Jerome I Rotter

List of Publications by Year
in descending order

346 papers	58,961 citations	1994 101 h-index	1461 220 g-index
382 all docs	382 docs citations	382 times ranked	62302 citing authors

#	Article	IF	Citations
1	Hostâ€“microbe interactions have shaped the genetic architecture of inflammatory bowel disease. Nature, 2012, 491, 119-124.	27.8	4,038
2	Meta-analysis of 74,046 individuals identifies 11 new susceptibility loci for Alzheimer's disease. Nature Genetics, 2013, 45, 1452-1458.	21.4	3,741
3	Biological, clinical and population relevance of 95 loci for blood lipids. Nature, 2010, 466, 707-713.	27.8	3,249
4	Discovery and refinement of loci associated with lipid levels. Nature Genetics, 2013, 45, 1274-1283.	21.4	2,641
5	Genetic meta-analysis of diagnosed Alzheimerâ€™s disease identifies new risk loci and implicates AÎ², tau, immunity and lipid processing. Nature Genetics, 2019, 51, 414-430.	21.4	1,962
6	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	21.4	1,818
7	Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. Nature Genetics, 2018, 50, 1505-1513.	21.4	1,331
8	Genome-wide association study of blood pressure and hypertension. Nature Genetics, 2009, 41, 677-687.	21.4	1,224
9	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. Nature Genetics, 2018, 50, 524-537.	21.4	1,124
10	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	27.8	1,069
11	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	21.4	924
12	Genetic Associations with Valvular Calcification and Aortic Stenosis. New England Journal of Medicine, 2013, 368, 503-512.	27.0	767
13	A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. Nature Genetics, 2012, 44, 659-669.	21.4	762
14	Common variants associated with plasma triglycerides and risk for coronary artery disease. Nature Genetics, 2013, 45, 1345-1352.	21.4	754
15	Genetic and Pharmacologic Inactivation of ANGPTL3 and Cardiovascular Disease. New England Journal of Medicine, 2017, 377, 211-221.	27.0	633
16	A structural variation reference for medical and population genetics. Nature, 2020, 581, 444-451.	27.8	614
17	Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. Nature Genetics, 2010, 42, 142-148.	21.4	591
18	Multi-ethnic genome-wide association study for atrial fibrillation. Nature Genetics, 2018, 50, 1225-1233.	21.4	552

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19	Meta-analyses of genome-wide association studies identify multiple loci associated with pulmonary function. Nature Genetics, 2010, 42, 45-52.	21.4	549
20	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	21.4	549
21	Association between alcohol and cardiovascular disease: Mendelian randomisation analysis based on individual participant data. BMJ, The, 2014, 349, g4164-g4164.	6.0	528
22	Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium. Circulation: Cardiovascular Genetics, 2009, 2, 73-80.	5.1	519
23	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. Nature Communications, 2018, 9, 2098.	12.8	484
24	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	21.4	470
25	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. Nature Communications, 2020, 11, 163.	12.8	466
26	Meta-Analysis of Genome-Wide Association Studies in >80 000 Subjects Identifies Multiple Loci for C-Reactive Protein Levels. Circulation, 2011, 123, 731-738.	1.6	461
27	Genomewide Association Studies of Stroke. New England Journal of Medicine, 2009, 360, 1718-1728.	27.0	420
28	Genome-wide association study of PR interval. Nature Genetics, 2010, 42, 153-159.	21.4	400
29	The Polygenic and Monogenic Basis of Blood Traits and Diseases. Cell, 2020, 182, 1214-1231.e11.	28.9	388
30	Inactivating Mutations in NPC1L1 and Protection from Coronary Heart Disease. New England Journal of Medicine, 2014, 371, 2072-2082.	27.0	386
31	Association Between Telomere Length and Risk of Cancer and Non-Neoplastic Diseases. JAMA Oncology, 2017, 3, 636.	7.1	376
32	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature, 2020, 586, 763-768.	27.8	376
33	Genome-wide association and large-scale follow up identifies 16 new loci influencing lung function. Nature Genetics, 2011, 43, 1082-1090.	21.4	367
34	Long-Range LD Can Confound Genome Scans in Admixed Populations. American Journal of Human Genetics, 2008, 83, 132-135.	6.2	366
35	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. Nature Genetics, 2016, 48, 1171-1184.	21.4	362
36	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

