *Aging*, **2016**, 8, 1844-1865	5.6	531
68	Epigenetic Signatures of Cigarette Smoking. *Circulation: Cardiovascular Genetics*, **2016**, 9, 436-447		442
67	Mendelian randomization of blood lipids for coronary heart disease. *European Heart Journal*, **2015**, 36, 539-50	9.5	417
66	Association between alcohol and cardiovascular disease: Mendelian randomisation analysis based on individual participant data. *BMJ, The*, **2014**, 349, g4164	5.9	406
65	Use of low-density lipoprotein cholesterol gene score to distinguish patients with polygenic and monogenic familial hypercholesterolaemia: a case-control study. *Lancet, The*, **2013**, 381, 1293-301	40	376
64	The epigenetic clock is correlated with physical and cognitive fitness in the Lothian Birth Cohort 1936. *International Journal of Epidemiology*, **2015**, 44, 1388-96	7.8	357
63	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. *Nature Genetics*, **2016**, 48, 1171-1184	36.3	251
62	Large-scale gene-centric meta-analysis across 39 studies identifies type 2 diabetes loci. *American Journal of Human Genetics*, **2012**, 90, 410-25	11	214
61	Contribution of genetic variation to transgenerational inheritance of DNA methylation. *Genome Biology*, **2014**, 15, R73	18.3	179
60	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. *Genome Biology*, **2016**, 17, 255	18.3	171
59	A DNA methylation biomarker of alcohol consumption. *Molecular Psychiatry*, **2018**, 23, 422-433	15.1	164

58	Gene-centric association signals for lipids and apolipoproteins identified via the HumanCVD BeadChip. *American Journal of Human Genetics*, **2009**, 85, 628-42	11	163
57	Association of Body Mass Index with DNA Methylation and Gene Expression in Blood Cells and Relations to Cardiometabolic Disease: A Mendelian Randomization Approach. *PLoS Medicine*, **2017**, 14, e1002215	11.6	162
56	The epigenetic clock and telomere length are independently associated with chronological age and mortality. *International Journal of Epidemiology*, **2018**, 45, 424-432	7.8	153
55	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. *Nature Communications*, **2020**, 11, 163	17.4	140
54	Blood pressure loci identified with a gene-centric array. *American Journal of Human Genetics*, **2011**, 89, 688-700	11	137
53	Gene-centric meta-analysis in 87,736 individuals of European ancestry identifies multiple blood-pressure-related loci. *American Journal of Human Genetics*, **2014**, 94, 349-60	11	131
52	Refinement of variant selection for the LDL cholesterol genetic risk score in the diagnosis of the polygenic form of clinical familial hypercholesterolemia and replication in samples from 6 countries. *Clinical Chemistry*, **2015**, 61, 231-8	5.5	130
51	Genetic and environmental exposures constrain epigenetic drift over the human life course. *Genome Research*, **2014**, 24, 1725-33	9.7	123
50	Loci influencing blood pressure identified using a cardiovascular gene-centric array. *Human Molecular Genetics*, **2013**, 22, 1663-78	5.6	119
49	Selecting instruments for Mendelian randomization in the wake of genome-wide association studies. *International Journal of Epidemiology*, **2016**, 45, 1600-1616	7.8	114
48	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. *American Journal of Human Genetics*, **2011**, 88, 6-18	11	103
47	Plasma urate concentration and risk of coronary heart disease: a Mendelian randomisation analysis. *Lancet Diabetes and Endocrinology,the*, **2016**, 4, 327-36	18.1	100
46	Prox1 maintains muscle structure and growth in the developing heart. *Development (Cambridge)*, **2009**, 136, 495-505	6.6	92
45	Improving Phenotypic Prediction by Combining Genetic and Epigenetic Associations. *American Journal of Human Genetics*, **2015**, 97, 75-85	11	85
44	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. *American Journal of Human Genetics*, **2012**, 90, 1116-1117	11	78
43	Identification of 55,000 Replicated DNA Methylation QTL. *Scientific Reports*, **2018**, 8, 17605	4.9	78
42	Comparative analysis of genome-wide association studies signals for lipids, diabetes, and coronary heart disease: Cardiovascular Biomarker Genetics Collaboration. *European Heart Journal*, **2012**, 33, 393-407	9.5	75
41	Epigenetic Patterns in Blood Associated With Lipid Traits Predict Incident Coronary Heart Disease Events and Are Enriched for Results From Genome-Wide Association Studies. *Circulation: Cardiovascular Genetics*, **2017**, 10,		72

