Stephen S Rich

List of Publications by Year
in descending order

562 papers	56,459 citations	1463 107 h-index	2127 203 g-index
590 all docs	590 docs citations	590 times ranked	61038 citing authors

#	Article	IF	Citations
1	Clonal Hematopoiesis Is Associated With Higher Risk of Stroke. Stroke, 2022, 53, 788-797.	2.0	88
2	Association of clonal hematopoiesis with chronic obstructive pulmonary disease. Blood, 2022, 139, 357-368.	1.4	106
3	Whole Genome Sequence Analysis of the Plasma Proteome in Black Adults Provides Novel Insights Into Cardiovascular Disease. Circulation, 2022, 145, 357-370.	1.6	39
4	ADA/EASD Precision Medicine in Diabetes Initiative: An International Perspective and Future Vision for Precision Medicine in Diabetes. Diabetes Care, 2022, 45, 261-266.	8.6	53
5	Heterogeneity of DKA Incidence and Age-Specific Clinical Characteristics in Children Diagnosed With Type 1 Diabetes in the TEDDY Study. Diabetes Care, 2022, 45, 624-633.	8.6	7
6	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. Cell Genomics, 2022, 2, 100084.	6.5	29
7	Toll-Like Receptor 1 Locus Re-examined in a Genome-Wide Association Study Update on Antiâ€“Helicobacter pylori IgG Titers. Gastroenterology, 2022, 162, 1705-1715.	1.3	7
8	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
9	Upregulated heme biosynthesis increases obstructive sleep apnea severity: a pathway-based Mendelian randomization study. Scientific Reports, 2022, 12, 1472.	3.3	2
10	Improving the Prediction of Type 1 Diabetes Across Ancestries. Diabetes Care, 2022, 45, e48-e50.	8.6	7
11	AtheroSpectrum Reveals Novel Macrophage Foam Cell Gene Signatures Associated With Atherosclerotic Cardiovascular Disease Risk. Circulation, 2022, 145, 206-218.	1.6	29
12	Multi-ethnic GWAS and fine-mapping of glycaemic traits identify novel loci in the PAGE Study. Diabetologia, 2022, 65, 477-489.	6.3	15
13	Protein prediction for trait mapping in diverse populations. PLoS ONE, 2022, 17, e0264341.	2.5	13
14	Rare Genetic Variants Associated With Myocardial Fibrosis: Multi-Ethnic Study of Atherosclerosis. Frontiers in Cardiovascular Medicine, 2022, 9, 804788.	2.4	6
15	Rare coding variants in RCN3 are associated with blood pressure. BMC Genomics, 2022, 23, 148.	2.8	2
16	Screening for Type 1 Diabetes in the General Population: A Status Report and Perspective. Diabetes, 2022, 71, 610-623.	0.6	59
17	Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data. Nature Genetics, 2022, 54, 263-273.	21.4	156
18	Telomere length is not a main factor for the development of islet autoimmunity and type 1 diabetes in the TEDDY study. Scientific Reports, 2022, 12, 4516.	3.3	6

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19	Associations between adherence to the dietary approaches to stop hypertension (DASH) diet and six glucose homeostasis traits in the Microbiome and Insulin Longitudinal Evaluation Study (MILES). Nutrition, Metabolism and Cardiovascular Diseases, 2022, 32, 1418-1426.	2.6	3
20	Polygenic transcriptome risk scores for COPD and lung function improve cross-ethnic portability of prediction in the NHLBI TOPMed program. American Journal of Human Genetics, 2022, 109, 857-870.	6.2	7
21	Monogenic and Polygenic Contributions to QTc Prolongation in the Population. Circulation, 2022, 145, 1524-1533.	1.6	14
22	Associations of Monocyte Count and Other Immune Cell Types with Interstitial Lung Abnormalities. American Journal of Respiratory and Critical Care Medicine, 2022, 205, 795-805.	5.6	11
23	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential. Science Advances, 2022, 8, eabl6579.	10.3	36
24	Integration of Infant Metabolite, Genetic, and Islet Autoimmunity Signatures to Predict Type 1 Diabetes by Age 6 Years. Journal of Clinical Endocrinology and Metabolism, 2022, 107, 2329-2338.	3.6	10
25	Childhood body size directly increases type 1 diabetes risk based on a lifecourse Mendelian randomization approach. Nature Communications, 2022, 13, 2337.	12.8	34
