Jerome I Rotter

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1048675/publications.pdf

Version: 2024-02-01

346 58,961 101 papers citations h-index

382 382 382 68040 all docs docs citations times ranked citing authors

219

g-index

#	Article	IF	CITATIONS
1	Whole genome sequence analysis of platelet traits in the NHLBI Trans-Omics for Precision Medicine (TOPMed) initiative. Human Molecular Genetics, 2022, 31, 347-361.	1.4	9
2	Clonal Hematopoiesis Is Associated With Higher Risk of Stroke. Stroke, 2022, 53, 788-797.	1.0	88
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	Gene-mapping study of extremes of cerebral small vessel disease reveals TRIM47 as a strong candidate. Brain, 2022, 145, 1992-2007.	3.7	6
5	Determinants of Incident Atherosclerotic Cardiovascular Disease Events Among Those With Absent Coronary Artery Calcium: Multi-Ethnic Study of Atherosclerosis. Circulation, 2022, 145, 259-267.	1.6	21
6	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. Cell Genomics, 2022, 2, 100084.	3.0	29
7	Upregulated heme biosynthesis increases obstructive sleep apnea severity: a pathway-based Mendelian randomization study. Scientific Reports, 2022, 12, 1472.	1.6	2
8	AtheroSpectrum Reveals Novel Macrophage Foam Cell Gene Signatures Associated With Atherosclerotic Cardiovascular Disease Risk. Circulation, 2022, 145, 206-218.	1.6	29
9	Circulating Metabolome and White Matter Hyperintensities in Women and Men. Circulation, 2022, 145, 1040-1052.	1.6	17
10	Multi-ethnic GWAS and fine-mapping of glycaemic traits identify novel loci in the PAGE Study. Diabetologia, 2022, 65, 477-489.	2.9	15
11	Protein prediction for trait mapping in diverse populations. PLoS ONE, 2022, 17, e0264341.	1.1	13
12	Rare Genetic Variants Associated With Myocardial Fibrosis: Multi-Ethnic Study of Atherosclerosis. Frontiers in Cardiovascular Medicine, 2022, 9, 804788.	1.1	6
13	Rare coding variants in RCN3 are associated with blood pressure. BMC Genomics, 2022, 23, 148.	1.2	2
14	Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data. Nature Genetics, 2022, 54, 263-273.	9.4	156
15	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.	1.1	3
16	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.	2.6	7
17	Ancestral diversity improves discovery and fine-mapping of genetic loci for anthropometric traits—The Hispanic/Latino Anthropometry Consortium. Human Genetics and Genomics Advances, 2022, 3, 100099.	1.0	3
18	Monogenic and Polygenic Contributions to QTc Prolongation in the Population. Circulation, 2022, 145, 1524-1533.	1.6	14

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19	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential. Science Advances, 2022, 8, eabl6579.	4.7	36
20	Estrogen-Related Receptor \hat{I}^3 Maintains Pancreatic Acinar Cell Function and Identity by Regulating Cellular Metabolism. Gastroenterology, 2022, 163, 239-256.	0.6	7
21	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
22	Cesarean Delivery and Insulin Sensitivity in the Older Adult: The Microbiome and Insulin Longitudinal Evaluation Study. Journal of the Endocrine Society, 2022, 6, .	0.1	4
23	The Value of Rare Genetic Variation in the Prediction of Common Obesity in European Ancestry Populations. Frontiers in Endocrinology, 2022, 13, 863893.	1.5	7
24	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.	9.4	68
25	0216 Environmental bright light exposure is associated with sleep timing: the Multi-Ethnic Study of Atherosclerosis. Sleep, 2022, 45, A98-A99.	0.6	0
26	Arsenic Exposure, Blood DNA Methylation, and Cardiovascular Disease. Circulation Research, 2022, 131,	2.0	20
27	A multi-ethnic polygenic risk score is associated with hypertension prevalence and progression throughout adulthood. Nature Communications, 2022, 13, .	5.8	27
28	Metabolomic Scores Mediate Associations between Dietary Patterns and Insulin Homeostasis in The Microbiome and Insulin Longitudinal Evaluation Study (MILES). Current Developments in Nutrition, 2022, 6, 958.	0.1	0
29	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. Communications Biology, 2022, 5, .	2.0	17
30	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.	1.4	2
31	Racial and Ethnic Differences in All-Cause and Cardiovascular Disease Mortality: The MESA Study. Circulation, 2022, 146, 229-239.	1.6	39
32	Insights From a Large-Scale Whole-Genome Sequencing Study of Systolic Blood Pressure, Diastolic Blood Pressure, and Hypertension. Hypertension, 2022, 79, 1656-1667.	1.3	12
33	Transethnic Transferability of a Genome-Wide Polygenic Score for Coronary Artery Disease. Circulation Genomic and Precision Medicine, 2021, 14, e003092.	1.6	25
34	rs641738C>T near MBOAT7 is associated with liver fat, ALT and fibrosis in NAFLD: A meta-analysis. Journal of Hepatology, 2021, 74, 20-30.	1.8	77
35	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	13.7	1,069
36	A multi-ethnic genome-wide association study implicates collagen matrix integrity and cell differentiation pathways in keratoconus. Communications Biology, 2021, 4, 266.	2.0	36

