Stephen S Rich

List of Publications by Year
in descending order

562 papers	56,459 citations	1713 107 h-index	2512 202 g-index
590 all docs	590 docs citations	590 times ranked	66478 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	Robust relationship inference in genome-wide association studies. Bioinformatics, 2010, 26, 2867-2873.	1.8	2,328
3	Genome-wide association study and meta-analysis find that over 40 loci affect risk of type 1 diabetes. Nature Genetics, 2009, 41, 703-707.	9.4	1,513
4	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. Nature Genetics, 2018, 50, 524-537.	9.4	1,124
5	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	13.7	1,069
6	Gut Microbiomes of Malawian Twin Pairs Discordant for Kwashiorkor. Science, 2013, 339, 548-554.	6.0	1,012
7	Familial Clustering of Diabetic Kidney Disease. New England Journal of Medicine, 1989, 320, 1161-1165.	13.9	976
8	Loss-of-Function Mutations inAPOC3,Triglycerides, and Coronary Disease. New England Journal of Medicine, 2014, 371, 22-31.	13.9	936
9	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. Nature Genetics, 2016, 48, 624-633.	9.4	870
10	Functional aspects of meningeal lymphatics in ageing and Alzheimerâ€™s disease. Nature, 2018, 560, 185-191.	13.7	839
11	Common variants associated with plasma triglycerides and risk for coronary artery disease. Nature Genetics, 2013, 45, 1345-1352.	9.4	754
12	Early-Onset Stroke and Vasculopathy Associated with Mutations in ADA2. New England Journal of Medicine, 2014, 370, 911-920.	13.9	687
13	Dense genotyping identifies and localizes multiple common and rare variant association signals in celiac disease. Nature Genetics, 2011, 43, 1193-1201.	9.4	682
14	A structural variation reference for medical and population genetics. Nature, 2020, 581, 444-451.	13.7	614
15	Fine mapping of type 1 diabetes susceptibility loci and evidence for colocalization of causal variants with lymphoid gene enhancers. Nature Genetics, 2015, 47, 381-386.	9.4	589
16	Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction. Nature, 2015, 518, 102-106.	13.7	581
17	Mendelian randomization of blood lipids for coronary heart disease. European Heart Journal, 2015, 36, 539-550.	1.0	567
18	High-density genetic mapping identifies new susceptibility loci for rheumatoid arthritis. Nature Genetics, 2012, 44, 1336-1340.	9.4	558

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19	Pervasive Sharing of Genetic Effects in Autoimmune Disease. PLoS Genetics, 2011, 7, e1002254.	1.5	540
20	Imputing Amino Acid Polymorphisms in Human Leukocyte Antigens. PLoS ONE, 2013, 8, e64683.	1.1	538
21	Role of Type 1 Diabetesâ€“Associated SNPs on Autoantibody Positivity in the Type 1 Diabetes Genetics Consortium: Overview. Diabetes Care, 2015, 38, S1-S3.	4.3	488
22	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	9.4	470
23	Genetics of Type 1A Diabetes. New England Journal of Medicine, 2009, 360, 1646-1654.	13.9	437
24	Multiancestry association study identifies new asthma risk loci that colocalize with immune-cell enhancer marks. Nature Genetics, 2018, 50, 42-53.	9.4	426
25	The Polygenic and Monogenic Basis of Blood Traits and Diseases. Cell, 2020, 182, 1214-1231.e11.	13.5	388
26	Inactivating Mutations in NPC1L1 and Protection from Coronary Heart Disease. New England Journal of Medicine, 2014, 371, 2072-2082.	13.9	386
27	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature, 2020, 586, 763-768.	13.7	376
28	Genome-wide association and large-scale follow up identifies 16 new loci influencing lung function. Nature Genetics, 2011, 43, 1082-1090.	9.4	367