26	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nature Genetics, 2022, 54, 560-572.	21.4	250
27	Cesarean Delivery and Insulin Sensitivity in the Older Adult: The Microbiome and Insulin Longitudinal Evaluation Study. Journal of the Endocrine Society, 2022, 6, .	0.2	4
28	Pulmonary Function and Blood DNA Methylation: A Multiancestry Epigenome-Wide Association Meta-analysis. American Journal of Respiratory and Critical Care Medicine, 2022, 206, 321-336.	5.6	15
29	TOP-LD: A tool to explore linkage disequilibrium with TOPMed whole-genome sequence data. American Journal of Human Genetics, 2022, 109, 1175-1181.	6.2	25
30	Lymphocyte activation gene-3-associated protein networks are associated with HDL-cholesterol and mortality in the Trans-omics for Precision Medicine program. Communications Biology, 2022, 5, 362.	4.4	5
31	The Value of Rare Genetic Variation in the Prediction of Common Obesity in European Ancestry Populations. Frontiers in Endocrinology, 2022, 13, 863893.	3.5	7
32	Arsenic Exposure, Blood DNA Methylation, and Cardiovascular Disease. Circulation Research, 2022, 131, .	4.5	20
33	A multi-ethnic polygenic risk score is associated with hypertension prevalence and progression throughout adulthood. Nature Communications, 2022, 13, .	12.8	27
34	Type 1 diabetes in diverse ancestries and the use of genetic risk scores. Lancet Diabetes and Endocrinology,the, 2022, 10, 597-608.	11.4	23
35	Assessing the contribution of rare genetic variants to phenotypes of chronic obstructive pulmonary disease using whole-genome sequence data. Human Molecular Genetics, 2022, 31, 3873-3885.	2.9	2
36	Editorial Cycles and Continuity of Diabetes Care. Diabetes Care, 2022, 45, 1493-1494.	8.6	0

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37	Insights From a Large-Scale Whole-Genome Sequencing Study of Systolic Blood Pressure, Diastolic Blood Pressure, and Hypertension. Hypertension, 2022, 79, 1656-1667.	2.7	12
38	Transethnic Transferability of a Genome-Wide Polygenic Score for Coronary Artery Disease. Circulation Genomic and Precision Medicine, 2021, 14, e003092.	3.6	25
39	PRF1 mutation alters immune system activation, inflammation, and risk of autoimmunity. Multiple Sclerosis Journal, 2021, 27, 1332-1340.	3.0	13
40	Prediction of the development of islet autoantibodies through integration of environmental, genetic, and metabolic markers. Journal of Diabetes, 2021, 13, 143-153.	1.8	25
41	Exercise during pregnancy mitigates negative effects of parental obesity on metabolic function in adult mouse offspring. Journal of Applied Physiology, 2021, 130, 605-616.	2.5	11
42	Whole genome sequence analyses of eGFR in 23,732 people representing multiple ancestries in the NHLBI trans-omics for precision medicine (TOPMed) consortium. EBioMedicine, 2021, 63, 103157.	6.1	14
43	An Age-Related Exponential Decline in the Risk of Multiple Islet Autoantibody Seroconversion During Childhood. Diabetes Care, 2021, 44, 2260-2268.	8.6	23
44	Childrenâ€™s erythrocyte fatty acids are associated with the risk of islet autoimmunity. Scientific Reports, 2021, 11, 3627.	3.3	10
45	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	27.8	1,069
46	Heterogeneous longâ€term trajectories of glycaemic control in type 1 diabetes. Diabetic Medicine, 2021, 38, e14545.	2.3	6
47	Epigenome-wide association study of kidney function identifies trans-ethnic and ethnic-specific loci. Genome Medicine, 2021, 13, 74.	8.2	20
48	Multi-ancestry genome-wide geneâ€“sleep interactions identify novel loci for blood pressure. Molecular Psychiatry, 2021, 26, 6293-6304.	7.9	13
49	Meningeal lymphatics affect microglia responses and anti-Aî² immunotherapy. Nature, 2021, 593, 255-260.	27.8	179
50	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. Nature Communications, 2021, 12, 2182.	12.8	17
51	Insulin resistance-associated genetic variants in type 1 diabetes. Journal of Diabetes and Its Complications, 2021, 35, 107842.	2.3	8
