Aaron Isaacs

List of Publications by Citations

71 papers	14,055 citations	36 h-index	80 g-index
80 ext. papers	17,108 ext. citations	15 avg, IF	4.68 L-index

#	Paper	IF	Citations
71	Biological, clinical and population relevance of 95 loci for blood lipids. *Nature*, **2010**, 466, 707-13	50.4	2742
70	Discovery and refinement of loci associated with lipid levels. *Nature Genetics*, **2013**, 45, 1274-1283	36.3	1904
69	GenABEL: an R library for genome-wide association analysis. *Bioinformatics*, **2007**, 23, 1294-6	7.2	1397
68	Defining the role of common variation in the genomic and biological architecture of adult human height. *Nature Genetics*, **2014**, 46, 1173-86	36.3	1339
67	New genetic loci link adipose and insulin biology to body fat distribution. *Nature*, **2015**, 518, 187-196	50.4	920
66	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. *Nature Genetics*, **2012**, 44, 991-1005	36.3	621
65	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. *Nature*, **2017**, 541, 81-86	50.4	511
64	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. *Nature Communications*, **2016**, 7, 10023	17.4	295
63	Meta-analysis of telomere length in 19,713 subjects reveals high heritability, stronger maternal inheritance and a paternal age effect. *European Journal of Human Genetics*, **2013**, 21, 1163-8	5.3	291
62	Disease variants alter transcription factor levels and methylation of their binding sites. *Nature Genetics*, **2017**, 49, 131-138	36.3	252
61	Common variants in 22 loci are associated with QRS duration and cardiac ventricular conduction. *Nature Genetics*, **2010**, 42, 1068-76	36.3	249
60	Identification of context-dependent expression quantitative trait loci in whole blood. *Nature Genetics*, **2017**, 49, 139-145	36.3	240
59	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, 223-32	11	233
58	The impact of low-frequency and rare variants on lipid levels. *Nature Genetics*, **2015**, 47, 589-97	36.3	229
57	Trans-ancestry genome-wide association study identifies 12 genetic loci influencing blood pressure and implicates a role for DNA methylation. *Nature Genetics*, **2015**, 47, 1282-1293	36.3	223
56	Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. *Nature Genetics*, **2013**, 45, 621-31	36.3	219
55	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. *Nature Genetics*, **2014**, 46, 826-36	36.3	199

54	Whole-exome sequencing identifies rare and low-frequency coding variants associated with LDL cholesterol. *American Journal of Human Genetics*, **2014**, 94, 233-45	11	170
53	Meta-analysis of genome-wide association studies from the CHARGE consortium identifies common variants associated with carotid intima media thickness and plaque. *Nature Genetics*, **2011**, 43, 940-7	36.3	168
52	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. *Nature Communications*, **2015**, 6, 5897	17.4	147
51	Gene-centric meta-analysis in 87,736 individuals of European ancestry identifies multiple blood-pressure-related loci. *American Journal of Human Genetics*, **2014**, 94, 349-60	11	131
50	Genome-wide association study identifies novel genetic variants contributing to variation in blood metabolite levels. *Nature Communications*, **2015**, 6, 7208	17.4	126
49	Novel loci affecting iron homeostasis and their effects in individuals at risk for hemochromatosis. *Nature Communications*, **2014**, 5, 4926	17.4	121
48	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. *Nature Communications*, **2016**, 7, 10494	17.4	107
47	Genome-wide association analysis identifies multiple loci related to resting heart rate. *Human Molecular Genetics*, **2010**, 19, 3885-94	5.6	106
46	The -514 C->T hepatic lipase promoter region polymorphism and plasma lipids: a meta-analysis. *Journal of Clinical Endocrinology and Metabolism*, **2004**, 89, 3858-63	5.6	81
45	52 Genetic Loci Influencing Myocardial Mass. *Journal of the American College of Cardiology*, **2016**, 68, 1435-1448	15.1	76
44	Genomewide meta-analysis identifies loci associated with IGF-I and IGFBP-3 levels with impact on age-related traits. *Aging Cell*, **2016**, 15, 811-24	9.9	71
43	GWAS and colocalization analyses implicate carotid intima-media thickness and carotid plaque loci in cardiovascular outcomes. *Nature Communications*, **2018**, 9, 5141	17.4	64
42	Discovery and Fine-Mapping of Glycaemic and Obesity-Related Trait Loci Using High-Density Imputation. *PLoS Genetics*, **2015**, 11, e1005230	6	59
41	A genome-wide association scan of RR and QT interval duration in 3 European genetically isolated populations: the EUROSPAN project. *Circulation: Cardiovascular Genetics*, **2009**, 2, 322-8		58
40	A metabolomic profile is associated with the risk of incident coronary heart disease. *American Heart Journal*, **2014**, 168, 45-52.e7	4.9	56
39	PNPLA3, TM6SF2, and MBOAT7 Genotypes and Coronary Artery Disease. *Gastroenterology*, **2017**, 152, 912-913	13.3	50
38	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. *Nature Communications*, **2016**, 7, 13357	17.4	46
37	Risk scores of common genetic variants for lipid levels influence atherosclerosis and incident coronary heart disease. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2013**, 33, 2233-9	9.4	40

