

# Jerome I Rotter

## List of Publications by Year in descending order

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Version: 2024-02-01

346  
papers

58,961  
citations

1992

101  
h-index

1461

220  
g-index

382  
all docs

382  
docs citations

382  
times ranked

62302  
citing authors

| #  | ARTICLE  | IF   | CITATIONS |
|----|--|------|-----------|
| 1  | Host-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 Alzheimer's disease identifies new risk loci and implicates A $\beta$ , 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. <i>Nature Genetics</i> , 2010, 42, 45-52.                 | 21.4 | 549       |
| 20 | A catalog of genetic loci associated with kidney function from analyses of a million individuals. <i>Nature Genetics</i> , 2019, 51, 957-972.                         | 21.4 | 549       |
| 21 | Association between alcohol and cardiovascular disease: Mendelian randomisation analysis based on individual participant data. <i>BMJ</i> , 2014, 349, g4164-g4164.   | 6.0  | 528       |
| 22 | Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium. <i>Circulation: Cardiovascular Genetics</i> , 2009, 2, 73-80.                       | 5.1  | 519       |
| 23 | Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. <i>Nature Communications</i> , 2018, 9, 2098.            | 12.8 | 484       |
| 24 | Exome-wide association study of plasma lipids in >300,000 individuals. <i>Nature Genetics</i> , 2017, 49, 1758-1766.  | 21.4 | 470       |
| 25 | Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. <i>Nature Communications</i> , 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. <i>Circulation</i> , 2011, 123, 731-738. | 1.6  | 461       |
| 27 | Genomewide Association Studies of Stroke. <i>New England Journal of Medicine</i> , 2009, 360, 1718-1728.  | 27.0 | 420       |
| 28 | Genome-wide association study of PR interval. <i>Nature Genetics</i> , 2010, 42, 153-159.   | 21.4 | 400       |
| 29 | The Polygenic and Monogenic Basis of Blood Traits and Diseases. <i>Cell</i> , 2020, 182, 1214-1231.e11.   | 28.9 | 388       |
| 30 | Inactivating Mutations in <i>NPC1L1</i> and Protection from Coronary Heart Disease. <i>New England Journal of Medicine</i> , 2014, 371, 2072-2082.                    | 27.0 | 386       |
| 31 | Association Between Telomere Length and Risk of Cancer and Non-Neoplastic Diseases. <i>JAMA Oncology</i> , 2017, 3, 636.  | 7.1  | 376       |
| 32 | Inherited causes of clonal haematopoiesis in 97,691 whole genomes. <i>Nature</i> , 2020, 586, 763-768.  | 27.8 | 376       |
| 33 | Genome-wide association and large-scale follow up identifies 16 new loci influencing lung function. <i>Nature Genetics</i> , 2011, 43, 1082-1090.                     | 21.4 | 367       |
| 34 | Long-Range LD Can Confound Genome Scans in Admixed Populations. <i>American Journal of Human Genetics</i> , 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. <i>Nature Genetics</i> , 2016, 48, 1171-1184.        | 21.4 | 362       |
| 36 | Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. <i>Nature Genetics</i> , 2018, 50, 559-571.          | 21.4 | 356       |

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|----|--|------|-----------|
| 37 | The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 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. <i>PLoS Medicine</i> , 2017, 14, e1002383.  | 8.4  | 341       |
| 39 | The trans-ancestral genomic architecture of glycemic traits. <i>Nature Genetics</i> , 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. <i>PLoS Genetics</i> , 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. <i>American Journal of Human Genetics</i> , 2018, 103, 691-706. | 6.2  | 326       |
| 42 | Multiple loci influence erythrocyte phenotypes in the CHARGE Consortium. <i>Nature Genetics</i> , 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. <i>Nature Communications</i> , 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. <i>PLoS Genetics</i> , 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. <i>American Journal of Human Genetics</i> , 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. <i>Nature Genetics</i> , 2018, 50, 26-41.  | 21.4 | 286       |
| 47 | Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. <i>Nature Genetics</i> , 2013, 45, 621-631.   | 21.4 | 282       |
| 48 | Identification of type 2 diabetes loci in 433,540 East Asian individuals. <i>Nature</i> , 2020, 582, 240-245.  | 27.8 | 282       |
| 49 | Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. <i>Nature Genetics</i> , 2014, 46, 826-836.  | 21.4 | 281       |
| 50 | Genome-Wide Association Study Identifies Variants Associated With Histologic Features of Nonalcoholic Fatty Liver Disease. <i>Gastroenterology</i> , 2010, 139, 1567-1576.e6.  | 1.3  | 270       |
| 51 | Genome-Wide Association Study for Coronary Artery Calcification With Follow-Up in Myocardial Infarction. <i>Circulation</i> , 2011, 124, 2855-2864.  | 1.6  | 269       |
| 52 | Genome-wide association analyses identify multiple loci associated with central corneal thickness and keratoconus. <i>Nature Genetics</i> , 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. <i>American Journal of Human Genetics</i> , 2016, 98, 165-184.      | 6.2  | 266       |
| 54 | GWAS of Longevity in CHARGE Consortium Confirms APOE and FOXO3 Candidacy. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2015, 70, 110-118.                                      | 3.6  | 250       |