52	A System for Phenotype Harmonization in the National Heart, Lung, and Blood Institute Trans-Omics for Precision Medicine (TOPMed) Program. American Journal of Epidemiology, 2021, 190, 1977-1992.	3.4	29
53	Whole-genome sequencing association analysis of quantitative red blood cell phenotypes: The NHLBI TOPMed program. American Journal of Human Genetics, 2021, 108, 874-893.	6.2	28
54	Nonclassical Monocytes (CD14dimCD16+) Are Associated With Carotid Intima-Media Thickness Progression for Men but Not Women. Arteriosclerosis, Thrombosis, and Vascular Biology, 2021, 41, 1810-1817.	2.4	10

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55	Clonal hematopoiesis associated with epigenetic aging and clinical outcomes. Aging Cell, 2021, 20, e13366.	6.7	72
56	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341
57	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. Genome Biology, 2021, 22, 194.	8.8	90
58	Fine-mapping, trans-ancestral and genomic analyses identify causal variants, cells, genes and drug targets for type 1 diabetes. Nature Genetics, 2021, 53, 962-971.	21.4	133
59	Determinants of penetrance and variable expressivity in monogenic metabolic conditions across 77,184 exomes. Nature Communications, 2021, 12, 3505.	12.8	49
60	Defining the Relative Role of Insulin Clearance in Early Dysglycemia in Relation to Insulin Sensitivity and Insulin Secretion: The Microbiome and Insulin Longitudinal Evaluation Study (MILES). Metabolites, 2021, 11, 420.	2.9	6
61	A systematic analysis of protein-altering exonic variants in chronic obstructive pulmonary disease. American Journal of Physiology - Lung Cellular and Molecular Physiology, 2021, 321, L130-L143.	2.9	11
62	Association of Coding Variants in Hydroxysteroid 17-beta Dehydrogenase 14 (HSD17B14) with Reduced Progression to End Stage Kidney Disease in Type 1 Diabetes. Journal of the American Society of Nephrology: JASN, 2021, 32, 2634-2651.	6.1	9
63	Transcriptome-Wide Association Study of Blood Cell Traits in African Ancestry and Hispanic/Latino Populations. Genes, 2021, 12, 1049.	2.4	11
64	BinomiRare: A robust test for association of a rare genetic variant with a binary outcome for mixed models and any case-control proportion. Human Genetics and Genomics Advances, 2021, 2, 100040.	1.7	2
65	Rare Coding Variants Associated With Electrocardiographic Intervals Identify Monogenic Arrhythmia Susceptibility Genes: A Multi-Ancestry Analysis. Circulation Genomic and Precision Medicine, 2021, 14, e003300.	3.6	7
66	Impact of Amerind ancestry and FADS genetic variation on omega-3 deficiency and cardiometabolic traits in Hispanic populations. Communications Biology, 2021, 4, 918.	4.4	11
67	The KAG motif of HLA-DRB1 (Î²71, Î²74, Î²86) predicts seroconversion and development of type 1 diabetes. EBioMedicine, 2021, 69, 103431.	6.1	6
68	Sugar-Sweetened Beverage Consumption May Modify Associations Between Genetic Variants in the CHREBP (Carbohydrate Responsive Element Binding Protein) Locus and HDL-C (High-Density Lipoprotein) Tj ETQq0 0 0 rgBT /Overlock 1 e003288.	3.6	8
69	Epigenome-wide association study of mitochondrial genome copy number. Human Molecular Genetics, 2021, 31, 309-319.	2.9	6
70	Associations between ambient air pollutants and clonal hematopoiesis of indeterminate potential (CHIP). ISEE Conference Abstracts, 2021, 2021, .	0.0	0
71	Population sequencing data reveal a compendium of mutational processes in the human germ line. Science, 2021, 373, 1030-1035.	12.6	43
72	Whole-genome association analyses of sleep-disordered breathing phenotypes in the NHLBI TOPMed program. Genome Medicine, 2021, 13, 136.	8.2	16

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73	Whole-genome sequencing in diverse subjects identifies genetic correlates of leukocyte traits: The NHLBI TOPMed program. American Journal of Human Genetics, 2021, 108, 1836-1851.	6.2	14
