Sonia Shah

List of Publications by Year
in descending order

76 papers	16,656 citations	70961 41 h-index	88477 70 g-index
83 all docs	83 docs citations	83 times ranked	24735 citing authors

#	Article	IF	Citations
1	Discovery and refinement of loci associated with lipid levels. Nature Genetics, 2013, 45, 1274-1283.	9.4	2,641
2	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
3	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
4	DNA methylation age of blood predicts all-cause mortality in later life. Genome Biology, 2015, 16, 25.	3.8	928
5	DNA methylation-based measures of biological age: meta-analysis predicting time to death. Aging, 2016, 8, 1844-1865.	1.4	786
6	Common variants associated with plasma triglycerides and risk for coronary artery disease. Nature Genetics, 2013, 45, 1345-1352.	9.4	754
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.	9.4	746
8	Epigenetic Signatures of Cigarette Smoking. Circulation: Cardiovascular Genetics, 2016, 9, 436-447.	5.1	678
9	Mendelian randomization of blood lipids for coronary heart disease. European Heart Journal, 2015, 36, 539-550.	1.0	567
10	Association between alcohol and cardiovascular disease: Mendelian randomisation analysis based on individual participant data. BMJ, The, 2014, 349, g4164-g4164.	3.0	528
11	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, 1293-1301.	6.3	485
12	The epigenetic clock is correlated with physical and cognitive fitness in the Lothian Birth Cohort 1936. International Journal of Epidemiology, 2015, 44, 1388-1396.	0.9	472
13	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. Nature Communications, 2020, 11, 163.	5.8	466
14	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. Nature Genetics, 2016, 48, 1171-1184.	9.4	362
15	A DNA methylation biomarker of alcohol consumption. Molecular Psychiatry, 2018, 23, 422-433.	4.1	280
16	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. Genome Biology, 2016, 17, 255.	3.8	251
17	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.	3.9	246
18	Large-Scale Gene-Centric Meta-Analysis across 39 Studies Identifies Type 2 Diabetes Loci. American Journal of Human Genetics, 2012, 90, 410-425.	2.6	239

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19	Selecting instruments for Mendelian randomization in the wake of genome-wide association studies. International Journal of Epidemiology, 2016, 45, 1600-1616.	0.9	232
20	Contribution of genetic variation to transgenerational inheritance of DNA methylation. Genome Biology, 2014, 15, R73.	13.9	231
21	The epigenetic clock and telomere length are independently associated with chronological age and mortality. International Journal of Epidemiology, 2016, 45, 424-432.	0.9	227
22	Gene-centric Association Signals for Lipids and Apolipoproteins Identified via the HumanCVD BeadChip. American Journal of Human Genetics, 2009, 85, 628-642.	2.6	183
23	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, 231-238.	1.5	166
24	Blood Pressure Loci Identified with a Gene-Centric Array. American Journal of Human Genetics, 2011, 89, 688-700.	2.6	159
25	Gene-centric Meta-analysis in 87,736 Individuals of European Ancestry Identifies Multiple Blood-Pressure-Related Loci. American Journal of Human Genetics, 2014, 94, 349-360.	2.6	158
26	Identification of 55,000 Replicated DNA Methylation QTL. Scientific Reports, 2018, 8, 17605.	1.6	157
27	Genetic and environmental exposures constrain epigenetic drift over the human life course. Genome Research, 2014, 24, 1725-1733.	2.4	152
28	Loci influencing blood pressure identified using a cardiovascular gene-centric array. Human Molecular Genetics, 2013, 22, 1663-1678.	1.4	141
29	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. American Journal of Human Genetics, 2011, 88, 6-18.	2.6	122
30	Plasma urate concentration and risk of coronary heart disease: a Mendelian randomisation analysis. Lancet Diabetes and Endocrinology,the, 2016, 4, 327-336.	5.5	122
31	GWAS and colocalization analyses implicate carotid intima-media thickness and carotid plaque loci in cardiovascular outcomes. Nature Communications, 2018, 9, 5141.	5.8	119
32	Improving Phenotypic Prediction by Combining Genetic and Epigenetic Associations. American Journal of Human Genetics, 2015, 97, 75-85.	2.6	116
33	Prox1 maintains muscle structure and growth in the developing heart. Development (Cambridge), 2009, 136, 495-505.	1.2	112
34	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, .	5.1	104
35	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.	1.0	93
36	Cross-ethnic meta-analysis identifies association of the GPX3-TNIP1 locus with amyotrophic lateral sclerosis. Nature Communications, 2017, 8, 611.	5.8	93