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|----|---|------|-----------|
| 55 | Novel genetic loci associated with hippocampal volume. <i>Nature Communications</i> , 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. <i>Nature Genetics</i> , 2022, 54, 560-572.  | 21.4 | 250       |
| 57 | Exome sequencing of 20,791 cases of type 2 diabetes and 24,440 controls. <i>Nature</i> , 2019, 570, 71-76.  | 27.8 | 248       |
| 58 | Large-Scale Gene-Centric Meta-analysis across 32 Studies Identifies Multiple Lipid Loci. <i>American Journal of Human Genetics</i> , 2012, 91, 823-838.   | 6.2  | 227       |
| 59 | Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. <i>Nature Genetics</i> , 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. <i>Nature Genetics</i> , 2017, 49, 1450-1457.  | 21.4 | 218       |
| 61 | A meta-analysis of genome-wide association studies identifies multiple longevity genes. <i>Nature Communications</i> , 2019, 10, 3669.  | 12.8 | 214       |
| 62 | Novel genetic loci underlying human intracranial volume identified through genome-wide association. <i>Nature Neuroscience</i> , 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. <i>Circulation</i> , 2019, 139, 1593-1602.   | 1.6  | 213       |
| 64 | Genome-wide meta-analysis of observational studies shows common genetic variants associated with macronutrient intake. <i>American Journal of Clinical Nutrition</i> , 2013, 97, 1395-1402.   | 4.7  | 210       |
| 65 | CUBN Is a Gene Locus for Albuminuria. <i>Journal of the American Society of Nephrology: JASN</i> , 2011, 22, 555-570.   | 6.1  | 208       |
| 66 | <i>KLB</i> is associated with alcohol drinking, and its gene product Klotho is necessary for FGF21 regulation of alcohol preference. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 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. <i>PLoS Genetics</i> , 2019, 15, e1008500. | 3.5  | 203       |
| 68 | Genome-wide association studies of cerebral white matter lesion burden. <i>Annals of Neurology</i> , 2011, 69, 928-939.   | 5.3  | 201       |
| 69 | Association of Mitochondrial DNA Copy Number With Cardiovascular Disease. <i>JAMA Cardiology</i> , 2017, 2, 1247.   | 6.1  | 194       |
| 70 | Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. <i>American Journal of Human Genetics</i> , 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. <i>Human Molecular Genetics</i> , 2014, 23, 5492-5504.  | 2.9  | 192       |
| 72 | Genetic architecture of subcortical brain structures in 38,851 individuals. <i>Nature Genetics</i> , 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. <i>PLoS Genetics</i> , 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. <i>American Journal of Human Genetics</i> , 2013, 93, 545-554. | 6.2  | 189       |
| 75 | Duodenal-Ulcer Disease Associated with Elevated Serum Pepsinogen I. <i>New England Journal of Medicine</i> , 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. <i>American Journal of Cardiology</i> , 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. <i>Nature Genetics</i> , 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. <i>Circulation: Cardiovascular Genetics</i> , 2010, 3, 256-266.   | 5.1  | 176       |
| 79 | Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. <i>Nature Communications</i> , 2015, 6, 5897.  | 12.8 | 173       |
| 80 | Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , 2015, 523, 459-462.   | 27.8 | 173       |
| 81 | Convergent genetic and expression data implicate immunity in Alzheimer's disease. <i>Alzheimer's and Dementia</i> , 2015, 11, 658-671.   | 0.8  | 173       |
| 82 | Genome-Wide Association Studies Identify <i>CHRNA5</i> and <i>HTR4</i> in the Development of Airflow Obstruction. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2012, 186, 622-632.                        | 5.6  | 164       |
| 83 | Multiethnic Genome-Wide Association Study of Cerebral White Matter Hyperintensities on MRI. <i>Circulation: Cardiovascular Genetics</i> , 2015, 8, 398-409.  | 5.1  | 162       |
| 84 | Assessing the contribution of rare variants to complex trait heritability from whole-genome sequence data. <i>Nature Genetics</i> , 2022, 54, 263-273.   | 21.4 | 156       |
| 85 | Identification of Novel Genetic Loci Associated with Thyroid Peroxidase Antibodies and Clinical Thyroid Disease. <i>PLoS Genetics</i> , 2014, 10, e1004123.  | 3.5  | 150       |