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37	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	27.8	353
38	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.	8.4	341
39	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341
40	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. PLoS Genetics, 2015, 11, e1005378.	3.5	331
41	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. American Journal of Human Genetics, 2018, 103, 691-706.	6.2	326
42	Multiple loci influence erythrocyte phenotypes in the CHARGE Consortium. Nature Genetics, 2009, 41, 1191-1198.	21.4	324
43	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
44	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.	3.5	290
45	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.	6.2	287
46	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	21.4	286
47	Identification of heart rateâ€“associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	21.4	282
48	Identification of type 2 diabetes loci in 433,540 East Asian individuals. Nature, 2020, 582, 240-245.	27.8	282
49	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836.	21.4	281
50	Genome-Wide Association Study Identifies Variants Associated With Histologic Features of Nonalcoholic Fatty Liver Disease. Gastroenterology, 2010, 139, 1567-1576.e6.	1.3	270
51	Genome-Wide Association Study for Coronary Artery Calcification With Follow-Up in Myocardial Infarction. Circulation, 2011, 124, 2855-2864.	1.6	269
52	Genome-wide association analyses identify multiple loci associated with central corneal thickness and keratoconus. Nature Genetics, 2013, 45, 155-163.	21.4	269
53	Genetic Diversity and Association Studies in US Hispanic/Latino Populations: Applications in the Hispanic Community Health Study/Study of Latinos. American Journal of Human Genetics, 2016, 98, 165-184.	6.2	266
54	GWAS of Longevity in CHARGE Consortium Confirms APOE and FOXO3 Candidacy. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2015, 70, 110-118.	3.6	250

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55	Novel genetic loci associated with hippocampal volume. Nature Communications, 2017, 8, 13624.	12.8	250
56	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
57	Exome sequencing of 20,791Âcases of type 2 diabetes and 24,440Âcontrols. Nature, 2019, 570, 71-76.	27.8	248
58	Large-Scale Gene-Centric Meta-analysis across 32 Studies Identifies Multiple Lipid Loci. American Journal of Human Genetics, 2012, 91, 823-838.	6.2	227
59	Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. Nature Genetics, 2016, 48, 1162-1170.	21.4	223
60	Identification of new susceptibility loci for type 2 diabetes and shared etiological pathways with coronary heart disease. Nature Genetics, 2017, 49, 1450-1457.	21.4	218
61	A meta-analysis of genome-wide association studies identifies multiple longevity genes. Nature Communications, 2019, 10, 3669.	12.8	214
62	Novel genetic loci underlying human intracranial volume identified through genome-wide association. Nature Neuroscience, 2016, 19, 1569-1582.	14.8	213
63	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
64	Genome-wide meta-analysis of observational studies shows common genetic variants associated with macronutrient intake. American Journal of Clinical Nutrition, 2013, 97, 1395-1402.	4.7	210
65	CUBN Is a Gene Locus for Albuminuria. Journal of the American Society of Nephrology: JASN, 2011, 22, 555-570.	6.1	208
66	KLB is associated with alcohol drinking, and its gene product Î²-Klotho is necessary for FGF21 regulation of alcohol preference. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 14372-14377.	7.1	208
67	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
68	Genomeâ€wide association studies of cerebral white matter lesion burden. Annals of Neurology, 2011, 69, 928-939.	5.3	201
69	Association of Mitochondrial DNA Copy Number With Cardiovascular Disease. JAMA Cardiology, 2017, 2, 1247.	6.1	194
70	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. American Journal of Human Genetics, 2014, 94, 233-245.	6.2	193
71	Meta-analysis of genome-wide association studies in East Asian-ancestry populations identifies four new loci for body mass index. Human Molecular Genetics, 2014, 23, 5492-5504.	2.9	192
72	Genetic architecture of subcortical brain structures in 38,851 individuals. Nature Genetics, 2019, 51, 1624-1636.	21.4	192

