Ron Do

List of Publications by Year
in descending order

88 papers	36,101 citations	57758 44 h-index	62596 80 g-index
104 all docs	104 docs citations	104 times ranked	54351 citing authors

#	Article	IF	Citations
1	Overcoming constraints on the detection of recessive selection in human genes from population frequency data. American Journal of Human Genetics, 2022, 109, 33-49.	6.2	5
2	Population-Based Penetrance of Deleterious Clinical Variants. JAMA - Journal of the American Medical Association, 2022, 327, 350.	7.4	34
3	Coronary Risk Estimation Based on Clinical Data in Electronic Health Records. Journal of the American College of Cardiology, 2022, 79, 1155-1166.	2.8	14
4	Genetic and phenotypic profiling of supranormal ejection fraction reveals decreased survival and underdiagnosed heart failure. European Journal of Heart Failure, 2022, 24, 2118-2127.	7.1	22
5	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential. Science Advances, 2022, 8, eabl6579.	10.3	36
6	Genome-First Recall of Healthy Individuals by Polygenic Risk Score Reveals Differences in Coronary Artery Calcium. American Heart Journal, 2022, 250, 29-29.	2.7	1
7	Penetrance of Deleterious Clinical Variantsâ€"Reply. JAMA - Journal of the American Medical Association, 2022, 327, 1927.	7.4	0
8	Statin Use in Relation to Intraocular Pressure, Glaucoma, and Ocular Coherence Tomography Parameters in the UK Biobank. , 2022, 63, 31.		7
9	Transethnic Transferability of a Genome-Wide Polygenic Score for Coronary Artery Disease. Circulation Genomic and Precision Medicine, 2021, 14, e003092.	3.6	25
10	A genotype-first approach to exploring Mendelian cardiovascular traits with clear external manifestations. Genetics in Medicine, 2021, 23, 94-102.	2.4	16
11	Prediction of Incident Heart Failure in TTR Val122Ile Carriers One Year Ahead of Diagnosis in a Multiethnic Biobank. American Journal of Cardiology, 2021, 142, 151-153.	1.6	1
12	Intraocular Pressure, Glaucoma, and Dietary Caffeine Consumption. Ophthalmology, 2021, 128, 866-876.	5.2	35
13	Exploiting the GTEx resources to decipher the mechanisms at GWAS loci. Genome Biology, 2021, 22, 49.	8.8	150
14	An integrative multiomic network model links lipid metabolism to glucose regulation in coronary artery disease. Nature Communications, 2021, 12, 547.	12.8	35
15	Exome-wide evaluation of rare coding variants using electronic health records identifies new geneâ€"phenotype associations. Nature Medicine, 2021, 27, 66-72.	30.7	44
16	Probing the aggregated effects of purifying selection per individual on 1,380 medical phenotypes in the UK Biobank. PLoS Genetics, 2021, 17, e1009337.	3.5	2
17	Genome-wide polygenic risk score for retinopathy of type 2 diabetes. Human Molecular Genetics, 2021, 30, 952-960.	2.9	14
18	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. Nature Communications, 2021, 12, 2182.	12.8	17

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19	Genetic pleiotropy of ERCC6 lossâ€ofâ€function and deleterious missense variants links retinal dystrophy, arrhythmia, and immunodeficiency in diverse ancestries. Human Mutation, 2021, 42, 969-977.	2.5	3
20	Non-invasive ventilation versus mechanical ventilation in hypoxemic patients with COVID-19. Infection, 2021, 49, 989-997.	4.7	13
21	Derivation and Validation of Genomeâ€Wide Polygenic Score for Ischemic Heart Failure. Journal of the American Heart Association, 2021, 10, e021916.	3.7	3
22	Whole-Genome Sequencing Association Analyses of Stroke and Its Subtypes in Ancestrally Diverse Populations From Trans-Omics for Precision Medicine Project. Stroke, 2021, , STROKEAHA120031792.	2.0	16
23	Tissue-specific genetic features inform prediction of drug side effects in clinical trials. Science Advances, 2020, 6, .	10.3	33
24	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.	2.8	88
25	Derivation and validation of genome-wide polygenic score for urinary tract stone diagnosis. Kidney International, 2020, 98, 1323-1330.	5.2	12
26	Minority-centric meta-analyses of blood lipid levels identify novel loci in the Population Architecture using Genomics and Epidemiology (PAGE) study. PLoS Genetics, 2020, 16, e1008684.	3.5	17
27	Title is missing!. , 2020, 16, e1008684.		0
28	Title is missing!. , 2020, 16, e1008684.		0
29	Title is missing!. , 2020, 16, e1008684.		0
30	Title is missing!. , 2020, 16, e1008684.		0
31	Title is missing!. , 2020, 16, e1008684.		0
32	Title is missing!. , 2020, 16, e1008684.		0
33	Augmented intelligence with natural language processing applied to electronic health records for identifying patients with non-alcoholic fatty liver disease at risk for disease progression. International Journal of Medical Informatics, 2019, 129, 334-341.	3.3	29
34	HOPS: a quantitative score reveals pervasive horizontal pleiotropy in human genetic variation is driven by extreme polygenicity of human traits and diseases. Genome Biology, 2019, 20, 222.	8.8	47
35	Whole Genome Sequencing Identifies CRISPLD2 as a Lung Function Gene in Children With Asthma. Chest, 2019, 156, 1068-1079.	0.8	5
36	Genetic analyses of diverse populations improves discovery for complex traits. Nature, 2019, 570, 514-518.	27.8	679