74	Rare and low-frequency exonic variants and gene-by-smoking interactions in pulmonary function. Scientific Reports, 2021, 11, 19365.	3.3	2
75	A Lesson From 2020: Public Health Matters for Both COVID-19 and Diabetes. Diabetes Care, 2021, 44, 8-10.	8.6	8
76	The 3p21.31 genetic locus promotes progression to type 1 diabetes through the CCR2/CCL2 pathway. Journal of Translational Autoimmunity, 2021, 4, 100127.	4.0	3
77	Association of mitochondrial DNA copy number with cardiometabolic diseases. Cell Genomics, 2021, 1, 100006.	6.5	26
78	A high-resolution HLA reference panel capturing global population diversity enables multi-ancestry fine-mapping in HIV host response. Nature Genetics, 2021, 53, 1504-1516.	21.4	69
79	Predicting diabetes risk in diverse populations: what next?. Lancet Diabetes and Endocrinology,the, 2021, 9, 808-810.	11.4	2
80	Whole-Genome Sequencing Association Analyses of Stroke and Its Subtypes in Ancestrally Diverse Populations From Trans-Omics for Precision Medicine Project. Stroke, 2021, , STROKEAHA120031792.	2.0	16
81	Dynamic changes in immune gene co-expression networks predict development of type 1 diabetes. Scientific Reports, 2021, 11, 22651.	3.3	3
82	Interpreting Clinical Trials With Omega-3 Supplements in the Context of Ancestry and FADS Genetic Variation. Frontiers in Nutrition, 2021, 8, 808054.	3.7	12
83	Pangenomics enables genotyping of known structural variants in 5202 diverse genomes. Science, 2021, 374, abg8871.	12.6	132
84	Associations between DNA methylation and BMI vary by metabolic health status: a potential link to disparate cardiovascular outcomes. Clinical Epigenetics, 2021, 13, 230.	4.1	11
85	Plasma ascorbic acid and the risk of islet autoimmunity and type 1 diabetes: the TEDDY study. Diabetologia, 2020, 63, 278-286.	6.3	18
86	Whole genome sequence analysis of pulmonary function and COPD in 19,996 multi-ethnic participants. Nature Communications, 2020, 11, 5182.	12.8	32
87	The Polygenic and Monogenic Basis of Blood Traits and Diseases. Cell, 2020, 182, 1214-1231.e11.	28.9	388
88	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature, 2020, 586, 763-768.	27.8	376
89	Rationale, design and baseline characteristics of the Microbiome and Insulin Longitudinal Evaluation Study (<scp>MILES</scp>). Diabetes, Obesity and Metabolism, 2020, 22, 1976-1984.	4.4	9
90	Monogenic Diabetes: From Genetic Insights to Population-Based Precision in Care. Reflections From a Diabetes Care Editorsâ€™ Expert Forum. Diabetes Care, 2020, 43, 3117-3128.	8.6	65

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91	Analysis of Glucocorticoid-Related Genes Reveal CCHCR1 as a New Candidate Gene for Type 2 Diabetes. Journal of the Endocrine Society, 2020, 4, bvaa121.	0.2	8
92	A combined risk score enhances prediction of type 1 diabetes among susceptible children. Nature Medicine, 2020, 26, 1247-1255.	30.7	83
93	Sexually Dimorphic Crosstalk at the Maternal-Fetal Interface. Journal of Clinical Endocrinology and Metabolism, 2020, 105, e4831-e4847.	3.6	48
94	Genome-Wide Association Study Meta-Analysis of Stroke in 22 000 Individuals of African Descent Identifies Novel Associations With Stroke. Stroke, 2020, 51, 2454-2463.	2.0	26
95	Chronic obstructive pulmonary disease and related phenotypes: polygenic risk scores in population-based and case-control cohorts. Lancet Respiratory Medicine,the, 2020, 8, 696-708.	10.7	69
96	Low oxygen saturation during sleep reduces CD1D and RAB20 expressions that are reversed by CPAP therapy. EBioMedicine, 2020, 56, 102803.	6.1	7
97	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. Cell, 2020, 182, 1198-1213.e14.	28.9	353
98	Next steps in the identification of gene targets for type 1 diabetes. Diabetologia, 2020, 63, 2260-2269.	6.3	12
99	Dynamic incorporation of multiple in silico functional annotations empowers rare variant association analysis of large whole-genome sequencing studies at scale. Nature Genetics, 2020, 52, 969-983.	21.4	146