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37	Multi-ancestry genome-wide gene–sleep interactions identify novel loci for blood pressure. Molecular Psychiatry, 2021, 26, 6293-6304.	4.1	13
38	Multi-omics analysis identifies CpGs near G6PC2 mediating the effects of genetic variants on fasting glucose. Diabetologia, 2021, 64, 1613-1625.	2.9	9
39	Transcriptome prediction performance across machine learning models and diverse ancestries. Human Genetics and Genomics Advances, 2021, 2, 100019.	1.0	14
40	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. Nature Communications, 2021, 12, 2182.	5.8	17
41	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.	1.6	29
42	Whole-genome sequencing association analysis of quantitative red blood cell phenotypes: The NHLBI TOPMed program. American Journal of Human Genetics, 2021, 108, 874-893.	2.6	28
43	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	9.4	341
44	Determinants of penetrance and variable expressivity in monogenic metabolic conditions across 77,184 exomes. Nature Communications, 2021, 12, 3505.	5.8	49
45	Genome-wide association study of body fat distribution traits in Hispanics/Latinos from the HCHS/SOL. Human Molecular Genetics, 2021, 30, 2190-2204.	1.4	8
46	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.	1.3	6
47	Sequencing of 640,000 exomes identifies <i>GPR75</i> variants associated with protection from obesity. Science, 2021, 373, .	6.0	130
48	Transcriptome-Wide Association Study of Blood Cell Traits in African Ancestry and Hispanic/Latino Populations. Genes, 2021, 12, 1049.	1.0	11
49	Rare Coding Variants Associated With Electrocardiographic Intervals Identify Monogenic Arrhythmia Susceptibility Genes: A Multi-Ancestry Analysis. Circulation Genomic and Precision Medicine, 2021, 14, e003300.	1.6	7
50	Epigenome-wide association study of mitochondrial genome copy number. Human Molecular Genetics, 2021, 31, 309-319.	1.4	6
51	Associations between ambient air pollutants and clonal hematopoiesis of indeterminate potential (CHIP). ISEE Conference Abstracts, 2021, 2021, .	0.0	0
52	Population sequencing data reveal a compendium of mutational processes in the human germ line. Science, 2021, 373, 1030-1035.	6.0	43
53	Whole-genome association analyses of sleep-disordered breathing phenotypes in the NHLBI TOPMed program. Genome Medicine, 2021, 13, 136.	3.6	16
54	The genomics of heart failure: design and rationale of the HERMES consortium. ESC Heart Failure, 2021, 8, 5531-5541.	1.4	11

