Helen R Warren

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7425451/publications.pdf

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159573 11,092 63 30 citations h-index papers

g-index 71 71 71 19476 citing authors docs citations times ranked all docs

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67

#	Article	IF	CITATIONS
1	Heteroplasmic mitochondrial DNA variants in cardiovascular diseases. PLoS Genetics, 2022, 18, e1010068.	3.5	19
2	Insights From a Large-Scale Whole-Genome Sequencing Study of Systolic Blood Pressure, Diastolic Blood Pressure, and Hypertension. Hypertension, 2022, 79, 1656-1667.	2.7	12
3	Phospholemman Phosphorylation Regulates Vascular Tone, Blood Pressure, and Hypertension in Mice and Humans. Circulation, 2021, 143, 1123-1138.	1.6	12
4	An Academic Clinician's Road Map to Hypertension Genomics. Hypertension, 2021, 77, 284-295.	2.7	9
5	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341
6	Genetically Determined Serum Calcium Levels and Markers of Ventricular Repolarization: A Mendelian Randomization Study in the UK Biobank. Circulation Genomic and Precision Medicine, 2021, 14, e003231.	3.6	11
7	Adverse Cardiovascular Outcomes and Antihypertensive Treatment: A Genomeâ€Wide Interaction Metaâ€Analysis in the International Consortium for Antihypertensive Pharmacogenomics Studies. Clinical Pharmacology and Therapeutics, 2021, 110, 723-732.	4.7	6
8	The Pharmacogenetics of Statin Therapy on Clinical Events: No Evidence that Genetic Variation Affects Statin Response on Myocardial Infarction. Frontiers in Pharmacology, 2021, 12, 679857.	3.5	2
9	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	27.8	353
10	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. Molecular Psychiatry, 2020, 25, 2392-2409.	7.9	83
11	Statin-induced LDL cholesterol response and type 2 diabetes: a bidirectional two-sample Mendelian randomization study. Pharmacogenomics Journal, 2020, 20, 462-470.	2.0	18
12	Hypertension and the roles of the 9p21.3 risk locus: Classic findings and new association data. International Journal of Cardiology: Hypertension, 2020, 7, 100050.	2.2	3
13	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. Nature Genetics, 2020, 52, 1314-1332.	21.4	91
14	Genetic Determinants of Electrocardiographic P-Wave Duration and Relation to Atrial Fibrillation. Circulation Genomic and Precision Medicine, 2020, 13, 387-395.	3.6	16
15	Cerebral small vessel disease genomics and its implications across the lifespan. Nature Communications, 2020, 11, 6285.	12.8	89
16	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. Molecular Psychiatry, 2020, 26, 2111-2125.	7.9	17
17	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	12.8	59
18	Gene Variants at Loci Related to Blood Pressure Account for Variation in Response to Antihypertensive Drugs Between Black and White Individuals. Hypertension, 2019, 74, 614-622.	2.7	14

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19	Effects of Calcium, Magnesium, and Potassium Concentrations on Ventricular Repolarization in Unselected Individuals. Journal of the American College of Cardiology, 2019, 73, 3118-3131.	2.8	27
20	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	12.8	84
21	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
22	Genome-Wide Association Study of Apparent Treatment-Resistant Hypertension in the CHARGE Consortium: The CHARGE Pharmacogenetics Working Group. American Journal of Hypertension, 2019, 32, 1146-1153.	2.0	17
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.	2.8	29
24	Genome-wide association study identifies loci for arterial stiffness index in 127,121 UK Biobank participants. Scientific Reports, 2019, 9, 9143.	3.3	28
25	A multi-ancestry genome-wide study incorporating gene–smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. Human Molecular Genetics, 2019, 28, 2615-2633.	2.9	31
26	Mendelian randomisation analyses find pulmonary factors mediate the effect of height on coronary artery disease. Communications Biology, 2019, 2, 119.	4.4	35
27	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	21.4	89
28	Trans-ethnic association study of blood pressure determinants in over 750,000 individuals. Nature Genetics, 2019, 51, 51-62.	21.4	328
29	The narrow-sense and common single nucleotide polymorphism heritability of early repolarization. International Journal of Cardiology, 2019, 279, 135-140.	1.7	7
30	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. Nature Genetics, 2018, 50, 559-571.	21.4	356
31	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. American Journal of Human Genetics, 2018, 102, 375-400.	6.2	123
32	Genetic Predisposition to High Blood Pressure and Lifestyle Factors. Circulation, 2018, 137, 653-661.	1.6	169
33	Postmortem Genetic Testing for Cardiac Ion Channelopathies in Stillbirths. Circulation Genomic and Precision Medicine, 2018, 11, e001817.	3.6	18
34	The biological impact of blood pressure-associated genetic variants in the natriuretic peptide receptor C gene on human vascular smooth muscle. Human Molecular Genetics, 2018, 27, 199-210.	2.9	21
35	Hypertension genomics and cardiovascular prevention. Annals of Translational Medicine, 2018, 6, 291-291.	1.7	21
36	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.	3.6	27