36	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. *Nature Communications*, **2018**, 9, 2904	17.4	39
35	Multiethnic Exome-Wide Association Study of Subclinical Atherosclerosis. *Circulation: Cardiovascular Genetics*, **2016**, 9, 511-520		34
34	Genome of The Netherlands population-specific imputations identify an ABCA6 variant associated with cholesterol levels. *Nature Communications*, **2015**, 6, 6065	17.4	32
33	An integrative cross-omics analysis of DNA methylation sites of glucose and insulin homeostasis. *Nature Communications*, **2019**, 10, 2581	17.4	31
32	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. *Nature Communications*, **2021**, 12, 24	17.4	30
31	Meta-analysis of 49 549 individuals imputed with the 1000 Genomes Project reveals an exonic damaging variant in ANGPTL4 determining fasting TG levels. *Journal of Medical Genetics*, **2016**, 53, 441-9	5.8	27
30	Exome-chip meta-analysis identifies novel loci associated with cardiac conduction, including ADAMTS6. *Genome Biology*, **2018**, 19, 87	18.3	25
29	Fifteen Genetic Loci Associated With the Electrocardiographic P Wave. *Circulation: Cardiovascular Genetics*, **2017**, 10,		24
28	Epistatic effect of cholesteryl ester transfer protein and hepatic lipase on serum high-density lipoprotein cholesterol levels. *Journal of Clinical Endocrinology and Metabolism*, **2007**, 92, 2680-7	5.6	22
27	Heritabilities, apolipoprotein E, and effects of inbreeding on plasma lipids in a genetically isolated population: the Erasmus Rucphen Family Study. *European Journal of Epidemiology*, **2007**, 22, 99-105	12.1	21
26	Twenty-eight genetic loci associated with ST-T-wave amplitudes of the electrocardiogram. *Human Molecular Genetics*, **2016**, 25, 2093-2103	5.6	20
25	Fine-mapping, novel loci identification, and SNP association transferability in a genome-wide association study of QRS duration in African Americans. *Human Molecular Genetics*, **2016**, 25, 4350-4368	5.6	20
24	Heritability in a SCN5A-mutation founder population with increased female susceptibility to non-nocturnal ventricular tachyarrhythmia and sudden cardiac death. *Heart Rhythm*, **2017**, 14, 1873-1881	6.7	19
23	Genome-wide association meta-analysis of 30,000 samples identifies seven novel loci for quantitative ECG traits. *European Journal of Human Genetics*, **2019**, 27, 952-962	5.3	18
22	Discovery of novel heart rate-associated loci using the Exome Chip. *Human Molecular Genetics*, **2017**, 26, 2346-2363	5.6	17
21	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. *Nature Communications*, **2020**, 11, 2542	17.4	16
20	Heritabilities, proportions of heritabilities explained by GWAS findings, and implications of cross-phenotype effects on PR interval. *Human Genetics*, **2015**, 134, 1211-9	6.3	16
19	The cholesteryl ester transfer protein I405V polymorphism is associated with increased high-density lipoprotein levels and decreased risk of myocardial infarction: the Rotterdam Study. *European Journal of Cardiovascular Prevention and Rehabilitation*, **2007**, 14, 419-21		15