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55	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.	2.6	14
56	Investigation of the interplay between circulating lipids and IGF-I and relevance to breast cancer risk: an observational and Mendelian randomization study. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, cebp.0315.2021.	1.1	9
57	Association of mitochondrial DNA copy number with cardiometabolic diseases. Cell Genomics, 2021, 1, 100006.	3.0	26
58	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.	9.4	69
59	Identification of Functional Genetic Determinants of Cardiac Troponin T and I in a Multiethnic Population and Causal Associations With Atrial Fibrillation. Circulation Genomic and Precision Medicine, 2021, 14, CIRCGEN121003460.	1.6	5
60	Whole-Genome Sequencing Association Analyses of Stroke and Its Subtypes in Ancestrally Diverse Populations From Trans-Omics for Precision Medicine Project. Stroke, 2021, , STROKEAHA120031792.	1.0	16
61	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	13.7	353
62	Pangenomics enables genotyping of known structural variants in 5202 diverse genomes. Science, 2021, 374, abg8871.	6.0	132
63	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. Nature Communications, 2020, 11, 163.	5.8	466
64	Association of Genetic Variation With Keratoconus. JAMA Ophthalmology, 2020, 138, 174.	1.4	34
65	Classification of Type 2 Diabetes Genetic Variants and a Novel Genetic Risk Score Association With Insulin Clearance. Journal of Clinical Endocrinology and Metabolism, 2020, 105, 1251-1260.	1.8	15
66	Whole genome sequence analysis of pulmonary function and COPD in 19,996 multi-ethnic participants. Nature Communications, 2020, 11, 5182.	5.8	32
67	Genetic correlations and genome-wide associations of cortical structure in general population samples of 22,824 adults. Nature Communications, 2020, 11, 4796.	5.8	61
68	The Polygenic and Monogenic Basis of Blood Traits and Diseases. Cell, 2020, 182, 1214-1231.e11.	13.5	388
69	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature, 2020, 586, 763-768.	13.7	376
70	Rationale, design and baseline characteristics of the Microbiome and Insulin Longitudinal Evaluation Study (<scp>MILES</scp>). Diabetes, Obesity and Metabolism, 2020, 22, 1976-1984.	2.2	9
71	Association of <i>APOL1</i> Genotypes With Measures of Microvascular and Endothelial Function, and Blood Pressure in MESA. Journal of the American Heart Association, 2020, 9, e017039.	1.6	7
72	Mitochondrial DNA copy number and incident atrial fibrillation. BMC Medicine, 2020, 18, 246.	2.3	21

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73	Genetic Studies of Leptin Concentrations Implicate Leptin in the Regulation of Early Adiposity. Diabetes, 2020, 69, 2806-2818.	0.3	26
74	Genetic Determinants of Electrocardiographic P-Wave Duration and Relation to Atrial Fibrillation. Circulation Genomic and Precision Medicine, 2020, 13, 387-395.	1.6	16
75	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
76	Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. Nature Communications, 2020, 11, 6417.	5.8	39
77	Cerebral small vessel disease genomics and its implications across the lifespan. Nature Communications, 2020, 11, 6285.	5.8	89
78	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. Molecular Psychiatry, 2020, 26, 2111-2125.	4.1	17
79	Identification of type 2 diabetes loci in 433,540 East Asian individuals. Nature, 2020, 582, 240-245.	13.7	282
80	Analysis of cardiac magnetic resonance imaging in $36,000$ individuals yields genetic insights into dilated cardiomyopathy. Nature Communications, $2020,11,2254.$	5.8	140
81	Comparison of Proteomic Assessment Methods in Multiple Cohort Studies. Proteomics, 2020, 20, e1900278.	1.3	103
82	An Outbreak of Polygenic Scores for Coronary Artery Disease. Journal of the American College of Cardiology, 2020, 75, 2781-2784.	1.2	11
83	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, $11,2542$.	5.8	59
84	A structural variation reference for medical and population genetics. Nature, 2020, 581, 444-451.	13.7	614
85	Role of Rare and Low-Frequency Variants in Gene-Alcohol Interactions on Plasma Lipid Levels. Circulation Genomic and Precision Medicine, 2020, 13, e002772.	1.6	11
86	Multi-Ethnic Genome-Wide Association Study of Decomposed Cardioelectric Phenotypes Illustrates Strategies to Identify and Characterize Evidence of Shared Genetic Effects for Complex Traits. Circulation Genomic and Precision Medicine, 2020, 13, e002680.	1.6	4
87	Allele-specific expression changes dynamically during T cell activation in HLA and other autoimmune loci. Nature Genetics, 2020, 52, 247-253.	9.4	85
88	Allelic Heterogeneity at the CRP Locus Identified by Whole-Genome Sequencing in Multi-ancestry Cohorts. American Journal of Human Genetics, 2020, 106, 112-120.	2.6	9
89	Evaluation of mitochondrial DNA copy number estimation techniques. PLoS ONE, 2020, 15, e0228166.	1.1	97
90	Physical Activity Associations with Bone Mineral Density and Modification by Metabolic Traits. Journal of the Endocrine Society, 2020, 4, bvaa092.	0.1	2