100	Novel genetic risk factors influence progression of islet autoimmunity to type 1 diabetes. Scientific Reports, 2020, 10, 19193.	3.3	5
101	Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. Nature Communications, 2020, 11, 6417.	12.8	39
102	Distinct Growth Phases in Early Life Associated With the Risk of Type 1 Diabetes: The TEDDY Study. Diabetes Care, 2020, 43, 556-562.	8.6	28
103	Analysis of cardiac magnetic resonance imaging in 36,000 individuals yields genetic insights into dilated cardiomyopathy. Nature Communications, 2020, 11, 2254.	12.8	140
104	Comparison of Proteomic Assessment Methods in Multiple Cohort Studies. Proteomics, 2020, 20, e1900278.	2.2	103
105	Genome-Wide Association Study of Cryptosporidiosis in Infants Implicates PRKCA. MBio, 2020, 11, .	4.1	20
106	Longitudinal Metabolome-Wide Signals Prior to the Appearance of a First Islet Autoantibody in Children Participating in the TEDDY Study. Diabetes, 2020, 69, 465-476.	0.6	30
107	A structural variation reference for medical and population genetics. Nature, 2020, 581, 444-451.	27.8	614
108	Precision medicine in diabetes: a Consensus Report from the American Diabetes Association (ADA) and the European Association for the Study of Diabetes (EASD). Diabetologia, 2020, 63, 1671-1693.	6.3	102

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109	Precision Medicine in Diabetes: A Consensus Report From the American Diabetes Association (ADA) and the European Association for the Study of Diabetes (EASD). Diabetes Care, 2020, 43, 1617-1635.	8.6	204
110	Role of Rare and Low-Frequency Variants in Gene-Alcohol Interactions on Plasma Lipid Levels. Circulation Genomic and Precision Medicine, 2020, 13, e002772.	3.6	11
111	Hierarchical Order of Distinct Autoantibody Spreading and Progression to Type 1 Diabetes in the TEDDY Study. Diabetes Care, 2020, 43, 2066-2073.	8.6	41
112	Allele-specific expression changes dynamically during T cell activation in HLA and other autoimmune loci. Nature Genetics, 2020, 52, 247-253.	21.4	85
113	Allelic Heterogeneity at the CRP Locus Identified by Whole-Genome Sequencing in Multi-ancestry Cohorts. American Journal of Human Genetics, 2020, 106, 112-120.	6.2	9
114	Associations of Innate and Adaptive Immune Cell Subsets With Incident Type 2 Diabetes Risk: The MESA Study. Journal of Clinical Endocrinology and Metabolism, 2020, 105, e848-e857.	3.6	10
115	A novel voluntary weightlifting model in mice promotes muscle adaptation and insulin sensitivity with simultaneous enhancement of autophagy and mTOR pathway. FASEB Journal, 2020, 34, 7330-7344.	0.5	42
116	Predictive Accuracy of a Polygenic Risk Score Compared With a Clinical Risk Score for Incident Coronary Heart Disease. JAMA - Journal of the American Medical Association, 2020, 323, 627.	7.4	234
117	Fatty Acid Desaturase Geneâ€Induced Omegaâ€3 Deficiency in Amerindianâ€Ancestry Hispanic Populations. FASEB Journal, 2020, 34, 1-1.	0.5	2
118	Genetic loci associated with prevalent and incident myocardial infarction and coronary heart disease in the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium. PLoS ONE, 2020, 15, e0230035.	2.5	5
119	Genome-wide meta-analysis of macronutrient intake of 91,114 European ancestry participants from the cohorts for heart and aging research in genomic epidemiology consortium. Molecular Psychiatry, 2019, 24, 1920-1932.	7.9	44
120	Overlap of Genetic Risk between Interstitial Lung Abnormalities and Idiopathic Pulmonary Fibrosis. American Journal of Respiratory and Critical Care Medicine, 2019, 200, 1402-1413.	5.6	77
121	Extending Classification Algorithms to Case-Control Studies. Biomedical Engineering and Computational Biology, 2019, 10, 117959721985895.	2.0	12
122	Genome-Wide Association Study of Diabetic Kidney Disease Highlights Biology Involved in Glomerular Basement Membrane Collagen. Journal of the American Society of Nephrology: JASN, 2019, 30, 2000-2016.	6.1	135