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37	Estimation of metabolic syndrome heritability in three large populations including full pedigree and genomic information. Human Genetics, 2019, 138, 739-748.	3.8	4
38	Association of the V122I Hereditary Transthyretin Amyloidosis Genetic Variant With Heart Failure Among Individuals of African or Hispanic/Latino Ancestry. JAMA - Journal of the American Medical Association, 2019, 322, 2191.	7.4	93
39	No causal effects of serum urate levels on the risk of chronic kidney disease: A Mendelian randomization study. PLoS Medicine, 2019, 16, e1002725.	8.4	97
40	Detection of widespread horizontal pleiotropy in causal relationships inferred from Mendelian randomization between complex traits and diseases. Nature Genetics, 2018, 50, 693-698.	21.4	3,593
41	Using Full Genomic Information to Predict Disease: Breaking Down the Barriers Between Complex and Mendelian Diseases. Annual Review of Genomics and Human Genetics, 2018, 19, 289-301.	6.2	9
42	Plasma biomarkers are associated with renal outcomes in individuals with APOL1 risk variants. Kidney International, 2018, 93, 1409-1416.	5.2	25
43	The Genetic Landscape of Diamond-Blackfan Anemia. American Journal of Human Genetics, 2018, 103, 930-947.	6.2	184
44	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated WithÂCoronary ArteryÂDisease. Journal of the American College of Cardiology, 2017, 69, 823-836.	2.8	214
45	Human knockouts and phenotypic analysis in a cohort with a high rate of consanguinity. Nature, 2017, 544, 235-239.	27.8	292
46	Loss of Cardioprotective Effects at the ADAMTS7 Locus as a Result of Gene-Smoking Interactions. Circulation, 2017, 135, 2336-2353.	1.6	51
47	Fifteen new risk loci for coronary artery disease highlight arterial-wall-specific mechanisms. Nature Genetics, 2017, 49, 1113-1119.	21.4	260
48	Association of Triglyceride-Related Genetic Variants With MitralÂAnnularÂCalcification. Journal of the American College of Cardiology, 2017, 69, 2941-2948.	2.8	25
49	What can we learn about lipoprotein metabolism and coronary heart disease from studying rare variants?. Current Opinion in Lipidology, 2016, 27, 99-104.	2.7	4
50	Coding Variation inANGPTL4,LPL,andSVEP1and the Risk of Coronary Disease. New England Journal of Medicine, 2016, 374, 1134-1144.	27.0	427
51	Insight into rheumatological cause and effect through the use of Mendelian randomization. Nature Reviews Rheumatology, 2016, 12, 486-496.	8.0	46
52	Analysis of protein-coding genetic variation in 60,706 humans. Nature, 2016, 536, 285-291.	27.8	9,051
53	No Association of Coronary Artery Disease with X-Chromosomal Variants in Comprehensive International Meta-Analysis. Scientific Reports, 2016, 6, 35278.	3.3	25
54	Systematic Functional Dissection of Common Genetic Variation Affecting Red Blood Cell Traits. Cell, 2016, 165, 1530-1545.	28.9	294