18	Dynamic risk assessment to improve quality of care in patients with atrial fibrillation: the 7th AFNET/EHRA Consensus Conference. *Europace*, **2021**, 23, 329-344	3.9	14
17	The challenges of genome-wide interaction studies: lessons to learn from the analysis of HDL blood levels. *PLoS ONE*, **2014**, 9, e109290	3.7	12
16	Common and Rare Coding Genetic Variation Underlying the Electrocardiographic PR Interval. *Circulation Genomic and Precision Medicine*, **2018**, 11, e002037	5.2	11
15	Genome-wide identification of genes regulating DNA methylation using genetic anchors for causal inference. *Genome Biology*, **2020**, 21, 220	18.3	10
14	A systematic SNP selection approach to identify mechanisms underlying disease aetiology: linking height to post-menopausal breast and colorectal cancer risk. *Scientific Reports*, **2017**, 7, 41034	4.9	7
13	DNA methylation signatures of aggression and closely related constructs: A meta-analysis of epigenome-wide studies across the lifespan. *Molecular Psychiatry*, **2021**, 26, 2148-2162	15.1	7
12	Fine mapping the region reveals a common intronic insertion associated to HDL-C. *Npj Aging and Mechanisms of Disease*, **2015**, 1, 15011	5.5	5
11	Association of the IGF1 gene with fasting insulin levels. *European Journal of Human Genetics*, **2016**, 24, 1337-43	5.3	4
10	Genetic Determinants of Electrocardiographic P-Wave Duration and Relation to Atrial Fibrillation. *Circulation Genomic and Precision Medicine*, **2020**, 13, 387-395	5.2	4
9	Genome-wide Association Study of Change in Fasting Glucose over time in 13,807 non-diabetic European Ancestry Individuals. *Scientific Reports*, **2019**, 9, 9439	4.9	3
8	A Combined Linkage and Exome Sequencing Analysis for Electrocardiogram Parameters in the Erasmus Rucphen Family Study. *Frontiers in Genetics*, **2016**, 7, 190	4.5	3
7	A combined linkage, microarray and exome analysis suggests MAP3K11 as a candidate gene for left ventricular hypertrophy. *BMC Medical Genomics*, **2018**, 11, 22	3.7	2
6	Metabolomics reveals a link between homocysteine and lipid metabolism and leukocyte telomere length: the ENGAGE consortium. *Scientific Reports*, **2019**, 9, 11623	4.9	2
5	Clinical and electrophysiological predictors of device-detected new-onset atrial fibrillation during 3 years after cardiac surgery. *Europace*, **2021**, 23, 1922-1930	3.9	2
4	Discovering patterns of pleiotropy in genome-wide association studies		1
3	Considerations for the Assessment of Substrates, Genetics and Risk Factors in Patients with Atrial Fibrillation. *Arrhythmia and Electrophysiology Review*, **2021**, 10, 132-139	3.2	0
2	Leukocyte gene expression in post-thrombotic syndrome. *Thrombosis Research*, **2021**, 202, 40-42	8.2	0
1	Low Density Lipoprotein Exposure of Plasmacytoid Dendritic Cells Blunts Toll-like Receptor 7/9 Signaling via NUR77. *Biomedicines*, **2022**, 10, 1152	4.8	