40	GWAS and colocalization analyses implicate carotid intima-media thickness and carotid plaque loci in cardiovascular outcomes. *Nature Communications*, **2018**, 9, 5141	17.4	64
39	Overexpression of MHC class I heavy chain protein in young skeletal muscle leads to severe myositis: implications for juvenile myositis. *American Journal of Pathology*, **2009**, 175, 1030-40	5.8	54
38	Cross-ethnic meta-analysis identifies association of the GPX3-TNIP1 locus with amyotrophic lateral sclerosis. *Nature Communications*, **2017**, 8, 611	17.4	45
37	Cholesteryl Ester Transfer Protein (CETP) polymorphisms affect mRNA splicing, HDL levels, and sex-dependent cardiovascular risk. *PLoS ONE*, **2012**, 7, e31930	3.7	45
36	C9orf72 hexanucleotide repeat expansions in Chinese sporadic amyotrophic lateral sclerosis. *Neurobiology of Aging*, **2015**, 36, 2660.e1-8	5.6	40
35	Identification of the BCAR1-CFDP1-TMEM170A locus as a determinant of carotid intima-media thickness and coronary artery disease risk. *Circulation: Cardiovascular Genetics*, **2012**, 5, 656-65		35
34	Gene-centric analysis identifies variants associated with interleukin-6 levels and shared pathways with other inflammation markers. *Circulation: Cardiovascular Genetics*, **2013**, 6, 163-70		34
33	Population genomics of cardiometabolic traits: design of the University College London-London School of Hygiene and Tropical Medicine-Edinburgh-Bristol (UCLEB) Consortium. *PLoS ONE*, **2013**, 8, e71345	3.7	33
32	Genetic determinants of circulating interleukin-1 receptor antagonist levels and their association with glycemic traits. *Diabetes*, **2014**, 63, 4343-59	0.9	32
31	Causal relevance of blood lipid fractions in the development of carotid atherosclerosis: Mendelian randomization analysis. *Circulation: Cardiovascular Genetics*, **2013**, 6, 63-72		32
30	A genomic atlas of human adrenal and gonad development. *Wellcome Open Research*, **2017**, 2, 25	4.8	31
29	Influence of common genetic variation on blood lipid levels, cardiovascular risk, and coronary events in two British prospective cohort studies. *European Heart Journal*, **2013**, 34, 972-81	9.5	28
28	Sex-Specific Effects of Adiponectin on Carotid Intima-Media Thickness and Incident Cardiovascular Disease. *Journal of the American Heart Association*, **2015**, 4, e001853	6	25
27	Genetic variants associated with Von Willebrand factor levels in healthy men and women identified using the HumanCVD BeadChip. *Annals of Human Genetics*, **2011**, 75, 456-67	2.2	24
26	Four genetic loci influencing electrocardiographic indices of left ventricular hypertrophy. *Circulation: Cardiovascular Genetics*, **2011**, 4, 626-35		22
25	ChIP-on-chip analysis reveals angiopoietin 2 (Ang2, ANGPT2) as a novel target of steroidogenic factor-1 (SF-1, NR5A1) in the human adrenal gland. *FASEB Journal*, **2011**, 25, 1166-75	0.9	21
24	Low levels of IgM antibodies against phosphorylcholine are associated with fast carotid intima media thickness progression and cardiovascular risk in men. *Atherosclerosis*, **2014**, 236, 394-9	3.1	19
23	Identifying differential exon splicing using linear models and correlation coefficients. *BMC Bioinformatics*, **2009**, 10, 26	3.6	19

22	Use of allele-specific FAIRE to determine functional regulatory polymorphism using large-scale genotyping arrays. *PLoS Genetics*, **2012**, 8, e1002908	6	19
21	Annotation of environmental OMICS data: application to the transcriptomics domain. *OMICS A Journal of Integrative Biology*, **2006**, 10, 172-8	3.8	18
20	Meta analysis of candidate gene variants outside the LPA locus with Lp(a) plasma levels in 14,500 participants of six White European cohorts. *Atherosclerosis*, **2011**, 217, 447-51	3.1	17
19	IRS1 gene variants, dysglycaemic metabolic changes and type-2 diabetes risk. *Nutrition, Metabolism and Cardiovascular Diseases*, **2012**, 22, 1024-30	4.5	15
18	Identification of 55,000 Replicated DNA Methylation QTL		14
17	Integration of genetics into a systems model of electrocardiographic traits using HumanCVD BeadChip. *Circulation: Cardiovascular Genetics*, **2012**, 5, 630-8		12
16	Whole exome sequencing and DNA methylation analysis in a clinical amyotrophic lateral sclerosis cohort. *Molecular Genetics & Genomic Medicine*, **2017**, 5, 418-428	2.3	8
15	Gene-centric association signals for haemostasis and thrombosis traits identified with the HumanCVD BeadChip. *Thrombosis and Haemostasis*, **2013**, 110, 995-1003	7	7
14	Sharing a Placenta is Associated With a Greater Similarity in DNA Methylation in Monochorionic Versus Dichorionic Twin Pars in Blood at Age 14. *Twin Research and Human Genetics*, **2015**, 18, 680-5	2.2	6
13	A gene-centric study of common carotid artery remodelling. *Atherosclerosis*, **2013**, 226, 440-6	3.1	5
12	rHVDM: an R package to predict the activity and targets of a transcription factor. *Bioinformatics*, **2009**, 25, 419-20	7.2	5
11	Comprehensive genetic analysis of the human lipidome identifies loci associated with lipid homeostasis with links to coronary artery disease. *Nature Communications*, **2022**, 13,	17.4	5
10	Large-Scale Gene-Centric Meta-Analysis across 39 Studies Identifies Type 2 Diabetes Loci. *American Journal of Human Genetics*, **2012**, 90, 753	11	4
9	Prox1 maintains muscle structure and growth in the developing heart. *Development (Cambridge)*, **2009**, 136, 699-699	6.6	4
8	Complex disease genetics: present and future translational applications. *Genome Medicine*, **2009**, 1, 104	14.4	2
7	Genome-wide association study provides new insights into the genetic architecture and pathogenesis of heart failure		2
6	A genetic model of ivabradine recapitulates results from randomized clinical trials. *PLoS ONE*, **2020**, 15, e0236193	3.7	1
5	The genomics of heart failure: design and rationale of the HERMES consortium. *ESC Heart Failure*, **2021**,	3.7	1

4 A genetic model of ivabradine recapitulates results from randomized clinical trials **2020**, 15, e0236193

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2 A genetic model of ivabradine recapitulates results from randomized clinical trials **2020**, 15, e0236193

1 A genetic model of ivabradine recapitulates results from randomized clinical trials **2020**, 15, e0236193