29	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. Nature Genetics, 2018, 50, 559-571.	9.4	356
30	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. Cell, 2020, 182, 1198-1213.e14.	13.5	353
31	Risk of Recurrent Seizures after Two Unprovoked Seizures. New England Journal of Medicine, 1998, 338, 429-434.	13.9	344
32	Impact of common genetic determinants of Hemoglobin A1c on type 2 diabetes risk and diagnosis in ancestrally diverse populations: A transethnic genome-wide meta-analysis. PLoS Medicine, 2017, 14, e1002383.	3.9	341
33	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	9.4	341
34	Dense genotyping of immune-related disease regions identifies nine new risk loci for primary sclerosing cholangitis. Nature Genetics, 2013, 45, 670-675.	9.4	339
35	Dense genotyping of immune-related disease regions identifies 14 new susceptibility loci for juvenile idiopathic arthritis. Nature Genetics, 2013, 45, 664-669.	9.4	337
36	Genetic Loci Associated with Plasma Phospholipid n-3 Fatty Acids: A Meta-Analysis of Genome-Wide Association Studies from the CHARGE Consortium. PLoS Genetics, 2011, 7, e1002193.	1.5	324

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37	The landscape of recombination in African Americans. Nature, 2011, 476, 170-175.	13.7	319
38	Actionable exomic incidental findings in 6503 participants: challenges of variant classification. Genome Research, 2015, 25, 305-315.	2.4	313
39	Genetic loci associated with chronic obstructive pulmonary disease overlap with loci for lung function and pulmonary fibrosis. Nature Genetics, 2017, 49, 426-432.	9.4	306
40	Genome-wide association study in 79,366 European-ancestry individuals informs the genetic architecture of 25-hydroxyvitamin D levels. Nature Communications, 2018, 9, 260.	5.8	295
41	Genome-Wide Association Study of Coronary Heart Disease and Its Risk Factors in 8,090 African Americans: The NHLBI CARe Project. PLoS Genetics, 2011, 7, e1001300.	1.5	290
42	Association of Low-Frequency and Rare Coding-Sequence Variants with Blood Lipids and Coronary Heart Disease in 56,000 Whites and Blacks. American Journal of Human Genetics, 2014, 94, 223-232.	2.6	287
43	Mapping Genes in Diabetes: Genetic Epidemiological Perspective. Diabetes, 1990, 39, 1315-1319.	0.3	273
44	Effect modification by population dietary folate on the association between MTHFR genotype, homocysteine, and stroke risk: a meta-analysis of genetic studies and randomised trials. Lancet, The, 2011, 378, 584-594.	6.3	273
45	A gene responsible for cavernous malformations of the brain maps to chromosome 7q. Human Molecular Genetics, 1995, 4, 453-458.	1.4	272
46	Genome-Wide Association Scan for Diabetic Nephropathy Susceptibility Genes in Type 1 Diabetes. Diabetes, 2009, 58, 1403-1410.	0.3	259
47	Microbiota alteration is associated with the development of stress-induced despair behavior. Scientific Reports, 2017, 7, 43859.	1.6	259
48	Genetics of Type 1 Diabetes: What's Next?. Diabetes, 2010, 59, 1561-1571.	0.3	256
49	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nature Genetics, 2022, 54, 560-572.	9.4	250
50	Genetic and Environmental Determinants of 25-Hydroxyvitamin D and 1,25-Dihydroxyvitamin D Levels in Hispanic and African Americans. Journal of Clinical Endocrinology and Metabolism, 2008, 93, 3381-3388.	1.8	239
51	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
52	Additive and interaction effects at three amino acid positions in HLA-DQ and HLA-DR molecules drive type 1 diabetes risk. Nature Genetics, 2015, 47, 898-905.	9.4	235
53	Functional IL6R 358Ala Allele Impairs Classical IL-6 Receptor Signaling and Influences Risk of Diverse Inflammatory Diseases. PLoS Genetics, 2013, 9, e1003444.	1.5	234
