Cristen J Willer

List of Publications by Year
in descending order

182 papers	68,477 citations	5876 81 h-index	3563 181 g-index
238 all docs	238 docs citations	238 times ranked	58628 citing authors

#	Article	IF	Citations
1	Gait speed is a preoperative indicator of postoperative events after elective proximal aortic surgery. Journal of Thoracic and Cardiovascular Surgery, 2022, 163, 886-894.e1.	0.4	7
2	Cardiorespiratory Fitness After Open Repair for Acute Type A Aortic Dissection â€“ A Prospective Study. Seminars in Thoracic and Cardiovascular Surgery, 2022, 34, 827-839.	0.4	11
3	Differences in Inflammation, Treatment, and Outcomes Between Black and Non-Black Patients Hospitalized for COVID-19: A Prospective Cohort Study. American Journal of Medicine, 2022, 135, 360-368.	0.6	5
4	Spontaneous coronary artery dissection is infrequent in individuals with heritable thoracic aortic disease despite partially shared genetic susceptibility. American Journal of Medical Genetics, Part A, 2022, 188, 1448-1456.	0.7	2
5	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.	2.6	24
6	A polygenic risk score improves risk stratification of coronary artery disease: a large-scale prospective Chinese cohort study. European Heart Journal, 2022, 43, 1702-1711.	1.0	58
7	Identification of cell type specific ACE2 modifiers by CRISPR screening. PLoS Pathogens, 2022, 18, e1010377.	2.1	9
8	Meta-analysis of sub-Saharan African studies provides insights into genetic architecture of lipid traits. Nature Communications, 2022, 13, 2578.	5.8	18
9	Within-sibship genome-wide association analyses decrease bias in estimates of direct genetic effects. Nature Genetics, 2022, 54, 581-592.	9.4	142
10	Genetic loci and prioritization of genes for kidney function decline derived from a meta-analysis of 62 longitudinal genome-wide association studies. Kidney International, 2022, 102, 624-639.	2.6	18
11	Genome-wide meta-analysis of iron status biomarkers and the effect of iron on all-cause mortality in HUNT. Communications Biology, 2022, 5, .	2.0	11
12	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. Communications Biology, 2022, 5, .	2.0	17
13	Receptor-Mediated ER Export of Lipoproteins Controls Lipid Homeostasis in Mice and Humans. Cell Metabolism, 2021, 33, 350-366.e7.	7.2	70
14	Complex and Potentially Harmful Medication Patterns in Heart Failure with Preserved Ejection Fraction. American Journal of Medicine, 2021, 134, 374-382.	0.6	14
15	Genome-scale CRISPR screening for modifiers of cellular LDL uptake. PLoS Genetics, 2021, 17, e1009285.	1.5	24
16	Exposure and risk factors for COVID-19 and the impact of staying home on Michigan residents. PLoS ONE, 2021, 16, e0246447.	1.1	13
17	Translating genetic association of lipid levels for biological and clinical application. Cardiovascular Drugs and Therapy, 2021, 35, 617-626.	1.3	4
18	Copy Number Variant Analysis and Genome-wide Association Study Identify Loci with Large Effect for Vesicoureteral Reflux. Journal of the American Society of Nephrology: JASN, 2021, 32, 805-820.	3.0	17

