Mark D Chaffin

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/2986131/publications.pdf

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46 papers	8,693 citations	117571 34 h-index	189801 50 g-index
65 all docs	65 docs citations	65 times ranked	14967 citing authors

#	Article	IF	Citations
1	Genome-wide polygenic scores for common diseases identify individuals with risk equivalent to monogenic mutations. Nature Genetics, 2018, 50, 1219-1224.	9.4	2,111
2	Multi-ethnic genome-wide association study for atrial fibrillation. Nature Genetics, 2018, 50, 1225-1233.	9.4	552
3	Polygenic Prediction of Weight and Obesity Trajectories from Birth to Adulthood. Cell, 2019, 177, 587-596.e9.	13.5	516
4	Genetics of blood lipids among ~300,000 multi-ethnic participants of the Million Veteran Program. Nature Genetics, 2018, 50, 1514-1523.	9.4	497
5	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. Nature Communications, 2020, 11, 163.	5.8	466
6	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature, 2020, 586, 763-768.	13.7	376
7	Transcriptional and Cellular Diversity of the Human Heart. Circulation, 2020, 142, 466-482.	1.6	326
8	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. Nature Genetics, 2017, 49, 946-952.	9.4	279
9	Single-cell meta-analysis of SARS-CoV-2 entry genes across tissues and demographics. Nature Medicine, 2021, 27, 546-559.	15.2	261
10	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
11	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.	9.4	191
12	Genetic analysis in UK Biobank links insulin resistance and transendothelial migration pathways to coronary artery disease. Nature Genetics, 2017, 49, 1392-1397.	9.4	190
13	Genome-wide association study of peripheral artery disease in the Million Veteran Program. Nature Medicine, 2019, 25, 1274-1279.	15.2	177
14	Genome-wide association analysis of venous thromboembolism identifies new risk loci and genetic overlap with arterial vascular disease. Nature Genetics, 2019, 51, 1574-1579.	9.4	152
15	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
16	Association Between Titin Loss-of-Function Variants and Early-Onset Atrial Fibrillation. JAMA - Journal of the American Medical Association, 2018, 320, 2354.	3.8	144
17	Deep-coverage whole genome sequences and blood lipids among 16,324 individuals. Nature Communications, 2018, 9, 3391.	5.8	140
18	Analysis of cardiac magnetic resonance imaging in 36,000 individuals yields genetic insights into dilated cardiomyopathy. Nature Communications, 2020, 11, 2254.	5.8	140

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19	Single-nucleus profiling of human dilated and hypertrophic cardiomyopathy. Nature, 2022, 608, 174-180.	13.7	115
20	Phenotypic Refinement of Heart Failure in a National Biobank Facilitates Genetic Discovery. Circulation, 2019, 139, 489-501.	1.6	109
21	A missense variant in Mitochondrial Amidoxime Reducing Component 1 gene and protection against liver disease. PLoS Genetics, 2020, 16, e1008629.	1.5	101
22	Deep learning enables genetic analysis of the human thoracic aorta. Nature Genetics, 2022, 54, 40-51.	9.4	90
23	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.	1.2	88
24	Deep coverage whole genome sequences and plasma lipoprotein(a) in individuals of European and African ancestries. Nature Communications, 2018, 9, 2606.	5.8	79
25	Monogenic and Polygenic Contributions to Atrial Fibrillation Risk. Circulation Research, 2020, 126, 200-209.	2.0	79
26	Analysis of predicted loss-of-function variants in UK Biobank identifies variants protective for disease. Nature Communications, 2018, 9, 1613.	5.8	78
27	Validation of a Genome-Wide PolygenicÂScore for Coronary ArteryÂDisease inÂSouth Asians. Journal of the American College of Cardiology, 2020, 76, 703-714.	1.2	76
28	Myocyte Specific Upregulation of ACE2 in Cardiovascular Disease: Implications for SARS-CoV-2 Mediated Myocarditis. Circulation, 2020, 142, 708-710.	1.6	73
29	Heritability of Atrial Fibrillation. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	72
30	Genome-Wide Polygenic Score, Clinical Risk Factors, and Long-Term Trajectories of Coronary Artery Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2020, 40, 2738-2746.	1.1	71
31	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
32	Analysis of rare genetic variation underlying cardiometabolic diseases and traits among 200,000 individuals in the UK Biobank. Nature Genetics, 2022, 54, 240-250.	9.4	68
33	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	5.8	59
34	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.	1.6	57
35	Integrative analysis of the plasma proteome and polygenic risk of cardiometabolic diseases. Nature Metabolism, 2021, 3, 1476-1483.	5.1	43
36	Genetic analysis of right heart structure and function in 40,000 people. Nature Genetics, 2022, 54, 792-803.	9.4	34

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37	Identification of Functional Variant Enhancers Associated With Atrial Fibrillation. Circulation Research, 2020, 127, 229-243.	2.0	33
38	DNA Sequence Variation in ACVR1C Encoding the Activin Receptor-Like Kinase 7 Influences Body Fat Distribution and Protects Against Type 2 Diabetes. Diabetes, 2019, 68, 226-234.	0.3	31
39	Genetic Variation in Cardiometabolic Traits and Medication Targets and the Risk of Hypertensive Disorders of Pregnancy. Circulation, 2020, 142, 711-713.	1.6	27
40	Rare coding variants in 35 genes associate with circulating lipid levelsâ€"A multi-ancestry analysis of 170,000 exomes. American Journal of Human Genetics, 2022, 109, 81-96.	2.6	24
41	Titin Truncating Variants in Adults Without Known Congestive HeartÂFailure. Journal of the American College of Cardiology, 2020, 75, 1239-1241.	1.2	22
42	Response by Aragam et al to Letter Regarding Article, â€œPhenotypic Refinement of Heart Failure in a National Biobank Facilitates Genetic Discoveryâ€• Circulation, 2019, 140, e7-e8.	1.6	20
43	Epigenetic Analyses of Human Left Atrial Tissue Identifies Gene Networks Underlying Atrial Fibrillation. Circulation Genomic and Precision Medicine, 2020, 13, e003085.	1.6	14
44	The genomics of heart failure: design and rationale of the HERMES consortium. ESC Heart Failure, 2021, 8, 5531-5541.	1.4	11
45	Rare variants lowering the levels of coagulation factor X are protective against ischemic heart disease. Haematologica, 2020, 105, e365-e369.	1.7	9
46	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