| 86 | Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. <i>Nature Communications</i> , 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. <i>Nature Genetics</i> , 2020, 52, 969-983.                     | 21.4 | 146       |
| 88 | Deep-coverage whole genome sequences and blood lipids among 16,324 individuals. <i>Nature Communications</i> , 2018, 9, 3391.  | 12.8 | 140       |
| 89 | Analysis of cardiac magnetic resonance imaging in 36,000 individuals yields genetic insights into dilated cardiomyopathy. <i>Nature Communications</i> , 2020, 11, 2254.   | 12.8 | 140       |
| 90 | Candidate Gene Association Resource (CARE). <i>Circulation: Cardiovascular Genetics</i> , 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. <i>Circulation</i> , 2019, 140, 1318-1330.  | 1.6  | 138       |
| 92  | Genetic predictors of medically refractory ulcerative colitis. <i>Inflammatory Bowel Diseases</i> , 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. <i>Human Molecular Genetics</i> , 2017, 26, 1770-1784.  | 2.9  | 135       |
| 94  | Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. <i>Nature Communications</i> , 2019, 10, 4130.   | 12.8 | 133       |
| 95  | Pangenomics enables genotyping of known structural variants in 5202 diverse genomes. <i>Science</i> , 2021, 374, abg8871.   | 12.6 | 132       |
| 96  | Genome-wide association analysis identifies six new loci associated with forced vital capacity. <i>Nature Genetics</i> , 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. <i>PLoS Genetics</i> , 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. <i>Lancet Neurology</i> , The, 2016, 15, 695-707.   | 10.2 | 130       |
| 99  | Sequencing of 640,000 exomes identifies <i>GPR75</i> variants associated with protection from obesity. <i>Science</i> , 2021, 373, .  | 12.6 | 130       |
| 100 | Familial Mediterranean fever in Armenians: Autosomal recessive inheritance with high gene frequency. <i>American Journal of Medical Genetics Part A</i> , 1989, 34, 168-172.  | 2.4  | 125       |
| 101 | GWAS and colocalization analyses implicate carotid intima-media thickness and carotid plaque loci in cardiovascular outcomes. <i>Nature Communications</i> , 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). <i>PLoS Genetics</i> , 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. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2010, 65A, 478-487. | 3.6  | 117       |
| 104 | Genetic architecture of gene expression traits across diverse populations. <i>PLoS Genetics</i> , 2018, 14, e1007586.   | 3.5  | 117       |
| 105 | Genome Scan for Blood Pressure in Dutch Dyslipidemic Families Reveals Linkage to a Locus on Chromosome 4p. <i>Hypertension</i> , 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 Myocardial Mass. <i>Journal of the American College of Cardiology</i> , 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. <i>American Journal of Human Genetics</i> , 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. <i>PLoS Genetics</i> , 2018, 14, e1007601.  | 3.5  | 112       |
| 110 | Multi-ancestry genome-wide gene-smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. <i>Nature Genetics</i> , 2019, 51, 636-648.   | 21.4 | 112       |
| 111 | Genome-Wide Association of Body Fat Distribution in African Ancestry Populations Suggests New Loci. <i>PLoS Genetics</i> , 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. <i>American Journal of Human Genetics</i> , 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. <i>Human Molecular Genetics</i> , 2012, 21, 421-429.                    | 2.9  | 108       |
| 114 | Pleiotropic genes for metabolic syndrome and inflammation. <i>Molecular Genetics and Metabolism</i> , 2014, 112, 317-338.  | 1.1  | 107       |
| 115 | Genetic Associations with Obstructive Sleep Apnea Traits in Hispanic/Latino Americans. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2016, 194, 886-897.   | 5.6  | 107       |
| 116 | Associations of Mitochondrial and Nuclear Mitochondrial Variants and Genes with Seven Metabolic Traits. <i>American Journal of Human Genetics</i> , 2019, 104, 112-138.  | 6.2  | 106       |
| 117 | Large-scale genome-wide analysis identifies genetic variants associated with cardiac structure and function. <i>Journal of Clinical Investigation</i> , 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. <i>American Journal of Human Genetics</i> , 2019, 104, 260-274.   | 6.2  | 103       |