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19	Genetic insight into sick sinus syndrome. European Heart Journal, 2021, 42, 1959-1971.	1.0	27
20	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	13.7	1,069
21	An Asian-specific MPL genetic variant alters JAKâ€“STAT signaling and influences platelet count in the population. Human Molecular Genetics, 2021, 30, 836-842.	1.4	4
22	Disclosure of clinically actionable genetic variants to thoracic aortic dissection biobank participants. BMC Medical Genomics, 2021, 14, 66.	0.7	10
23	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. Nature Communications, 2021, 12, 2182.	5.8	17
24	Genome-wide association study of cardiac troponin I in the general population. Human Molecular Genetics, 2021, 30, 2027-2039.	1.4	11
25	Development and Validation of a Polygenic Risk Score for Stroke in the Chinese Population. Neurology, 2021, 97, e619-e628.	1.5	19
26	The causal effects of serum lipids and apolipoproteins on kidney function: multivariable and bidirectional Mendelian-randomization analyses. International Journal of Epidemiology, 2021, 50, 1569-1579.	0.9	18
27	Discovery and prioritization of variants and genes for kidney function in >1.2 million individuals. Nature Communications, 2021, 12, 4350.	5.8	125
28	Mapping the human genetic architecture of COVID-19. Nature, 2021, 600, 472-477.	13.7	640
29	GWAS Identifies LINC01184/SLC12A2 as a Risk Locus for Skin and Soft Tissue Infections. Journal of Investigative Dermatology, 2021, 141, 2083-2086.e8.	0.3	4
30	Regulatory variants in TCF7L2 are associated with thoracic aortic aneurysm. American Journal of Human Genetics, 2021, 108, 1578-1589.	2.6	17
31	A genome-wide association study with 1,126,563 individuals identifies new risk loci for Alzheimerâ€™s disease. Nature Genetics, 2021, 53, 1276-1282.	9.4	430
32	Deciphering osteoarthritis genetics across 826,690 individuals from 9 populations. Cell, 2021, 184, 4784-4818.e17.	13.5	188
33	A survey of aortic disease biorepository participantsâ€™ preferences for return of research genetic results. Journal of Genetic Counseling, 2021, 30, 645-655.	0.9	6
34	Type 2 diabetes sex-specific effects associated with E167K coding variant in TM6SF2. IScience, 2021, 24, 103196.	1.9	10
35	Responsible use of polygenic risk scores in the clinic: potential benefits, risks and gaps. Nature Medicine, 2021, 27, 1876-1884.	15.2	214
36	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	13.7	353

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37	The emerging landscape of health research based on biobanks linked to electronic health records: Existing resources, statistical challenges, and potential opportunities. Statistics in Medicine, 2020, 39, 773-800.	0.8	57
38	Genetic Architecture of Abdominal Aortic Aneurysm in the Million Veteran Program. Circulation, 2020, 142, 1633-1646.	1.6	78
39	Exome sequencing and characterization of 49,960 individuals in the UK Biobank. Nature, 2020, 586, 749-756.	13.7	369
40	Genome-wide association study of intracranial aneurysms identifies 17 risk loci and genetic overlap with clinical risk factors. Nature Genetics, 2020, 52, 1303-1313.	9.4	163
41	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. Nature Genetics, 2020, 52, 1314-1332.	9.4	91
42	GWAS of thyroid stimulating hormone highlights pleiotropic effects and inverse association with thyroid cancer. Nature Communications, 2020, 11, 3981.	5.8	86
43	Avoiding dynastic, assortative mating, and population stratification biases in Mendelian randomization through within-family analyses. Nature Communications, 2020, 11, 3519.	5.8	213
44	MEPE loss-of-function variant associates with decreased bone mineral density and increased fracture risk. Nature Communications, 2020, 11, 4093.	5.8	24
45	Mendelian randomization study of maternal influences on birthweight and future cardiometabolic risk in the HUNT cohort. Nature Communications, 2020, 11, 5404.	5.8	48
46	Cardiometabolic Traits, Sepsis, and Severe COVID-19. Circulation, 2020, 142, 1791-1793.	1.6	93
47	Genetic Predisposition to Coronary Artery Disease in Type 2 Diabetes Mellitus. Circulation Genomic and Precision Medicine, 2020, 13, e002769.	1.6	5
48	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
49	Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. Nature Communications, 2020, 11, 6417.	5.8	39
50	Scalable generalized linear mixed model for region-based association tests in large biobanks and cohorts. Nature Genetics, 2020, 52, 634-639.	9.4	124
51	Use of a Polygenic Risk Score Improves Prediction of Myocardial Injury After Non-Cardiac Surgery. Circulation Genomic and Precision Medicine, 2020, 13, e002817.	1.6	9
52	Exploring and visualizing large-scale genetic associations by using PheWeb. Nature Genetics, 2020, 52, 550-552.	9.4	129
53	Causal relationships between NAFLD, T2D and obesity have implications for disease subphenotyping. Journal of Hepatology, 2020, 73, 263-276.	1.8	137
54	Aortic progression and reintervention in patients with pathogenic variants after a thoracic aortic dissection. Journal of Thoracic and Cardiovascular Surgery, 2020, 162, 1436-1448.e6.	0.4	11