54	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.	3.8	234

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55	Large-Scale Gene-Centric Meta-analysis across 32 Studies Identifies Multiple Lipid Loci. American Journal of Human Genetics, 2012, 91, 823-838.	2.6	227
56	Genomewide Screen and Identification of Gene-Gene Interactions for Asthma-Susceptibility Loci in Three U.S. Populations: Collaborative Study on the Genetics of Asthma. American Journal of Human Genetics, 2001, 68, 1437-1446.	2.6	225
57	Type 1 Diabetes: Evidence for Susceptibility Loci from Four Genome-Wide Linkage Scans in 1,435 Multiplex Families. Diabetes, 2005, 54, 2995-3001.	0.3	221
58	Best Practices and Joint Calling of the HumanExome BeadChip: The CHARGE Consortium. PLoS ONE, 2013, 8, e68095.	1.1	219
59	Loci associated with ischaemic stroke and its subtypes (SiGN): a genome-wide association study. Lancet Neurology, The, 2016, 15, 174-184.	4.9	217
60	Genome Screening in Human Systemic Lupus Erythematosus: Results from a Second Minnesota Cohort and Combined Analyses of 187 Sib-Pair Families. American Journal of Human Genetics, 2000, 66, 547-556.	2.6	213
61	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
62	ImmunoChip Study Implicates Antigen Presentation to T Cells in Narcolepsy. PLoS Genetics, 2013, 9, e1003270.	1.5	206
63	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.	4.3	204
64	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.	1.5	203
65	Causal Effects of Body Mass Index on Cardiometabolic Traits and Events: A Mendelian Randomization Analysis. American Journal of Human Genetics, 2014, 94, 198-208.	2.6	199
66	Visualizing Human Leukocyte Antigen Class II Risk Haplotypes in Human Systemic Lupus Erythematosus. American Journal of Human Genetics, 2002, 71, 543-553.	2.6	197
67	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. American Journal of Human Genetics, 2014, 94, 233-245.	2.6	193
68	Meta-Analysis of Genome-Wide Association Studies in African Americans Provides Insights into the Genetic Architecture of Type 2 Diabetes. PLoS Genetics, 2014, 10, e1004517.	1.5	191
69	Cellular Basis of Diabetic Nephropathy: 1. Study Design and Renal Structural-Functional Relationships in Patients With Long-Standing Type 1 Diabetes. Diabetes, 2002, 51, 506-513.	0.3	188
70	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.	4.3	187
71	Negligible impact of rare autoimmune-locus coding-region variants on missing heritability. Nature, 2013, 498, 232-235.	13.7	184
72	Association of Low-Density Lipoprotein Cholesterolâ€“Related Genetic Variants With Aortic Valve Calcium and Incident Aortic Stenosis. JAMA - Journal of the American Medical Association, 2014, 312, 1764.	3.8	184

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73	Meningeal lymphatics affect microglia responses and anti-Aî² immunotherapy. Nature, 2021, 593, 255-260.	13.7	179
74	A genome-wide genotyping study in patients with ischaemic stroke: initial analysis and data release. Lancet Neurology, The, 2007, 6, 414-420.	4.9	175
75	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. Nature Communications, 2015, 6, 5897.	5.8	173
76	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	13.7	173
77	Autoimmune diseases â€" connecting risk alleles with molecular traits of the immune system. Nature Reviews Genetics, 2016, 17, 160-174.	7.7	173
78	Association of Sickle Cell Trait With Chronic Kidney Disease and Albuminuria in African Americans. JAMA - Journal of the American Medical Association, 2014, 312, 2115.	3.8	167