| 119 | Comparison of Proteomic Assessment Methods in Multiple Cohort Studies. <i>Proteomics</i> , 2020, 20, e1900278.   | 2.2  | 103       |
| 120 | A genomic approach to therapeutic target validation identifies a glucose-lowering <i>GLP1R</i> variant protective for coronary heart disease. <i>Science Translational Medicine</i> , 2016, 8, 341ra76.  | 12.4 | 100       |
| 121 | A Genome-Wide Association Study for Venous Thromboembolism: The Extended Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium. <i>Genetic Epidemiology</i> , 2013, 37, 512-521.                                      | 1.3  | 99        |
| 122 | Natural Selection on Genes Related to Cardiovascular Health in High-Altitude Adapted Andeans. <i>American Journal of Human Genetics</i> , 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. <i>PLoS Genetics</i> , 2017, 13, e1006719. | 3.5  | 98        |
| 124 | Evaluation of mitochondrial DNA copy number estimation techniques. <i>PLoS ONE</i> , 2020, 15, e0228166.   | 2.5  | 97        |
| 125 | Measuring the genetic contribution of a single locus to a multilocus disease. <i>Clinical Genetics</i> , 1984, 26, 529-542.  | 2.0  | 96        |
| 126 | Genetic loci associated with heart rate variability and their effects on cardiac disease risk. <i>Nature Communications</i> , 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. <i>PLoS ONE</i> , 2018, 13, e0198166.  | 2.5  | 94        |
| 128 | Analysis commons, a team approach to discovery in a big-data environment for genetic epidemiology. <i>Nature Genetics</i> , 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. <i>PLoS Genetics</i> , 2011, 7, e1002322.               | 3.5  | 92        |
| 130 | HDAC9 is implicated in atherosclerotic aortic calcification and affects vascular smooth muscle cell phenotype. <i>Nature Genetics</i> , 2019, 51, 1580-1587.                       | 21.4 | 92        |
| 131 | Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. <i>Nature Genetics</i> , 2019, 51, 452-469.                      | 21.4 | 89        |
| 132 | Cerebral small vessel disease genomics and its implications across the lifespan. <i>Nature Communications</i> , 2020, 11, 6285.  | 12.8 | 89        |
| 133 | A three-allele model for heterogeneity of juvenile onset insulin-dependent diabetes. <i>Annals of Human Genetics</i> , 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. <i>PLoS Genetics</i> , 2017, 13, e1006728.   | 3.5  | 88        |
| 135 | Clonal Hematopoiesis Is Associated With Higher Risk of Stroke. <i>Stroke</i> , 2022, 53, 788-797.  | 2.0  | 88        |
| 136 | Genetic Risk Prediction of Atrial Fibrillation. <i>Circulation</i> , 2017, 135, 1311-1320.   | 1.6  | 87        |
| 137 | Increased risk for type I (insulin-dependent) diabetes in relatives of patients with alopecia areata (AA). <i>American Journal of Medical Genetics Part A</i> , 1994, 51, 234-239. | 2.4  | 86        |
| 138 | Insulin Clearance and the Incidence of Type 2 Diabetes in Hispanics and African Americans. <i>Diabetes Care</i> , 2013, 36, 901-907.   | 8.6  | 85        |
| 139 | Challenges in Elucidating the Genetics of Diabetic Retinopathy. <i>JAMA Ophthalmology</i> , 2014, 132, 96.   | 2.5  | 85        |
| 140 | Multiethnic meta-analysis identifies ancestry-specific and cross-ancestry loci for pulmonary function. <i>Nature Communications</i> , 2018, 9, 2976.                               | 12.8 | 85        |
| 141 | Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. <i>American Journal of Epidemiology</i> , 2019, 188, 1033-1054.               | 3.4  | 85        |
| 142 | Allele-specific expression changes dynamically during T cell activation in HLA and other autoimmune loci. <i>Nature Genetics</i> , 2020, 52, 247-253.                              | 21.4 | 85        |
| 143 | Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019, 10, 4957.  | 12.8 | 84        |
| 144 | Genomewide meta-analysis identifies loci associated with IGF and IGFBP levels with impact on age-related traits. <i>Aging Cell</i> , 2016, 15, 811-824.                            | 6.7  | 83        |

| #   | ARTICLE  | IF   | CITATIONS |
|-----|--|------|-----------|
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