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55	Higher admission rates and in-hospital mortality for acute type A aortic dissection during Influenza season: a single center experience. Scientific Reports, 2020, 10, 4723.	1.6	15
56	Age-of-onset information helps identify 76 genetic variants associated with allergic disease. PLoS Genetics, 2020, 16, e1008725.	1.5	27
57	Mitochondrial genome-wide association study of migraine â€“ the HUNT Study. Cephalalgia, 2020, 40, 625-634.	1.8	19
58	Variants associated with HHIP expression have sex-differential effects on lung function. Wellcome Open Research, 2020, 5, 111.	0.9	3
59	Genetic mutations associated with susceptibility to perioperative complications in a longitudinal biorepository with integrated genomic and electronic health records. British Journal of Anaesthesia, 2020, 125, 986-994.	1.5	9
60	A Novel Variant in APOB Gene Causes Extremely Low LDL-C Without Known Adverse Effects. JACC: Case Reports, 2020, 2, 775-779.	0.3	0
61	Genetic associations with temporal shifts in obesity and severe obesity during the obesity epidemic in Norway: A longitudinal population-based cohort (the HUNT Study). PLoS Medicine, 2020, 17, e1003452.	3.9	13
62	Title is missing!. , 2020, 17, e1003452.		0
63	Title is missing!. , 2020, 17, e1003452.		0
64	Title is missing!. , 2020, 17, e1003452.		0
65	Title is missing!. , 2020, 17, e1003452.		0
66	Title is missing!. , 2020, 17, e1003452.		0
67	Title is missing!. , 2020, 17, e1003452.		0
68	Title is missing!. , 2020, 17, e1003452.		0
69	Genome-wide association analysis of self-reported daytime sleepiness identifies 42 loci that suggest biological subtypes. Nature Communications, 2019, 10, 3503.	5.8	117
70	Clinical Implications of Identifying Pathogenic Variants in Individuals With Thoracic Aortic Dissection. Circulation Genomic and Precision Medicine, 2019, 12, e002476.	1.6	51
71	Sex-specific and pleiotropic effects underlying kidney function identified from GWAS meta-analysis. Nature Communications, 2019, 10, 1847.	5.8	55
72	Robust metaâ€analysis of biobankâ€based genomeâ€wide association studies with unbalanced binary phenotypes. Genetic Epidemiology, 2019, 43, 462-476.	0.6	7

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73	Biological and clinical insights from genetics of insomnia symptoms. Nature Genetics, 2019, 51, 387-393.	9.4	250
74	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	9.4	89
75	Lower Extremity Function Is Independently Associated With Hospitalization Burden in Heart Failure With Preserved Ejection Fraction. Journal of Cardiac Failure, 2019, 25, 2-9.	0.7	27
76	Effects of the coronary artery disease associated LPA and 9p21 loci on risk of aortic valve stenosis. International Journal of Cardiology, 2019, 276, 212-217.	0.8	9
77	Association studies of up to 1.2 million individuals yield new insights into the genetic etiology of tobacco and alcohol use. Nature Genetics, 2019, 51, 237-244.	9.4	1,307
78	Variation in Serum PCSK9 (Proprotein Convertase Subtilisin/Kexin Type 9), Cardiovascular Disease Risk, and an Investigation of Potential Unanticipated Effects of PCSK9 Inhibition. Circulation Genomic and Precision Medicine, 2019, 12, e002335.	1.6	11
79	Genome-wide analysis yields new loci associating with aortic valve stenosis. Nature Communications, 2018, 9, 987.	5.8	91
80	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
81	Genome-wide Study of Atrial Fibrillation Identifies Seven Risk Loci and Highlights Biological Pathways and Regulatory Elements Involved in Cardiac Development. American Journal of Human Genetics, 2018, 102, 103-115.	2.6	86
82	Electronic health records: the next wave of complex disease genetics. Human Molecular Genetics, 2018, 27, R14-R21.	1.4	38
83	Genetics of blood lipids among ~300,000 multi-ethnic participants of the Million Veteran Program. Nature Genetics, 2018, 50, 1514-1523.	9.4	497
84	A novel homozygous ABCA1 variant in an asymptomatic man with profound hypoalphalipoproteinemia. Journal of Clinical Lipidology, 2018, 12, 878-882.	0.6	4
85	Biobank-driven genomic discovery yields new insight into atrial fibrillation biology. Nature Genetics, 2018, 50, 1234-1239.	9.4	547
86	A genome scan for genes underlying adult body size differences between Central African hunter-gatherers and farmers. Human Genetics, 2018, 137, 487-509.	1.8	15
87	Coding variants in RPL3L and MYZAP increase risk of atrial fibrillation. Communications Biology, 2018, 1, 68.	2.0	42
88	Efficiently controlling for case-control imbalance and sample relatedness in large-scale genetic association studies. Nature Genetics, 2018, 50, 1335-1341.	9.4	896
89	Deep-coverage whole genome sequences and blood lipids among 16,324 individuals. Nature Communications, 2018, 9, 3391.	5.8	140
90	Genetic inactivation of ANGPTL4 improves glucose homeostasis and is associated with reduced risk of diabetes. Nature Communications, 2018, 9, 2252.	5.8	99