123	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	12.8	84
124	Rare Genetic Variants Associated With Sudden Cardiac Death in Adults. Journal of the American College of Cardiology, 2019, 74, 2623-2634.	2.8	27
125	Multi-ancestry sleep-by-SNP interaction analysis in 126,926 individuals reveals lipid loci stratified by sleep duration. Nature Communications, 2019, 10, 5121.	12.8	62
126	Sequencing Analysis at 8p23 Identifies Multiple Rare Variants in DLC1 Associated with Sleep-Related Oxyhemoglobin Saturation Level. American Journal of Human Genetics, 2019, 105, 1057-1068.	6.2	10

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127	Persistent C-peptide secretion in Type 1 diabetes and its relationship to the genetic architecture of diabetes. BMC Medicine, 2019, 17, 165.	5.5	43
128	Whole Genome Sequencing Identifies CRISPLD2 as a Lung Function Gene in Children With Asthma. Chest, 2019, 156, 1068-1079.	0.8	5
129	Impact of Rare and Common Genetic Variants on Diabetes Diagnosis by Hemoglobin A1c in Multi-Ancestry Cohorts: The Trans-Omics for Precision Medicine Program. American Journal of Human Genetics, 2019, 105, 706-718.	6.2	44
130	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	3.4	85
131	Genetic Contribution to the Divergence in Type 1 Diabetes Risk Between Children From the General Population and Children From Affected Families. Diabetes, 2019, 68, 847-857.	0.6	22
132	Type 1 Diabetes Risk in African-Ancestry Participants and Utility of an Ancestry-Specific Genetic Risk Score. Diabetes Care, 2019, 42, 406-415.	8.6	62
133	Whole-Genome Sequencing to Characterize Monogenic and Polygenic Contributions in Patients Hospitalized With Early-Onset Myocardial Infarction. Circulation, 2019, 139, 1593-1602.	1.6	213
134	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	12.8	64
135	Leveraging linkage evidence to identify low-frequency and rare variants on 16p13 associated with blood pressure using TOPMed whole genome sequencing data. Human Genetics, 2019, 138, 199-210.	3.8	29
136	Autoantibodies Directed Toward a Novel IA-2 Variant Protein Enhance Prediction of Type 1 Diabetes. Diabetes, 2019, 68, 1819-1829.	0.6	12
137	0291 Sleep Disordered Breathing Associated with Epigenetic Age Acceleration: Evidence from the Multi-Ethnic Study of Atherosclerosis. Sleep, 2019, 42, A118-A119.	1.1	0
138	Innovation in Genomic Data Sharing at the NIH. New England Journal of Medicine, 2019, 380, 2192-2195.	27.0	4
139	Genome-wide association study identifies novel loci for type 2 diabetes-attributed end-stage kidney disease in African Americans. Human Genomics, 2019, 13, 21.	2.9	32
140	Predicting Islet Cell Autoimmunity and Type 1 Diabetes: An 8-Year TEDDY Study Progress Report. Diabetes Care, 2019, 42, 1051-1060.	8.6	75
141	Multi-ancestry genome-wide geneâ€“smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. Nature Genetics, 2019, 51, 636-648.	21.4	112
142	A Genetic Risk Score Associated with Chronic Obstructive Pulmonary Disease Susceptibility and Lung Structure on Computed Tomography. American Journal of Respiratory and Critical Care Medicine, 2019, 200, 721-731.	5.6	40
143	Differences in First-Trimester Maternal Metabolomic Profiles in Pregnancies Conceived From Fertility Treatments. Journal of Clinical Endocrinology and Metabolism, 2019, 104, 1005-1019.	3.6	15
144	OP0190â€…META-ANALYSIS OF IMMUNOCHIP DATA OF FOUR AUTOIMMUNE DISEASES REVEALS NOVEL SINGLE-DISEASE AND CROSS-PHENOTYPE ASSOCIATIONS. , 2019, , .		0

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145	Use of >100,000 NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium whole genome sequences improves imputation quality and detection of rare variant associations in admixed African and Hispanic/Latino populations. PLoS Genetics, 2019, 15, e1008500.	3.5	203