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37	Cholesteryl Ester Transfer Protein (CETP) Polymorphisms Affect mRNA Splicing, HDL Levels, and Sex-Dependent Cardiovascular Risk. PLoS ONE, 2012, 7, e31930.	1.1	59
38	Overexpression of MHC Class I Heavy Chain Protein in Young Skeletal Muscle Leads to Severe Myositis. American Journal of Pathology, 2009, 175, 1030-1040.	1.9	57
39	A genomic atlas of human adrenal and gonad development. Wellcome Open Research, 2017, 2, 25.	0.9	55
40	C9orf72 hexanucleotide repeat expansions in Chinese sporadic amyotrophic lateral sclerosis. Neurobiology of Aging, 2015, 36, 2660.e1-2660.e8.	1.5	50
41	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, 656-665.	5.1	47
42	Gene-Centric Analysis Identifies Variants Associated With Interleukin-6 Levels and Shared Pathways With Other Inflammation Markers. Circulation: Cardiovascular Genetics, 2013, 6, 163-170.	5.1	44
43	Genetic Determinants of Circulating Interleukin-1 Receptor Antagonist Levels and Their Association With Glycemic Traits. Diabetes, 2014, 63, 4343-4359.	0.3	40
44	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.	1.1	39
45	Causal Relevance of Blood Lipid Fractions in the Development of Carotid Atherosclerosis. Circulation: Cardiovascular Genetics, 2013, 6, 63-72.	5.1	36
46	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, 972-981.	1.0	33
47	Sexâ€Specific Effects of Adiponectin on Carotid Intimaâ€Media Thickness and Incident Cardiovascular Disease. Journal of the American Heart Association, 2015, 4, e001853.	1.6	33
48	Comprehensive genetic analysis of the human lipidome identifies loci associated with lipid homeostasis with links to coronary artery disease. Nature Communications, 2022, 13, .	5.8	30
49	Genetic Variants Associated with von Willebrand Factor Levels in Healthy Men and Women Identified Using the HumanCVD BeadChip. Annals of Human Genetics, 2011, 75, 456-467.	0.3	28
50	Four Genetic Loci Influencing Electrocardiographic Indices of Left Ventricular Hypertrophy. Circulation: Cardiovascular Genetics, 2011, 4, 626-635.	5.1	28
51	ChIPâ€onâ€chip analysis reveals angiopoietin 2 (Ang2, ANGPT2) as a novel target of steroidogenic factorâ€1 (SFâ€1, NR5A1) in the human adrenal gland. FASEB Journal, 2011, 25, 1166-1175.	0.2	27
52	Low levels of IgM antibodies against phosphorylcholine are associated with fast carotid intima media thickness progression and cardiovascular risk in men. Atherosclerosis, 2014, 236, 394-399.	0.4	23
53	Standard Annotation of Environmental OMICS Data: Application to the Transcriptomics Domain. OMICS A Journal of Integrative Biology, 2006, 10, 172-178.	1.0	21
54	Use of Allele-Specific FAIRE to Determine Functional Regulatory Polymorphism Using Large-Scale Genotyping Arrays. PLoS Genetics, 2012, 8, e1002908.	1.5	21

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55	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, 447-451.	0.4	20
56	IRS1 gene variants, dysglycaemic metabolic changes and type-2 diabetes risk. Nutrition, Metabolism and Cardiovascular Diseases, 2012, 22, 1024-1030.	1.1	20
57	Identifying differential exon splicing using linear models and correlation coefficients. BMC Bioinformatics, 2009, 10, 26.	1.2	19
58	Whole exome sequencing and <scp>DNA</scp> methylation analysis in a clinical amyotrophic lateral sclerosis cohort. Molecular Genetics & Genomic Medicine, 2017, 5, 418-428.	0.6	14
59	Integration of Genetics into a Systems Model of Electrocardiographic Traits Using HumanCVD BeadChip. Circulation: Cardiovascular Genetics, 2012, 5, 630-638.	5.1	12
60	The genomics of heart failure: design and rationale of the HERMES consortium. ESC Heart Failure, 2021, 8, 5531-5541.	1.4	11
61	A gene-centric study of common carotid artery remodelling. Atherosclerosis, 2013, 226, 440-446.	0.4	9
62	rHVDM: an R package to predict the activity and targets of a transcription factor. Bioinformatics, 2009, 25, 419-420.	1.8	8
63	Gene-centric association signals for haemostasis and thrombosis traits identified with the HumanCVD BeadChip. Thrombosis and Haemostasis, 2013, 110, 995-1003.	1.8	8
64	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, 680-685.	0.3	6
65	Prox1 maintains muscle structure and growth in the developing heart. Development (Cambridge), 2009, 136, 699-699.	1.2	4
66	Large-Scale Gene-Centric Meta-Analysis across 39 Studies Identifies Type 2 Diabetes Loci. American Journal of Human Genetics, 2012, 90, 753.	2.6	4
67	Complex disease genetics: present and future translational applications. Genome Medicine, 2009, 1, 104.	3.6	3
68	A genetic model of ivabradine recapitulates results from randomized clinical trials. PLoS ONE, 2020, 15, e0236193.	1.1	3
69	Loci influencing blood pressure identified using a cardiovascular gene-centric array. Human Molecular Genetics, 2013, 22, 3394-3395.	1.4	1
70	EXPLORING THE GENETIC ARCHITECTURE OF LIPID TRAITS IN WHITEHALL II HEALTHY MEN AND WOMEN USING THE 50K-SNP CARDIO-METABOLIC CHIP. Atherosclerosis, 2009, 207, 306.	0.4	0
71	IDENTIFICATION OF GENES ASSOCIATED WITH QT INTERVAL USING THE 50K CARDIO-METABOLIC SNP CHIP: RESULTS FROM THE WHITEHALL II STUDY. Atherosclerosis, 2009, 207, e11.	0.4	0
72	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. American Journal of Human Genetics, 2012, 90, 1116-1117.	2.6	0

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73	A genetic model of ivabradine recapitulates results from randomized clinical trials. , 2020, 15, e0236193.		0
74	A genetic model of ivabradine recapitulates results from randomized clinical trials. , 2020, 15, e0236193.		0
75	A genetic model of ivabradine recapitulates results from randomized clinical trials. , 2020, 15, e0236193.		0
76	A genetic model of ivabradine recapitulates results from randomized clinical trials. , 2020, 15, e0236193.		0