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91	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	9.4	286
92	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	13.7	544
93	Association of Rare and Common Variation in the Lipoprotein Lipase Gene With Coronary Artery Disease. JAMA - Journal of the American Medical Association, 2017, 317, 937.	3.8	148
94	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated WithÂCoronary ArteryÂDisease. Journal of the American College of Cardiology, 2017, 69, 823-836.	1.2	214
95	Protein-Truncating Variants at the Cholesteryl Ester Transfer Protein Gene and Risk for Coronary Heart Disease. Circulation Research, 2017, 121, 81-88.	2.0	68
96	Protein-altering and regulatory genetic variants near GATA4 implicated in bicuspid aortic valve. Nature Communications, 2017, 8, 15481.	5.8	90
97	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	9.4	470
98	Exome chip meta-analysis identifies novel loci and East Asianâ€“specific coding variants that contribute to lipid levels and coronary artery disease. Nature Genetics, 2017, 49, 1722-1730.	9.4	129
99	Shared genetic origin of asthma, hay fever and eczema elucidates allergic disease biology. Nature Genetics, 2017, 49, 1752-1757.	9.4	432
100	New Blood Pressureâ€“Associated Loci Identified in Meta-Analyses of 475â€‰000 Individuals. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	48
101	Improving power of association tests using multiple sets of imputed genotypes from distributed reference panels. Genetic Epidemiology, 2017, 41, 744-755.	0.6	27
102	A genomic exploration identifies mechanisms that may explain adverse cardiovascular effects of COX-2 inhibitors. Scientific Reports, 2017, 7, 10252.	1.6	16
103	Genomic correlates of glatiramer acetate adverse cardiovascular effects lead to a novel locus mediating coronary risk. PLoS ONE, 2017, 12, e0182999.	1.1	5
104	Phenotypic Characterization of GeneticallyÂLowered Human Lipoprotein(a) Levels. Journal of the American College of Cardiology, 2016, 68, 2761-2772.	1.2	186
105	Coding Variation inANGPTL4,LPL,andSVEP1and the Risk of Coronary Disease. New England Journal of Medicine, 2016, 374, 1134-1144.	13.9	427
106	Genetic Variants in LRP1 and ULK4 Are Associated with Acute Aortic Dissections. American Journal of Human Genetics, 2016, 99, 762-769.	2.6	73
107	A reference panel of 64,976 haplotypes for genotype imputation. Nature Genetics, 2016, 48, 1279-1283.	9.4	2,421
108	Reply. Gastroenterology, 2016, 151, 1034-1035.	0.6	0

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109	Genetic variants inCETPincrease risk of intracerebral hemorrhage. Annals of Neurology, 2016, 80, 730-740.	2.8	33
110	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	9.4	261
111	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
112	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. American Journal of Human Genetics, 2016, 99, 40-55.	2.6	82
113	Hepatic Transmembrane 6 Superfamily Member 2 Regulates Cholesterol Metabolism in Mice. Gastroenterology, 2016, 150, 1208-1218.	0.6	78
114	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. Science, 2016, 351, 1166-1171.	6.0	438
115	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. Nature Communications, 2016, 7, 10495.	5.8	245
116	Association of exome sequences with plasma C-reactive protein levels in >9000 participants. Human Molecular Genetics, 2015, 24, 559-571.	1.4	36
117	Exome-wide association analysis reveals novel coding sequence variants associated with lipid traits in Chinese. Nature Communications, 2015, 6, 10206.	5.8	86
118	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	13.7	1,328
119	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	13.7	3,823
120	Methods for Association Analysis and Metaâ€Analysis of Rare Variants in Families. Genetic Epidemiology, 2015, 39, 227-238.	0.6	16
121	GREGOR: evaluating global enrichment of trait-associated variants in epigenomic features using a systematic, data-driven approach. Bioinformatics, 2015, 31, 2601-2606.	1.8	146
122	Recent developments in genome and exome-wide analyses of plasma lipids. Current Opinion in Lipidology, 2015, 26, 96-102.	1.2	24
123	Genetically Determined Height and Coronary Artery Disease. New England Journal of Medicine, 2015, 372, 1608-1618.	13.9	220
124	Insights into blood lipids from rare variant discovery. Current Opinion in Genetics and Development, 2015, 33, 25-31.	1.5	4
125	Perhexiline activates KLF14 and reduces atherosclerosis by modulating ApoA-I production. Journal of Clinical Investigation, 2015, 125, 3819-3830.	3.9	72
126	Whole-exome imputation of sequence variants identified two novel alleles associated with adult body height in African Americans. Human Molecular Genetics, 2014, 23, 6607-6615.	1.4	14