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73	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.	3.5	191
74	Genome-wide Association Analysis of Blood-Pressure Traits in African-Ancestry Individuals Reveals Common Associated Genes in African and Non-African Populations. American Journal of Human Genetics, 2013, 93, 545-554.	6.2	189
75	Duodenal-Ulcer Disease Associated with Elevated Serum Pepsinogen I. New England Journal of Medicine, 1979, 300, 63-66.	27.0	180
76	Phenotypic Predictors of Response to Simvastatin Therapy Among African-Americans and Caucasians: The Cholesterol and Pharmacogenetics (CAP) Study. American Journal of Cardiology, 2006, 97, 843-850.	1.6	179
77	HLA class II alleles and susceptibility and resistance to insulin dependent diabetes mellitus in Mexican-American families. Nature Genetics, 1993, 3, 358-364.	21.4	176
78	Association of Genome-Wide Variation With the Risk of Incident Heart Failure in Adults of European and African Ancestry. Circulation: Cardiovascular Genetics, 2010, 3, 256-266.	5.1	176
79	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. Nature Communications, 2015, 6, 5897.	12.8	173
80	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	27.8	173
81	Convergent genetic and expression data implicate immunity in Alzheimer's disease. Alzheimer's and Dementia, 2015, 11, 658-671.	0.8	173
82	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.	5.6	164
83	Multiethnic Genome-Wide Association Study of Cerebral White Matter Hyperintensities on MRI. Circulation: Cardiovascular Genetics, 2015, 8, 398-409.	5.1	162
84	Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data. Nature Genetics, 2022, 54, 263-273.	21.4	156
85	Identification of Novel Genetic Loci Associated with Thyroid Peroxidase Antibodies and Clinical Thyroid Disease. PLoS Genetics, 2014, 10, e1004123.	3.5	150
86	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. Nature Communications, 2017, 8, 80.	12.8	147
87	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
88	Deep-coverage whole genome sequences and blood lipids among 16,324 individuals. Nature Communications, 2018, 9, 3391.	12.8	140
89	Analysis of cardiac magnetic resonance imaging in 36,000 individuals yields genetic insights into dilated cardiomyopathy. Nature Communications, 2020, 11, 2254.	12.8	140
90	Candidate Gene Association Resource (CARe). Circulation: Cardiovascular Genetics, 2010, 3, 267-275.	5.1	139