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91	Evaluation of mitochondrial DNA copy number estimation techniques. , 2020, 15, e0228166.		O
92	Evaluation of mitochondrial DNA copy number estimation techniques. , 2020, 15, e0228166.		0
93	Evaluation of mitochondrial DNA copy number estimation techniques. , 2020, 15, e0228166.		0
94	Evaluation of mitochondrial DNA copy number estimation techniques., 2020, 15, e0228166.		0
95	Genome-wide meta-analysis of SNP-by9-ACEI/ARB and SNP-by-thiazide diuretic and effect on serum potassium in cohorts of European and African ancestry. Pharmacogenomics Journal, 2019, 19, 97-108.	0.9	3
96	A meta-analysis of genome-wide association studies identifies multiple longevity genes. Nature Communications, 2019, 10, 3669.	5.8	214
97	A Genome-Wide Association Study Identifies Blood Disorder–Related Variants Influencing Hemoglobin A1c With Implications for Glycemic Status in U.S. Hispanics/Latinos. Diabetes Care, 2019, 42, 1784-1791.	4.3	9
98	New alcohol-related genes suggest shared genetic mechanisms with neuropsychiatric disorders. Nature Human Behaviour, 2019, 3, 950-961.	6.2	75
99	GWAS of QRS duration identifies new loci specific to Hispanic/Latino populations. PLoS ONE, 2019, 14, e0217796.	1.1	8
100	Effects of Calcium, Magnesium, and Potassium Concentrations on Ventricular Repolarization in Unselected Individuals. Journal of the American College of Cardiology, 2019, 73, 3118-3131.	1.2	27
101	Disentangling the genetics of lean mass. American Journal of Clinical Nutrition, 2019, 109, 276-287.	2.2	38
102	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	5.8	84
103	Association of Genetic Variants With Primary Open-Angle Glaucoma Among Individuals With African Ancestry. JAMA - Journal of the American Medical Association, 2019, 322, 1682.	3.8	50
104	Genome-Wide Association Studies. JAMA - Journal of the American Medical Association, 2019, 322, 1705.	3.8	17
105	Multi-ancestry sleep-by-SNP interaction analysis in 126,926 individuals reveals lipid loci stratified by sleep duration. Nature Communications, 2019, 10, 5121.	5.8	62
106	HDAC9 is implicated in atherosclerotic aortic calcification and affects vascular smooth muscle cell phenotype. Nature Genetics, 2019, 51, 1580-1587.	9.4	92
107	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. Nature Communications, 2019, 10, 4130.	5.8	133
108	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