146	Association between sleep disordered breathing and epigenetic age acceleration: Evidence from the Multi-Ethnic Study of Atherosclerosis. EBioMedicine, 2019, 50, 387-394.	6.1	12
147	Omega-3 Fatty Acids and Genome-Wide Interaction Analyses Reveal DPP10â€“Pulmonary Function Association. American Journal of Respiratory and Critical Care Medicine, 2019, 199, 631-642.	5.6	14
148	Trans-ethnic kidney function association study reveals putative causal genes and effects on kidney-specific disease aetiologies. Nature Communications, 2019, 10, 29.	12.8	113
149	Variations in Risk of End-Stage Renal Disease and Risk of Mortality in an International Study of Patients With Type 1 Diabetes and Advanced Nephropathy. Diabetes Care, 2019, 42, 93-101.	8.6	37
150	Differential gene expression during placentation in pregnancies conceived with different fertility treatments compared with spontaneous pregnancies. Fertility and Sterility, 2019, 111, 535-546.	1.0	12
151	Development and Standardization of an Improved Type 1 Diabetes Genetic Risk Score for Use in Newborn Screening and Incident Diagnosis. Diabetes Care, 2019, 42, 200-207.	8.6	187
152	Efficient Variant Set Mixed Model Association Tests for Continuous and Binary Traits in Large-Scale Whole-Genome Sequencing Studies. American Journal of Human Genetics, 2019, 104, 260-274.	6.2	103
153	Progression from islet autoimmunity to clinical type 1 diabetes is influenced by genetic factors: results from the prospective TEDDY study. Journal of Medical Genetics, 2019, 56, 602-605.	3.2	22
154	Genomeâ€wide interaction with the insulin secretion locus MTNR1B reveals CMIP as a novel type 2 diabetes susceptibility gene in African Americans. Genetic Epidemiology, 2018, 42, 559-570.	1.3	17
155	Analysis of predicted loss-of-function variants in UK Biobank identifies variants protective for disease. Nature Communications, 2018, 9, 1613.	12.8	78
156	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
157	A Genome-Wide Association Study in Hispanics/Latinos Identifies Novel Signals for Lung Function. The Hispanic Community Health Study/Study of Latinos. American Journal of Respiratory and Critical Care Medicine, 2018, 198, 208-219.	5.6	37
158	Genetics of type 1 diabetes. Current Opinion in Genetics and Development, 2018, 50, 7-16.	3.3	58
159	Human airway branch variation and chronic obstructive pulmonary disease. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E974-E981.	7.1	80
160	Genome-wide association study in 79,366 European-ancestry individuals informs the genetic architecture of 25-hydroxyvitamin D levels. Nature Communications, 2018, 9, 260.	12.8	295
161	Multiancestry association study identifies new asthma risk loci that colocalize with immune-cell enhancer marks. Nature Genetics, 2018, 50, 42-53.	21.4	426
162	Genome-wide association study of homocysteine in African Americans from the Jackson Heart Study, the Multi-Ethnic Study of Atherosclerosis, and the Coronary Artery Risk in Young Adults study. Journal of Human Genetics, 2018, 63, 327-337.	2.3	7

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163	Identification of non-HLA genes associated with development of islet autoimmunity and type 1 diabetes in the prospective TEDDY cohort. Journal of Autoimmunity, 2018, 89, 90-100.	6.5	46
164	A Genome-Wide Association Study of Diabetic Kidney Disease in Subjects With Type 2 Diabetes. Diabetes, 2018, 67, 1414-1427.	0.6	136
165	Plasma 25-Hydroxyvitamin D Concentration and Risk of Islet Autoimmunity. Diabetes, 2018, 67, 146-154.	0.6	72
166	Sugar-sweetened beverage intake associations with fasting glucose and insulin concentrations are not modified by selected genetic variants in a ChREBP-FGF21 pathway: a meta-analysis. Diabetologia, 2018, 61, 317-330.	6.3	32
167	Genomeâ€Wide Interactions with Dairy Intake for Body Mass Index in Adults of European Descent. Molecular Nutrition and Food Research, 2018, 62, 1700347.	3.3	9
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