79	Laws Restricting Health Insurers' Use of Genetic Information: Impact on Genetic Discrimination. American Journal of Human Genetics, 2000, 66, 293-307.	2.6	166
80	Genome-Wide Association Studies Identify CHRNA5/3 and HTR4 in the Development of Airflow Obstruction. American Journal of Respiratory and Critical Care Medicine, 2012, 186, 622-632.	2.5	164
81	Genome-Wide Association Study of Plasma N6 Polyunsaturated Fatty Acids Within the Cohorts for Heart and Aging Research in Genomic Epidemiology Consortium. Circulation: Cardiovascular Genetics, 2014, 7, 321-331.	5.1	164
82	Widespread non-additive and interaction effects within HLA loci modulate the risk of autoimmune diseases. Nature Genetics, 2015, 47, 1085-1090.	9.4	164
83	Mutations at the BLK locus linked to maturity onset diabetes of the young and Î²-cell dysfunction. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 14460-14465.	3.3	156
84	Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data. Nature Genetics, 2022, 54, 263-273.	9.4	156
85	A genome scan for diabetic nephropathy in African Americans. Kidney International, 2004, 66, 1517-1526.	2.6	151
86	Accuracy of proband reported family history: The NHLBI Family Heart Study (FHS). , 1999, 17, 141-150.		149
87	Heritability of Carotid Artery Intima-Medial Thickness in Type 2 Diabetes. Stroke, 2002, 33, 1876-1881.	1.0	146
88	Evidence for gene-environment interactions in a linkage study of asthma and smoking exposure. Journal of Allergy and Clinical Immunology, 2003, 111, 840-846.	1.5	146
89	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.	9.4	146
90	Circulating and Dietary Omegaâ€3 and Omegaâ€6 Polyunsaturated Fatty Acids and Incidence of CVD in the Multiâ€Ethnic Study of Atherosclerosis. Journal of the American Heart Association, 2013, 2, e000506.	1.6	145

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91	Apolipoprotein E genotype, cardiovascular biomarkers and risk of stroke: Systematic review and meta-analysis of 14 015 stroke cases and pooled analysis of primary biomarker data from up to 60 883 individuals. International Journal of Epidemiology, 2013, 42, 475-492.	0.9	145
92	Promoter (4G/5G) Plasminogen Activator Inhibitor-1 Genotype and Plasminogen Activator Inhibitor-1 Levels in Blacks, Hispanics, and Non-Hispanic Whites. Circulation, 2003, 107, 2422-2427.	1.6	140
93	Genome-Wide Scans for Diabetic Nephropathy and Albuminuria in Multiethnic Populations: The Family Investigation of Nephropathy and Diabetes (FIND). Diabetes, 2007, 56, 1577-1585.	0.3	140
94	Deep-coverage whole genome sequences and blood lipids among 16,324 individuals. Nature Communications, 2018, 9, 3391.	5.8	140
95	Analysis of cardiac magnetic resonance imaging in 36,000 individuals yields genetic insights into dilated cardiomyopathy. Nature Communications, 2020, 11, 2254.	5.8	140
96	Candidate Gene Association Resource (CARe). Circulation: Cardiovascular Genetics, 2010, 3, 267-275.	5.1	139
97	Quantitative-Trait Loci Influencing Body-Mass Index Reside on Chromosomes 7 and 13: The National Heart, Lung, and Blood Institute Family Heart Study. American Journal of Human Genetics, 2002, 70, 72-82.	2.6	138
98	Genetic Epidemiology of Insulin Resistance and Visceral Adiposity The IRAS Family Study Design and Methods. Annals of Epidemiology, 2003, 13, 211-217.	0.9	138
99	A Genome-Wide Association Study of Diabetic Kidney Disease in Subjects With Type 2 Diabetes. Diabetes, 2018, 67, 1414-1427.	0.3	136
100	Association analyses of East Asian individuals and trans-ancestry analyses with European individuals reveal new loci associated with cholesterol and triglyceride levels. Human Molecular Genetics, 2017, 26, 1770-1784.	1.4	135