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109	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.	2.6	44
110	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	1.6	85
111	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
112	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	5.8	64
113	Home use of a compact, 12â€'lead ECG recording system for newborns. Journal of Electrocardiology, 2019, 53, 89-94.	0.4	7
114	Genomeâ€Wide Association Study Identifies Loci for Liver Enzyme Concentrations in Mexican Americans: The GUARDIAN Consortium. Obesity, 2019, 27, 1331-1337.	1.5	20
115	0291 Sleep Disordered Breathing Associated with Epigenetic Age Acceleration: Evidence from the Multi-Ethnic Study of Atherosclerosis. Sleep, 2019, 42, A118-A119.	0.6	0
116	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	9.4	549
117	An integrative cross-omics analysis of DNA methylation sites of glucose and insulin homeostasis. Nature Communications, 2019, 10, 2581.	5.8	62
118	Exome sequencing of 20,791Âcases of type 2 diabetes and 24,440Âcontrols. Nature, 2019, 570, 71-76.	13.7	248
119	Associations of variants In the hexokinase 1 and interleukin 18 receptor regions with oxyhemoglobin saturation during sleep. PLoS Genetics, 2019, 15, e1007739.	1.5	28
120	Multi-ancestry genome-wide gene–smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. Nature Genetics, 2019, 51, 636-648.	9.4	112
121	Adiposityâ€Independent Effects of Aging on Insulin Sensitivity and Clearance in Mice and Humans. Obesity, 2019, 27, 434-443.	1.5	34
122	Genetic meta-analysis of diagnosed Alzheimer's disease identifies new risk loci and implicates Aβ, tau, immunity and lipid processing. Nature Genetics, 2019, 51, 414-430.	9.4	1,962
123	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	9.4	89
124	Differences in First-Trimester Maternal Metabolomic Profiles in Pregnancies Conceived From Fertility Treatments. Journal of Clinical Endocrinology and Metabolism, 2019, 104, 1005-1019.	1.8	15
125	PPIP5K2 and PCSK1 are Candidate Genetic Contributors to Familial Keratoconus. Scientific Reports, 2019, 9, 19406.	1.6	34
126	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

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127	Association between sleep disordered breathing and epigenetic age acceleration: Evidence from the Multi-Ethnic Study of Atherosclerosis. EBioMedicine, 2019, 50, 387-394.	2.7	12
128	Genetic architecture of subcortical brain structures in 38,851 individuals. Nature Genetics, 2019, 51, 1624-1636.	9.4	192
129	Omega-3 Fatty Acids and Genome-Wide Interaction Analyses Reveal <i>DPP10–</i> Pulmonary Function Association. American Journal of Respiratory and Critical Care Medicine, 2019, 199, 631-642.	2.5	14
130	Associations of Mitochondrial and Nuclear Mitochondrial Variants and Genes with Seven Metabolic Traits. American Journal of Human Genetics, 2019, 104, 112-138.	2.6	106
131	Genetic Architecture of Primary Open-Angle Glaucoma in Individuals of African Descent. Ophthalmology, 2019, 126, 38-48.	2.5	40
132	Genetic and lifestyle risk factors for MRI-defined brain infarcts in a population-based setting. Neurology, 2019, 92, .	1.5	30
133	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
134	The triglyceride to high-density lipoprotein cholesterol (TG/HDL-C) ratio as a predictor of insulin resistance, \hat{I}^2 -cell function, and diabetes in Hispanics and African Americans. Journal of Diabetes and Its Complications, 2019, 33, 118-122.	1.2	71
135	Multiethnic Genome-Wide Association Study of Diabetic Retinopathy Using Liability Threshold Modeling of Duration of Diabetes and Glycemic Control. Diabetes, 2019, 68, 441-456.	0.3	54
136	The African Descent and Glaucoma Evaluation Study (ADAGES) III. Ophthalmology, 2019, 126, 156-170.	2.5	13
137	Association of severity of primary open-angle glaucoma with serum vitamin D levels in patients of African descent. Molecular Vision, 2019, 25, 438-445.	1.1	9
138	Genetic Variants Associated With Obesity and Insulin Resistance in Hispanic Boys With Nonalcoholic Fatty Liver Disease. Journal of Pediatric Gastroenterology and Nutrition, 2018, 66, 789-796.	0.9	11
139	Genomeâ€wide interaction with the insulin secretion locus <i>MTNR1B</i> reveals <i>CMIP</i> as a novel type 2 diabetes susceptibility gene in African Americans. Genetic Epidemiology, 2018, 42, 559-570.	0.6	17
140	Analysis of predicted loss-of-function variants in UK Biobank identifies variants protective for disease. Nature Communications, 2018, 9, 1613.	5.8	78
141	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
142	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
143	Association between siteâ€specific bone mineral density and glucose homeostasis and anthropometric traits in healthy men and women. Clinical Endocrinology, 2018, 88, 848-855.	1.2	4
144	Prognostic Significance of Large Airway Dimensions on Computed Tomography in the General Population. The Multi-Ethnic Study of Atherosclerosis (MESA) Lung Study. Annals of the American Thoracic Society, 2018, 15, 718-727.	1.5	24

