Mark D Chaffin

List of Publications by Citations

55 papers	3,930 citations	27 h-index	62 g-index
65 ext. papers	6,522 ext. citations	22.3 avg, IF	4.98 L-index

#	Paper	IF	Citations
55	Genome-wide polygenic scores for common diseases identify individuals with risk equivalent to monogenic mutations. *Nature Genetics*, **2018**, 50, 1219-1224	36.3	1073
54	Multi-ethnic genome-wide association study for atrial fibrillation. *Nature Genetics*, **2018**, 50, 1225-1233	36.3	277
53	Polygenic Prediction of Weight and Obesity Trajectories from Birth to Adulthood. *Cell*, **2019**, 177, 587-596.e9	36.2	265
52	Genetics of blood lipids among ~300,000 multi-ethnic participants of the Million Veteran Program. *Nature Genetics*, **2018**, 50, 1514-1523	36.3	260
51	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. *Nature Genetics*, **2017**, 49, 946-952	36.3	176
50	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. *Nature Communications*, **2020**, 11, 163	17.4	140
49	Genetic analysis in UK Biobank links insulin resistance and transendothelial migration pathways to coronary artery disease. *Nature Genetics*, **2017**, 49, 1392-1397	36.3	127
48	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. *Nature*, **2020**, 586, 763-768	50.4	127
47	Transcriptional and Cellular Diversity of the Human Heart. *Circulation*, **2020**, 142, 466-482	16.7	124
46	Whole-Genome Sequencing to Characterize Monogenic and Polygenic Contributions in Patients Hospitalized With Early-Onset Myocardial Infarction. *Circulation*, **2019**, 139, 1593-1602	16.7	112
45	Integrated analyses of single-cell atlases reveal age, gender, and smoking status associations with cell type-specific expression of mediators of SARS-CoV-2 viral entry and highlights inflammatory programs in putative target cells		107
44	A genome-wide cross-trait analysis from UK Biobank highlights the shared genetic architecture of asthma and allergic diseases. *Nature Genetics*, **2018**, 50, 857-864	36.3	93
43	Single-cell meta-analysis of SARS-CoV-2 entry genes across tissues and demographics. *Nature Medicine*, **2021**, 27, 546-559	50.5	91
42	Deep-coverage whole genome sequences and blood lipids among 16,324 individuals. *Nature Communications*, **2018**, 9, 3391	17.4	90
41	Association Between Titin Loss-of-Function Variants and Early-Onset Atrial Fibrillation. *JAMA - Journal of the American Medical Association*, **2018**, 320, 2354-2364	27.4	75
40	Genome-wide association study of peripheral artery disease in the Million Veteran Program. *Nature Medicine*, **2019**, 25, 1274-1279	50.5	73
39	Genome-wide association analysis of venous thromboembolism identifies new risk loci and genetic overlap with arterial vascular disease. *Nature Genetics*, **2019**, 51, 1574-1579	36.3	56