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55	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. Science, 2016, 351, 1166-1171.	12.6	438
56	Whole-exome sequencing of over 4100 men of African ancestry and prostate cancer risk. Human Molecular Genetics, 2016, 25, 371-381.	2.9	26
57	Dominance of Deleterious Alleles Controls the Response to a Population Bottleneck. PLoS Genetics, 2015, 11, e1005436.	3.5	78
58	Disproportionate Contributions of Select Genomic Compartments and Cell Types to Genetic Risk for Coronary Artery Disease. PLoS Genetics, 2015, 11, e1005622.	3.5	70
59	No evidence that selection has been less effective at removing deleterious mutations in Europeans than in Africans. Nature Genetics, 2015, 47, 126-131.	21.4	182
60	Myocardial Infarctionâ€“Associated SNP at 6p24 Interferes With MEF2 Binding and Associates With PHACTR1 Expression Levels in Human Coronary Arteries. Arteriosclerosis, Thrombosis, and Vascular Biology, 2015, 35, 1472-1479.	2.4	78
61	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	6.2	1,098
62	Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction. Nature, 2015, 518, 102-106.	27.8	581
63	Searching for missing heritability: Designing rare variant association studies. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E455-64.	7.1	570
64	Association of Low-Density Lipoprotein Cholesterolâ€“Related Genetic Variants With Aortic Valve Calcium and Incident Aortic Stenosis. JAMA - Journal of the American Medical Association, 2014, 312, 1764.	7.4	184
65	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. American Journal of Human Genetics, 2014, 94, 233-245.	6.2	193
66	Inactivating Mutations in NPC1L1 and Protection from Coronary Heart Disease. New England Journal of Medicine, 2014, 371, 2072-2082.	27.0	386
67	Loss-of-Function Mutations inAPOC3,Triglycerides, and Coronary Disease. New England Journal of Medicine, 2014, 371, 22-31.	27.0	936
68	Discovery and refinement of loci associated with lipid levels. Nature Genetics, 2013, 45, 1274-1283.	21.4	2,641
69	Common variants associated with plasma triglycerides and risk for coronary artery disease. Nature Genetics, 2013, 45, 1345-1352.	21.4	754
70	Large-scale association analysis identifies new risk loci for coronary artery disease. Nature Genetics, 2013, 45, 25-33.	21.4	1,439
71	Exome sequencing and complex disease: practical aspects of rare variant association studies. Human Molecular Genetics, 2012, 21, R1-R9.	2.9	114
72	Advances in genetics show the need for extending screening strategies for autosomal dominant hypercholesterolaemia. European Heart Journal, 2012, 33, 1360-1366.	2.2	76

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73	Plasma HDL cholesterol and risk of myocardial infarction: a mendelian randomisation study. Lancet, The, 2012, 380, 572-580.	13.7	1,937
74	Bayesian inference analyses of the polygenic architecture of rheumatoid arthritis. Nature Genetics, 2012, 44, 483-489.	21.4	402
75	A High-Coverage Genome Sequence from an Archaic Denisovan Individual. Science, 2012, 338, 222-226.	12.6	1,695
76	Evolution and Functional Impact of Rare Coding Variation from Deep Sequencing of Human Exomes. Science, 2012, 337, 64-69.	12.6	1,535
77	Exome sequencing and the genetic basis of complex traits. Nature Genetics, 2012, 44, 623-630.	21.4	340
78	Exome sequencing identifies GATA1 mutations resulting in Diamond-Blackfan anemia. Journal of Clinical Investigation, 2012, 122, 2439-2443.	8.2	292
79	Large-scale association analysis identifies 13 new susceptibility loci for coronary artery disease. Nature Genetics, 2011, 43, 333-338.	21.4	1,685
80	The Effect of Chromosome 9p21 Variants on Cardiovascular Disease May Be Modified by Dietary Intake: Evidence from a Case/Control and a Prospective Study. PLoS Medicine, 2011, 8, e1001106.	8.4	76
81	Fine Mapping of the Insulin-Induced Gene 2 Identifies a Variant Associated With LDL Cholesterol and Total Apolipoprotein B Levels. Circulation: Cardiovascular Genetics, 2010, 3, 454-461.	5.1	7
82	Variation at the NFATC2 Locus Increases the Risk of Thiazolidinedione-Induced Edema in the Diabetes REduction Assessment with ramipril and rosiglitazone Medication (DREAM) Study. Diabetes Care, 2010, 33, 2250-2253.	8.6	34
83	Lack of Association Between the Trp719Arg Polymorphism in Kinesin-Like Protein-6 and Coronary Artery Disease in 19 Case-Control Studies. Journal of the American College of Cardiology, 2010, 56, 1552-1563.	2.8	84
84	Exome Sequencing,ANGPTL3Mutations, and Familial Combined Hypolipidemia. New England Journal of Medicine, 2010, 363, 2220-2227.	27.0	640
85	Genetic Variation at the Proprotein Convertase Subtilisin/Kexin Type 5 Gene Modulates High-Density Lipoprotein Cholesterol Levels. Circulation: Cardiovascular Genetics, 2009, 2, 467-475.	5.1	33
86	Genome-wide association of early-onset myocardial infarction with single nucleotide polymorphisms and copy number variants. Nature Genetics, 2009, 41, 334-341.	21.4	990
87	K45R variant of squalene synthase increases total cholesterol levels in two study samples from a French Canadian population. Human Mutation, 2008, 29, 689-694.	2.5	5
88	Genetic Variants of FTO Influence Adiposity, Insulin Sensitivity, Leptin Levels, and Resting Metabolic Rate in the Quebec Family Study. Diabetes, 2008, 57, 1147-1150.	0.6	206