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145	Genome-wide association study of depressive symptoms in the Hispanic Community Health Study/Study of Latinos. Journal of Psychiatric Research, 2018, 99, 167-176.	1.5	15
146	P2â€003: ACETYLCHOLINESTERASE INHIBITOR THERAPY IN MILD COGNITIVE IMPAIRMENT: YES OR NO?. Alzheimer's and Dementia, 2018, 14, P665.	0.4	0
147	Community Partnership in Precision Medicine: Themes from a Community Engagement Conference. Ethnicity and Disease, 2018, 28, 503-510.	1.0	6
148	GWAS and colocalization analyses implicate carotid intima-media thickness and carotid plaque loci in cardiovascular outcomes. Nature Communications, 2018, 9, 5141.	5.8	119
149	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.	9.4	1,331
150	Genome-wide meta-analysis of 158,000 individuals of European ancestry identifies three loci associated with chronic back pain. PLoS Genetics, 2018, 14, e1007601.	1.5	112
151	ExomeChip-Wide Analysis of 95 626 Individuals Identifies 10 Novel Loci Associated With QT and JT Intervals. Circulation Genomic and Precision Medicine, 2018, 11, e001758.	1.6	27
152	Genome-wide association study of primary open-angle glaucoma in continental and admixed African populations. Human Genetics, 2018, 137, 847-862.	1.8	40
153	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.	2.6	326
154	Genetic Variants Associated with Circulating Fibroblast Growth Factor 23. Journal of the American Society of Nephrology: JASN, 2018, 29, 2583-2592.	3.0	35
155	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	9.4	924
156	A genomeâ€wide association study suggests new evidence for an association of the <scp>NADPH</scp> Oxidase 4 (<i><scp>NOX</scp>4</i>) gene with severe diabetic retinopathy in type 2 diabetes. Acta Ophthalmologica, 2018, 96, e811-e819.	0.6	52
157	Common and Rare Coding Genetic Variation Underlying the Electrocardiographic PR Interval. Circulation Genomic and Precision Medicine, 2018, 11, e002037.	1.6	19
158	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. Nature Communications, 2018, 9, 2098.	5.8	484
159	Common Coding Variants in <i>SCN10A</i> Are Associated With the Nav1.8 Late Current and Cardiac Conduction. Circulation Genomic and Precision Medicine, 2018, 11, e001663.	1.6	26
160	Cross-ancestry genome-wide association analysis of corneal thickness strengthens link between complex and Mendelian eye diseases. Nature Communications, 2018, 9, 1864.	5.8	63
161	Outdoor air pollution and mosaic loss of chromosome Y in older men from the Cardiovascular Health Study. Environment International, 2018, 116, 239-247.	4.8	32
162	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. Nature Communications, 2018, 9, 2904.	5.8	71

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163	Exome Chip Analysis Identifies Low-Frequency and Rare Variants in <i>MRPL38</i> for White Matter Hyperintensities on Brain Magnetic Resonance Imaging. Stroke, 2018, 49, 1812-1819.	1.0	17
164	Deep coverage whole genome sequences and plasma lipoprotein(a) in individuals of European and African ancestries. Nature Communications, 2018, 9, 2606.	5.8	79
165	Genetic architecture of gene expression traits across diverse populations. PLoS Genetics, 2018, 14, e1007586.	1.5	117
166	Deep-coverage whole genome sequences and blood lipids among 16,324 individuals. Nature Communications, 2018, 9, 3391.	5.8	140
167	Multiethnic meta-analysis identifies ancestry-specific and cross-ancestry loci for pulmonary function. Nature Communications, 2018, 9, 2976.	5.8	85
168	Multi-ethnic genome-wide association study for atrial fibrillation. Nature Genetics, 2018, 50, 1225-1233.	9.4	552
169	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. PLoS ONE, 2018, 13, e0198166.	1.1	94
170	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
171	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
172	Genomeâ€wide association study of generalized anxiety symptoms in the Hispanic Community Health Study/Study of Latinos. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2017, 174, 132-143.	1.1	37
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