101	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.	3.0	135
102	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.	9.4	133
103	Pangenomics enables genotyping of known structural variants in 5202 diverse genomes. Science, 2021, 374, abg8871.	6.0	132
104	Genome-wide association analysis identifies six new loci associated with forced vital capacity. Nature Genetics, 2014, 46, 669-677.	9.4	131
105	Genome-Wide Joint Meta-Analysis of SNP and SNP-by-Smoking Interaction Identifies Novel Loci for Pulmonary Function. PLoS Genetics, 2012, 8, e1003098.	1.5	130
106	Identification of additional risk loci for stroke and small vessel disease: a meta-analysis of genome-wide association studies. Lancet Neurology, The, 2016, 15, 695-707.	4.9	130
107	Pericardial and Visceral Adipose Tissues Measured Volumetrically With Computed Tomography Are Highly Associated in Type 2 Diabetic Families. Investigative Radiology, 2005, 40, 97-101.	3.5	129
108	Genetic linkage and association of Fc? receptor IIIA (CD16A) on chromosome 1q23 with human systemic lupus erythematosus. Arthritis and Rheumatism, 2002, 46, 2132-2140.	6.7	127

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109	Heritability of GFR and albuminuria in Caucasians with type 2 diabetes mellitus. American Journal of Kidney Diseases, 2004, 43, 796-800.	2.1	127
110	Imputation of Exome Sequence Variants into Population- Based Samples and Blood-Cell-Trait-Associated Loci in African Americans: NHLBI GO Exome Sequencing Project. American Journal of Human Genetics, 2012, 91, 794-808.	2.6	123
111	Fine-mapping and functional studies highlight potential causal variants for rheumatoid arthritis and type 1 diabetes. Nature Genetics, 2018, 50, 1366-1374.	9.4	122
112	Minimal Model-Based Insulin Sensitivity Has Greater Heritability and a Different Genetic Basis Than Homeostasis Model Assessment or Fasting Insulin. Diabetes, 2003, 52, 2168-2174.	0.3	118
113	The Type 1 Diabetes Genetics Consortium. Annals of the New York Academy of Sciences, 2006, 1079, 1-8.	1.8	116
114	Association of Protein Tyrosine Phosphatase 1B Gene Polymorphisms With Type 2 Diabetes. Diabetes, 2004, 53, 3007-3012.	0.3	113
115	Trans-ethnic kidney function association study reveals putative causal genes and effects on kidney-specific disease aetiologies. Nature Communications, 2019, 10, 29.	5.8	113
116	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.	9.4	112
117	A leucine repeat in the carnosinase gene CNDP1 is associated with diabetic end-stage renal disease in European Americans. Nephrology Dialysis Transplantation, 2007, 22, 1131-1135.	0.4	111
118	Sex differences in the late first trimester human placenta transcriptome. Biology of Sex Differences, 2018, 9, 4.	1.8	109
119	Phosphodiesterase 4D and 5-lipoxygenase activating protein in ischemic stroke. Annals of Neurology, 2005, 58, 351-361.	2.8	108
120	Role of Type 1 Diabetesâ€“Associated SNPs on Risk of Autoantibody Positivity in the TEDDY Study. Diabetes, 2015, 64, 1818-1829.	0.3	108
121	DNA Methylation of the Aryl Hydrocarbon Receptor Repressor Associations With Cigarette Smoking and Subclinical Atherosclerosis. Circulation: Cardiovascular Genetics, 2015, 8, 707-716.	5.1	107
122	Association of clonal hematopoiesis with chronic obstructive pulmonary disease. Blood, 2022, 139, 357-368.	0.6	106
123	Early Progression of Diabetic Nephropathy Correlates With Methylglyoxal-Derived Advanced Glycation End Products. Diabetes Care, 2013, 36, 3234-3239.	4.3	105
124	Links Between Insulin Resistance, Adenosine A2B Receptors, and Inflammatory Markers in Mice and Humans. Diabetes, 2011, 60, 669-679.	0.3	104