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127	No large-effect low-frequency coding variation found for myocardial infarction. Human Molecular Genetics, 2014, 23, 4721-4728.	1.4	16
128	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
129	Systematic evaluation of coding variation identifies a candidate causal variant in TM6SF2 influencing total cholesterol and myocardial infarction risk. Nature Genetics, 2014, 46, 345-351.	9.4	268
130	Effects of Long-Term Averaging of Quantitative Blood Pressure Traits on the Detection of Genetic Associations. American Journal of Human Genetics, 2014, 95, 49-65.	2.6	73
131	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	9.4	1,818
132	Meta-analysis of gene-level tests for rare variant association. Nature Genetics, 2014, 46, 200-204.	9.4	178
133	Loss-of-Function Mutations inAPOC3,Triglycerides, and Coronary Disease. New England Journal of Medicine, 2014, 371, 22-31.	13.9	936
134	Discovery and refinement of loci associated with lipid levels. Nature Genetics, 2013, 45, 1274-1283.	9.4	2,641
135	Common variants associated with plasma triglycerides and risk for coronary artery disease. Nature Genetics, 2013, 45, 1345-1352.	9.4	754
136	Large-scale association analysis identifies new risk loci for coronary artery disease. Nature Genetics, 2013, 45, 25-33.	9.4	1,439
137	Accurate Local-Ancestry Inference in Exome-Sequenced Admixed Individuals via Off-Target Sequence Reads. American Journal of Human Genetics, 2013, 93, 891-899.	2.6	21
138	WikiGWA: an open platform for collecting and using genome-wide association results. European Journal of Human Genetics, 2013, 21, 471-473.	1.4	3
139	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. Nature Genetics, 2013, 45, 501-512.	9.4	578
140	Identification of heart rateâ€“associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	9.4	282
141	The Power of Meta-Analysis in Genome-Wide Association Studies. Annual Review of Genomics and Human Genetics, 2013, 14, 441-465.	2.5	107
142	Abstract 050: Meta-analysis of Genetic Associations in up to 339,224 Individuals Identify 66 New Loci for Bmi, Confirming a Neuronal Contribution to Body Weight Regulation and Implicating Several Novel Pathways. Circulation, 2013, 127, .	1.6	0
143	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.	1.5	419
144	Finding genes and variants for lipid levels after genome-wide association analysis. Current Opinion in Lipidology, 2012, 23, 98-103.	1.2	46

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145	Plasma HDL cholesterol and risk of myocardial infarction: a mendelian randomisation study. Lancet, The, 2012, 380, 572-580.	6.3	1,937
146	A Genome-Wide Association Search for Type 2 Diabetes Genes in African Americans. PLoS ONE, 2012, 7, e29202.	1.1	197
147	Genomic inflation factors under polygenic inheritance. European Journal of Human Genetics, 2011, 19, 807-812.	1.4	460
148	Common Variants Show Predicted Polygenic Effects on Height in the Tails of the Distribution, Except in Extremely Short Individuals. PLoS Genetics, 2011, 7, e1002439.	1.5	49
149	MaCH: using sequence and genotype data to estimate haplotypes and unobserved genotypes. Genetic Epidemiology, 2010, 34, 816-834.	0.6	1,718
150	Biological, clinical and population relevance of 95 loci for blood lipids. Nature, 2010, 466, 707-713.	13.7	3,249
151	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	13.7	1,789
152	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. Nature Genetics, 2010, 42, 579-589.	9.4	1,631
153	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. Nature Genetics, 2010, 42, 949-960.	9.4	836
154	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nature Genetics, 2010, 42, 937-948.	9.4	2,634
155	METAL: fast and efficient meta-analysis of genomewide association scans. Bioinformatics, 2010, 26, 2190-2191.	1.8	4,046
156	LocusZoom: regional visualization of genome-wide association scan results. Bioinformatics, 2010, 26, 2336-2337.	1.8	2,349
157	Genome-Wide Association Scan Meta-Analysis Identifies Three Loci Influencing Adiposity and Fat Distribution. PLoS Genetics, 2009, 5, e1000508.	1.5	453
158	Six new loci associated with body mass index highlight a neuronal influence on body weight regulation. Nature Genetics, 2009, 41, 25-34.	9.4	1,572
159	Common variants at 30 loci contribute to polygenic dyslipidemia. Nature Genetics, 2009, 41, 56-65.	9.4	1,234
160	Genome-wide association study identifies eight loci associated with blood pressure. Nature Genetics, 2009, 41, 666-676.	9.4	1,104
161	Genotype Imputation. Annual Review of Genomics and Human Genetics, 2009, 10, 387-406.	2.5	920
162	A first stage genomeâ€wide screen for regions shared identicalâ€byâ€descent in hutterite families with multiple sclerosis. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2008, 147B, 467-472.	1.1	4