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91	Genome-Wide Analysis of Left Ventricular Image-Derived Phenotypes Identifies Fourteen Loci Associated With Cardiac Morphogenesis and Heart Failure Development. Circulation, 2019, 140, 1318-1330.	1.6	138
92	Genetic predictors of medically refractory ulcerative colitis. Inflammatory Bowel Diseases, 2010, 16, 1830-1840.	1.9	135
93	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.	2.9	135
94	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. Nature Communications, 2019, 10, 4130.	12.8	133
95	Pangenomics enables genotyping of known structural variants in 5202 diverse genomes. Science, 2021, 374, abg8871.	12.6	132
96	Genome-wide association analysis identifies six new loci associated with forced vital capacity. Nature Genetics, 2014, 46, 669-677.	21.4	131
97	Genome-Wide Joint Meta-Analysis of SNP and SNP-by-Smoking Interaction Identifies Novel Loci for Pulmonary Function. PLoS Genetics, 2012, 8, e1003098.	3.5	130
98	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.	10.2	130
99	Sequencing of 640,000 exomes identifies GPR75 variants associated with protection from obesity. Science, 2021, 373, .	12.6	130
100	Familial Mediterranean fever in Armenians: Autosomal recessive inheritance with high gene frequency. American Journal of Medical Genetics Part A, 1989, 34, 168-172.	2.4	125
101	GWAS and colocalization analyses implicate carotid intima-media thickness and carotid plaque loci in cardiovascular outcomes. Nature Communications, 2018, 9, 5141.	12.8	119
102	Genome-Wide Association and Trans-ethnic Meta-Analysis for Advanced Diabetic Kidney Disease: Family Investigation of Nephropathy and Diabetes (FIND). PLoS Genetics, 2015, 11, e1005352.	3.5	118
103	A Meta-analysis of Four Genome-Wide Association Studies of Survival to Age 90 Years or Older: The Cohorts for Heart and Aging Research in Genomic Epidemiology Consortium. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2010, 65A, 478-487.	3.6	117
104	Genetic architecture of gene expression traits across diverse populations. PLoS Genetics, 2018, 14, e1007586.	3.5	117
105	Genome Scan for Blood Pressure in Dutch Dyslipidemic Families Reveals Linkage to a Locus on Chromosome 4p. Hypertension, 2001, 38, 773-778.	2.7	116
106	Association of Polymorphisms in the Hepatocyte Growth Factor Gene Promoter with Keratoconus. , 2011, 52, 8514.		114
107	52 Genetic Loci Influencing MyocardialÂMass. Journal of the American College of Cardiology, 2016, 68, 1435-1448.	2.8	113
108	Low-Frequency Synonymous Coding Variation in CYP2R1 Has Large Effects on Vitamin D Levels and Risk of Multiple Sclerosis. American Journal of Human Genetics, 2017, 101, 227-238.	6.2	112

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109	Genome-wide meta-analysis of 158,000 individuals of European ancestry identifies three loci associated with chronic back pain. PLoS Genetics, 2018, 14, e1007601.	3.5	112
110	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
111	Genome-Wide Association of Body Fat Distribution in African Ancestry Populations Suggests New Loci. PLoS Genetics, 2013, 9, e1003681.	3.5	109
112	Gene-Age Interactions in Blood Pressure Regulation: A Large-Scale Investigation with the CHARGE, Global BPgen, and ICBP Consortia. American Journal of Human Genetics, 2014, 95, 24-38.	6.2	109
113	A genome-wide association study identifies a potential novel gene locus for keratoconus, one of the commonest causes for corneal transplantation in developed countries. Human Molecular Genetics, 2012, 21, 421-429.	2.9	108
114	Pleiotropic genes for metabolic syndrome and inflammation. Molecular Genetics and Metabolism, 2014, 112, 317-338.	1.1	107
115	Genetic Associations with Obstructive Sleep Apnea Traits in Hispanic/Latino Americans. American Journal of Respiratory and Critical Care Medicine, 2016, 194, 886-897.	5.6	107
116	Associations of Mitochondrial and Nuclear Mitochondrial Variants and Genes with Seven Metabolic Traits. American Journal of Human Genetics, 2019, 104, 112-138.	6.2	106
117	Large-scale genome-wide analysis identifies genetic variants associated with cardiac structure and function. Journal of Clinical Investigation, 2017, 127, 1798-1812.	8.2	106
118	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
119	Comparison of Proteomic Assessment Methods in Multiple Cohort Studies. Proteomics, 2020, 20, e1900278.	2.2	103
120	A genomic approach to therapeutic target validation identifies a glucose-lowering GLP1R variant protective for coronary heart disease. Science Translational Medicine, 2016, 8, 341ra76.	12.4	100
121	A Genomeâ€Wide Association Study for Venous Thromboembolism: The Extended Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium. Genetic Epidemiology, 2013, 37, 512-521.	1.3	99
122	Natural Selection on Genes Related to Cardiovascular Health in High-Altitude Adapted Andeans. American Journal of Human Genetics, 2017, 101, 752-767.	6.2	99
123	Discovery and fine-mapping of adiposity loci using high density imputation of genome-wide association studies in individuals of African ancestry: African Ancestry Anthropometry Genetics Consortium. PLoS Genetics, 2017, 13, e1006719.	3.5	98
124	Evaluation of mitochondrial DNA copy number estimation techniques. PLoS ONE, 2020, 15, e0228166.	2.5	97
125	Measuring the genetic contribution of a single locus to a multilocus disease. Clinical Genetics, 1984, 26, 529-542.	2.0	96
126	Genetic loci associated with heart rate variability and their effects on cardiac disease risk. Nature Communications, 2017, 8, 15805.	12.8	95