125	A Human Type 1 Diabetes Susceptibility Locus Maps to Chromosome 21q22.3. Diabetes, 2008, 57, 2858-2861.	0.3	103
126	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.	2.6	103

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127	Comparison of Proteomic Assessment Methods in Multiple Cohort Studies. Proteomics, 2020, 20, e1900278.	1.3	103
128	Studies of Kidney and Muscle Biopsy Specimens from Identical Twins Discordant for Type I Diabetes Mellitus. New England Journal of Medicine, 1985, 312, 1282-1287.	13.9	102
129	Confirmation of Genetic Associations at ELMO1 in the GoKinD Collection Supports Its Role as a Susceptibility Gene in Diabetic Nephropathy. Diabetes, 2009, 58, 2698-2702.	0.3	102
130	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.	2.9	102
131	Evidence for major genes influencing pulmonary function in the NHLBI Family Heart Study. Genetic Epidemiology, 2000, 19, 81-94.	0.6	101
132	The Genetic Landscape of Renal Complications in Type 1 Diabetes. Journal of the American Society of Nephrology: JASN, 2017, 28, 557-574.	3.0	101
133	Genetic scores to stratify risk of developing multiple islet autoantibodies and type 1 diabetes: A prospective study in children. PLoS Medicine, 2018, 15, e1002548.	3.9	101
134	Urinary albumin excretion in families with type 2 diabetes is heritable and genetically correlated to blood pressure. Kidney International, 2000, 57, 250-257.	2.6	100
135	Ethnic differences in asthma and associated phenotypes: Collaborative Study on the Genetics of Asthma. Journal of Allergy and Clinical Immunology, 2001, 108, 357-362.	1.5	99
136	Biomarkers of Dairy Fatty Acids and Risk of Cardiovascular Disease in the Multiâ€Ethnic Study of Atherosclerosis. Journal of the American Heart Association, 2013, 2, e000092.	1.6	97
137	Genetic Polymorphisms of the IL-1Î± and IL-1Î² Genes in African-American LJP Patients and an African-American Control Population. Journal of Periodontology, 2000, 71, 723-728.	1.7	93
138	Habitual sleep duration is associated with BMI and macronutrient intake and may be modified by CLOCK genetic variants. American Journal of Clinical Nutrition, 2015, 101, 135-143.	2.2	93
139	Analysis commons, a team approach to discovery in a big-data environment for genetic epidemiology. Nature Genetics, 2017, 49, 1560-1563.	9.4	93
140	Genome-Wide Scan for Estimated Glomerular Filtration Rate in Multi-Ethnic Diabetic Populations: The Family Investigation of Nephropathy and Diabetes (FIND). Diabetes, 2008, 57, 235-243.	0.3	92
141	Genome-Wide Association Study Identifies Novel Loci Associated With Concentrations of Four Plasma Phospholipid Fatty Acids in the De Novo Lipogenesis Pathway. Circulation: Cardiovascular Genetics, 2013, 6, 171-183.	5.1	91
142	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. Genome Biology, 2021, 22, 194.	3.8	90
143	Association of Stein-Leventhal syndrome with the incidence of postmenopausal breast carcinoma in a large prospective study of women in Iowa. , 1997, 79, 494-499.		89
144	Linkage Analysis of a Composite Factor for the Multiple Metabolic Syndrome: The National Heart, Lung, and Blood Institute Family Heart Study. Diabetes, 2003, 52, 2840-2847.	0.3	89

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145	Variants of the Transcription Factor 7-Like 2 (TCF7L2) Gene Are Associated With Type 2 Diabetes in an African-American Population Enriched for Nephropathy. Diabetes, 2007, 56, 2638-2642.	0.3	89
146	Clonal Hematopoiesis Is Associated With Higher Risk of Stroke. Stroke, 2022, 53, 788-797.	1.0	88
147	Linkage of the Metabolic Syndrome to 1q23-q31 in Hispanic Families: The Insulin Resistance Atherosclerosis Study Family Study. Diabetes, 2004, 53, 1170-1174.	0.3	87