38	Analysis of predicted loss-of-function variants in UK Biobank identifies variants protective for disease. *Nature Communications*, **2018**, 9, 1613	17.4	55
37	Deep coverage whole genome sequences and plasma lipoprotein(a) in individuals of European and African ancestries. *Nature Communications*, **2018**, 9, 2606	17.4	53
36	Phenotypic Refinement of Heart Failure in a National Biobank Facilitates Genetic Discovery. *Circulation*, **2018**,	16.7	51
35	A missense variant in Mitochondrial Amidoxime Reducing Component 1 gene and protection against liver disease. *PLoS Genetics*, **2020**, 16, e1008629	6	49
34	Myocyte-Specific Upregulation of in Cardiovascular Disease: Implications for SARS-CoV-2-Mediated Myocarditis. *Circulation*, **2020**, 142, 708-710	16.7	47
33	Analysis of cardiac magnetic resonance imaging in 36,000 individuals yields genetic insights into dilated cardiomyopathy. *Nature Communications*, **2020**, 11, 2254	17.4	40
32	Heritability of Atrial Fibrillation. *Circulation: Cardiovascular Genetics*, **2017**, 10,		39
31	Limitations of Contemporary Guidelines for Managing Patients at High Genetic Risk of Coronary Artery Disease. *Journal of the American College of Cardiology*, **2020**, 75, 2769-2780	15.1	33
30	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	36.3	33
29	Rare Protein-Truncating Variants in APOB, Lower Low-Density Lipoprotein Cholesterol, and Protection Against Coronary Heart Disease. *Circulation Genomic and Precision Medicine*, **2019**, 12, e002376	5.2	30
28	Monogenic and Polygenic Contributions to Atrial Fibrillation Risk: Results From a National Biobank. *Circulation Research*, **2020**, 126, 200-209	15.7	26
27	Genome-Wide Polygenic Score, Clinical Risk Factors, and Long-Term Trajectories of Coronary Artery Disease. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2020**, 40, 2738-2746	9.4	24
26	Validation of a Genome-Wide Polygenic Score for Coronary Artery Disease in South Asians. *Journal of the American College of Cardiology*, **2020**, 76, 703-714	15.1	22
25	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. *Nature Communications*, **2020**, 11, 2542	17.4	16
24	Genome-wide polygenic score to identify a monogenic risk-equivalent for coronary disease		13
23	DNA Sequence Variation in Encoding the Activin Receptor-Like Kinase 7 Influences Body Fat Distribution and Protects Against Type 2 Diabetes. *Diabetes*, **2019**, 68, 226-234	0.9	12
22	Identification of Functional Variant Enhancers Associated With Atrial Fibrillation. *Circulation Research*, **2020**, 127, 229-243	15.7	12
21	Titin Truncating Variants in Adults Without Known Congestive Heart Failure. *Journal of the American College of Cardiology*, **2020**, 75, 1239-1241	15.1	10

20	Genetic Variation in Cardiometabolic Traits and Medication Targets and the Risk of Hypertensive Disorders of Pregnancy. *Circulation*, **2020**, 142, 711-713	16.7	9
19	Myocyte Specific Upregulation of ACE2 in Cardiovascular Disease: Implications for SARS-CoV-2 mediated myocarditis **2020**,		8
18	Epigenetic Analyses of Human Left Atrial Tissue Identifies Gene Networks Underlying Atrial Fibrillation. *Circulation Genomic and Precision Medicine*, **2020**, 13, e003085	5.2	7
17	Rare variants lowering the levels of coagulation factor X are protective against ischemic heart disease. *Haematologica*, **2020**, 105, e365-e369	6.6	7
16	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	36.3	7
15	Integrative analysis of the plasma proteome and polygenic risk of cardiometabolic diseases. *Nature Metabolism*, **2021**, 3, 1476-1483	14.6	6
14	Deep learning enables genetic analysis of the human thoracic aorta. *Nature Genetics*, **2021**,	36.3	6
13	Deep learning enables genetic analysis of the human thoracic aorta		6
12	Response by Aragam et al to Letter Regarding Article, "Phenotypic Refinement of Heart Failure in a National Biobank Facilitates Genetic Discovery". *Circulation*, **2019**, 140, e7-e8	16.7	6
11	Single-nucleus profiling of human dilated and hypertrophic cardiomyopathy. *Nature*,	50.4	6
10	Integrative analysis of the plasma proteome and polygenic risk of cardiometabolic diseases		4
9	Transcriptional and Cellular Diversity of the Human Heart		4
8	A missense variant in Mitochondrial Amidoxime Reducing Component 1 gene and protection against liver disease		4
7	Analysis of rare genetic variation underlying cardiometabolic diseases and traits among 200,000 individuals in the UK Biobank.. *Nature Genetics*, **2022**,	36.3	4
6	Rare Genetic Variation Underlying Human Diseases and Traits: Results from 200,000 Individuals in the UK Biobank		3
5	Genome-wide association study provides new insights into the genetic architecture and pathogenesis of heart failure		2
4	Rare coding variants in 35 genes associate with circulating lipid levels a multi-ancestry analysis of 170,000 exomes		2
3	Genetic Analysis of Right Heart Structure and Function in 40,000 People		1

2	The genomics of heart failure: design and rationale of the HERMES consortium. *ESC Heart Failure*, **2021**,	3.7	1
1	Rare Coding Variants Associated With Electrocardiographic Intervals Identify Monogenic Arrhythmia Susceptibility Genes: A Multi-Ancestry Analysis. *Circulation Genomic and Precision Medicine*, **2021**, 14, e003300	5.2	0