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127	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. PLoS ONE, 2018, 13, e0198166.	2.5	94
128	Analysis commons, a team approach to discovery in a big-data environment for genetic epidemiology. Nature Genetics, 2017, 49, 1560-1563.	21.4	93
129	A Phenomics-Based Strategy Identifies Loci on APOC1, BRAP, and PLCG1 Associated with Metabolic Syndrome Phenotype Domains. PLoS Genetics, 2011, 7, e1002322.	3.5	92
130	HDAC9 is implicated in atherosclerotic aortic calcification and affects vascular smooth muscle cell phenotype. Nature Genetics, 2019, 51, 1580-1587.	21.4	92
131	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	21.4	89
132	Cerebral small vessel disease genomics and its implications across the lifespan. Nature Communications, 2020, 11, 6285.	12.8	89
133	A threeâ€allele model for heterogeneity of juvenile onset insulinâ€dependent diabetes. Annals of Human Genetics, 1980, 43, 399-412.	0.8	88
134	Single-trait and multi-trait genome-wide association analyses identify novel loci for blood pressure in African-ancestry populations. PLoS Genetics, 2017, 13, e1006728.	3.5	88
135	Clonal Hematopoiesis Is Associated With Higher Risk of Stroke. Stroke, 2022, 53, 788-797.	2.0	88
136	Genetic Risk Prediction of Atrial Fibrillation. Circulation, 2017, 135, 1311-1320.	1.6	87
137	Increased risk for type I (insulin-dependent) diabetes in relatives of patients with alopecia areata (AA). American Journal of Medical Genetics Part A, 1994, 51, 234-239.	2.4	86
138	Insulin Clearance and the Incidence of Type 2 Diabetes in Hispanics and African Americans. Diabetes Care, 2013, 36, 901-907.	8.6	85
139	Challenges in Elucidating the Genetics of Diabetic Retinopathy. JAMA Ophthalmology, 2014, 132, 96.	2.5	85
140	Multiethnic meta-analysis identifies ancestry-specific and cross-ancestry loci for pulmonary function. Nature Communications, 2018, 9, 2976.	12.8	85
141	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	3.4	85
142	Allele-specific expression changes dynamically during T cell activation in HLA and other autoimmune loci. Nature Genetics, 2020, 52, 247-253.	21.4	85
143	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	12.8	84
144	Genomewide metaâ€analysis identifies loci associated with <scp>IGF</scp> â€I and <scp>IGFBP</scp> â€3 levels with impact on ageâ€related traits. Aging Cell, 2016, 15, 811-824.	6.7	83