148	Genome-Wide Scan for Linkage to Type 1 Diabetes in 2,496 Multiplex Families From the Type 1 Diabetes Genetics Consortium. Diabetes, 2009, 58, 1018-1022.	0.3	87
149	Genome-Wide Study of Percent Emphysema on Computed Tomography in the General Population. The Multi-Ethnic Study of Atherosclerosis Lung/SNP Health Association Resource Study. American Journal of Respiratory and Critical Care Medicine, 2014, 189, 408-418.	2.5	87
150	Crossâ€validation of protein structural class prediction using statistical clustering and neural networks. Protein Science, 1993, 2, 1171-1182.	3.1	86
151	Multiethnic meta-analysis identifies ancestry-specific and cross-ancestry loci for pulmonary function. Nature Communications, 2018, 9, 2976.	5.8	85
152	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	1.6	85
153	Allele-specific expression changes dynamically during T cell activation in HLA and other autoimmune loci. Nature Genetics, 2020, 52, 247-253.	9.4	85
154	HLA-DRB1*07:01 is associated with a higher risk of asparaginase allergies. Blood, 2014, 124, 1266-1276.	0.6	84
155	Gene Ã— dietary pattern interactions in obesity: analysis of up to 68 317 adults of European ancestry. Human Molecular Genetics, 2015, 24, 4728-4738.	1.4	84
156	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	5.8	84
157	HLA class II â€œtypingâ€• Direct sequencing of DRB, DQB, and DQA genes. Human Immunology, 1992, 33, 69-81.	1.2	83
158	A combined risk score enhances prediction of type 1 diabetes among susceptible children. Nature Medicine, 2020, 26, 1247-1255.	15.2	83
159	Determinants of the Development of Diabetes (Maturity-Onset Diabetes of the Young-3) in Carriers of HNF-1Â Mutations: Evidence for parent-of-origin effect. Diabetes Care, 2002, 25, 2292-2301.	4.3	82
160	Quantifying rare, deleterious variation in 12 human cytochrome P450 drug-metabolism genes in a large-scale exome dataset. Human Molecular Genetics, 2014, 23, 1957-1963.	1.4	82
161	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. American Journal of Human Genetics, 2016, 99, 40-55.	2.6	82
162	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.	3.3	80

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163	Population Structure of Hispanics in the United States: The Multi-Ethnic Study of Atherosclerosis. PLoS Genetics, 2012, 8, e1002640.	1.5	79
164	Guidelines for Large-Scale Sequence-Based Complex Trait Association Studies: Lessons Learned from the NHLBI Exome Sequencing Project. American Journal of Human Genetics, 2016, 99, 791-801.	2.6	79
165	Deep coverage whole genome sequences and plasma lipoprotein(a) in individuals of European and African ancestries. Nature Communications, 2018, 9, 2606.	5.8	79
166	Pathogenic Variants for Mendelian and Complex Traits in Exomes of 6,517 European and African Americans: Implications for the Return of Incidental Results. American Journal of Human Genetics, 2014, 95, 183-193.	2.6	78
167	Analysis of predicted loss-of-function variants in UK Biobank identifies variants protective for disease. Nature Communications, 2018, 9, 1613.	5.8	78
168	Genetic Variants Associated With Quantitative Glucose Homeostasis Traits Translate to Type 2 Diabetes in Mexican Americans: The GUARDIAN (Genetics Underlying Diabetes in Hispanics) Consortium. Diabetes, 2015, 64, 1853-1866.	0.3	77
169	Overlap of Genetic Risk between Interstitial Lung Abnormalities and Idiopathic Pulmonary Fibrosis. American Journal of Respiratory and Critical Care Medicine, 2019, 200, 1402-1413.	2.5	77
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