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163	Common variants near MC4R are associated with fat mass, weight and risk of obesity. Nature Genetics, 2008, 40, 768-775.	9.4	1,179
164	Common variants in the GDF5-UQCC region are associated with variation in human height. Nature Genetics, 2008, 40, 198-203.	9.4	369
165	Newly identified loci that influence lipid concentrations and risk of coronary artery disease. Nature Genetics, 2008, 40, 161-169.	9.4	1,488
166	Meta-analysis of genome-wide association data and large-scale replication identifies additional susceptibility loci for type 2 diabetes. Nature Genetics, 2008, 40, 638-645.	9.4	1,683
167	Comprehensive Association Study of Type 2 Diabetes and Related Quantitative Traits With 222 Candidate Genes. Diabetes, 2008, 57, 3136-3144.	0.3	104
168	Variations in the G6PC2/ABCB11 genomic region are associated with fasting glucose levels. Journal of Clinical Investigation, 2008, 118, 2620-8.	3.9	146
169	Screening of 134 Single Nucleotide Polymorphisms (SNPs) Previously Associated With Type 2 Diabetes Replicates Association With 12 SNPs in Nine Genes. Diabetes, 2007, 56, 256-264.	0.3	109
170	A Genome-Wide Association Study of Type 2 Diabetes in Finns Detects Multiple Susceptibility Variants. Science, 2007, 316, 1341-1345.	6.0	2,534
171	A genome-wide scan in forty large pedigrees with multiple sclerosis. Journal of Human Genetics, 2007, 52, 955-962.	1.1	30
172	Association between microchimerism and multiple sclerosis in Canadian twins. Journal of Neuroimmunology, 2006, 179, 145-151.	1.1	41
173	Tag SNP selection for Finnish individuals based on the CEPH Utah HapMap database. Genetic Epidemiology, 2006, 30, 180-190.	0.6	54
174	Common Variants in Maturity-Onset Diabetes of the Young Genes Contribute to Risk of Type 2 Diabetes in Finns. Diabetes, 2006, 55, 2534-2540.	0.3	69
175	Association of Transcription Factor 7-Like 2 (TCF7L2) Variants With Type 2 Diabetes in a Finnish Sample. Diabetes, 2006, 55, 2649-2653.	0.3	224
176	Complex interactions among MHC haplotypes in multiple sclerosis: susceptibility and resistance. Human Molecular Genetics, 2005, 14, 2019-2026.	1.4	212
177	Timing of birth and risk of multiple sclerosis: population based study. BMJ: British Medical Journal, 2005, 330, 120.	2.4	380
178	An extended genome scan in 442 Canadian multiple sclerosis-affected sibships: a report from the Canadian Collaborative Study Group. Human Molecular Genetics, 2004, 13, 1005-1015.	1.4	52
179	Microchimerism in autoimmunity and transplantation: potential relevance to multiple sclerosis. Journal of Neuroimmunology, 2002, 126, 126-133.	1.1	24
180	Evidence of Linkage with HLA-DR in DRB1*15-Negative Families with Multiple Sclerosis. American Journal of Human Genetics, 2001, 69, 900-903.	2.6	72

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181	Genetic susceptibility to MS: a second stage analysis in Canadian MS families. Neurogenetics, 2001, 3, 145-151.	0.7	40
182	Susceptibility to multiple sclerosis: interplay between genes and environment. Current Opinion in Neurology, 2000, 13, 241-247.	1.8	64