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145	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. American Journal of Human Genetics, 2016, 99, 40-55.	6.2	82
146	Deep coverage whole genome sequences and plasma lipoprotein(a) in individuals of European and African ancestries. Nature Communications, 2018, 9, 2606.	12.8	79
147	Analysis of predicted loss-of-function variants in UK Biobank identifies variants protective for disease. Nature Communications, 2018, 9, 1613.	12.8	78
148	Combined admixture mapping and association analysis identifies a novel blood pressure genetic locus on 5p13: contributions from the CARe consortium. Human Molecular Genetics, 2011, 20, 2285-2295.	2.9	77
149	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.	0.6	77
150	rs641738C>T near MBOAT7 is associated with liver fat, ALT and fibrosis in NAFLD: A meta-analysis. Journal of Hepatology, 2021, 74, 20-30.	3.7	77
151	New alcohol-related genes suggest shared genetic mechanisms with neuropsychiatric disorders. Nature Human Behaviour, 2019, 3, 950-961.	12.0	75
152	Pooled analysis of iron-related genes in Parkinson's disease: Association with transferrin. Neurobiology of Disease, 2014, 62, 172-178.	4.4	74
153	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.	6.2	73
154	Genome-wide Association Study of Platelet Count Identifies Ancestry-Specific Loci in Hispanic/Latino Americans. American Journal of Human Genetics, 2016, 98, 229-242.	6.2	71
155	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. Nature Communications, 2018, 9, 2904.	12.8	71
156	The triglyceride to high-density lipoprotein cholesterol (TG/HDL-C) ratio as a predictor of insulin resistance, Î²-cell function, and diabetes in Hispanics and African Americans. Journal of Diabetes and Its Complications, 2019, 33, 118-122.	2.3	71
157	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
158	A multiancestry genome-wide association study of unexplained chronic ALT elevation as a proxy for nonalcoholic fatty liver disease with histological and radiological validation. Nature Genetics, 2022, 54, 761-771.	21.4	68
159	Genome-wide Studies of Verbal Declarative Memory in Nondemented Older People: The Cohorts for Heart and Aging Research in Genomic Epidemiology Consortium. Biological Psychiatry, 2015, 77, 749-763.	1.3	67
160	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	12.8	64
161	Cross-ancestry genome-wide association analysis of corneal thickness strengthens link between complex and Mendelian eye diseases. Nature Communications, 2018, 9, 1864.	12.8	63
162	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

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163	An integrative cross-omics analysis of DNA methylation sites of glucose and insulin homeostasis. Nature Communications, 2019, 10, 2581.	12.8	62
164	Multiple Nonglycemic Genomic Loci Are Newly Associated With Blood Level of Glycated Hemoglobin in East Asians. Diabetes, 2014, 63, 2551-2562.	0.6	61
165	Genetic correlations and genome-wide associations of cortical structure in general population samples of 22,824 adults. Nature Communications, 2020, 11, 4796.	12.8	61
166	Trans-ethnic meta-analysis of white blood cell phenotypes. Human Molecular Genetics, 2014, 23, 6944-6960.	2.9	60
167	Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. American Journal of Human Genetics, 2016, 99, 8-21.	6.2	60
168	Genetics of Type 2 Diabetes in U.S. Hispanic/Latino Individuals: Results From the Hispanic Community Health Study/Study of Latinos (HCHS/SOL). Diabetes, 2017, 66, 1419-1425.	0.6	60
169	Common genetic variants and subclinical atherosclerosis: The Multi-Ethnic Study of Atherosclerosis (MESA). Atherosclerosis, 2016, 245, 230-236.	0.8	59
170	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	12.8	59
171	African Ancestryâ€“Specific Alleles and Kidney Disease Risk in Hispanics/Latinos. Journal of the American Society of Nephrology: JASN, 2017, 28, 915-922.	6.1	57
172	Trans-ethnic Meta-analysis and Functional Annotation Illuminates theÂGenetic Architecture of Fasting Glucose and Insulin. American Journal of Human Genetics, 2016, 99, 56-75.	6.2	55
173	Multiethnic Exome-Wide Association Study of Subclinical Atherosclerosis. Circulation: Cardiovascular Genetics, 2016, 9, 511-520.	5.1	54
174	Multiethnic Genome-Wide Association Study of Diabetic Retinopathy Using Liability Threshold Modeling of Duration of Diabetes and Glycemic Control. Diabetes, 2019, 68, 441-456.	0.6	54
175	Genome-wide association study of red blood cell traits in Hispanics/Latinos: The Hispanic Community Health Study/Study of Latinos. PLoS Genetics, 2017, 13, e1006760.	3.5	53
176	A genomeâ€wide association study suggests new evidence for an association of the <scp>NADPH</scp> Oxidase 4 (<scp>NOX</scp>4) gene with severe diabetic retinopathy in type 2 diabetes. Acta Ophthalmologica, 2018, 96, e811-e819.	1.1	52
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