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37	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
38	Common and Rare Coding Genetic Variation Underlying the Electrocardiographic PR Interval. Circulation Genomic and Precision Medicine, 2018, 11, e002037.	3.6	19
39	Thirty loci identified for heart rate response to exercise and recovery implicate autonomic nervous system. Nature Communications, 2018, 9, 1947.	12.8	70
40	Exome-chip meta-analysis identifies novel loci associated with cardiac conduction, including ADAMTS6. Genome Biology, 2018, 19, 87.	8.8	47
41	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. PLoS ONE, 2018, 13, e0198166.	2.5	94
42	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	21.4	286
43	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. Nature Genetics, 2017, 49, 403-415.	21.4	492
44	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	27.8	544
45	A genome-wide interaction analysis of tricyclic/tetracyclic antidepressants and RR and QT intervals: a pharmacogenomics study from the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) consortium. Journal of Medical Genetics, 2017, 54, 313-323.	3.2	9
46	Discovery of novel heart rate-associated loci using the Exome Chip. Human Molecular Genetics, 2017, 26, 2346-2363.	2.9	29
47	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	21.4	470
48	Genome-Wide Association Study of Blood Pressure Traits by Hispanic/Latino Background: the Hispanic Community Health Study/Study of Latinos. Scientific Reports, 2017, 7, 10348.	3.3	24
49	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. Hypertension, 2017, 70, .	2.7	123
50	Randomised, double-blind, placebo-controlled study investigating the effects of inorganic nitrate on vascular function, platelet reactivity and restenosis in stable angina: protocol of the NITRATE-OCT study. BMJ Open, 2016, 6, e012728.	1.9	6
51	Meta-analysis of genome-wide association studies of HDL cholesterol response to statins. Journal of Medical Genetics, 2016, 53, 835-845.	3.2	28
52	<i> <scp>IGSF</scp> 10 </i> mutations dysregulate gonadotropinâ€releasing hormone neuronal migration resulting in delayed puberty. EMBO Molecular Medicine, 2016, 8, 626-642.	6.9	109
53	A genetic risk score is associated with statin-induced low-density lipoprotein cholesterol lowering. Pharmacogenomics, 2016, 17, 583-591.	1.3	9
54	Analysis with the exome array identifies multiple new independent variants in lipid loci. Human Molecular Genetics, 2016, 25, 4094-4106.	2.9	19

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55	Rooted in risk: genetic predisposition for low-density lipoprotein cholesterol level associates with diminished low-density lipoprotein cholesterol response to statin treatment. Pharmacogenomics, 2016, 17, 1621-1628.	1.3	11
56	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	21.4	261
57	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. Nature Genetics, 2016, 48, 1171-1184.	21.4	362
58	Plasma urate concentration and risk of coronary heart disease: a Mendelian randomisation analysis. Lancet Diabetes and Endocrinology,the, 2016, 4, 327-336.	11.4	122
59	Exploring hypertension genomeâ€wide association studies findings and impact on pathophysiology, pathways, and pharmacogenetics. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2015, 7, 73-90.	6.6	30
60	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823
61	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984.	2.9	40
62	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	27.8	173
63	Pharmacogenetic meta-analysis of genome-wide association studies of LDL cholesterol response to statins. Nature Communications, 2014, 5, 5068.	12.8	216