

Ron Do

List of Articles by Year in descending order

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142

PR articles

34,276

PR citations

35956

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14640

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53

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75438

citing authors

#	ARTICLE	IF	CITATIONS
1	The Clinical Usefulness of a Glaucoma Polygenic Risk Score in 4 Population-Based European Ancestry Cohorts. <i>Ophthalmology</i> , 2025, 132, 228-237.	7.8	18
2	Evaluation of a machine learning-based metabolic marker for coronary artery disease in the UK Biobank. <i>Atherosclerosis</i> , 2025, 401, 119103.	1.5	5
3	Association between genetically predicted leisure and social activities and cardiovascular disease and other health outcomes. <i>Nature Cardiovascular Research</i> , 2025, 4, 15-25.	8.4	0
4	Unveiling the Genetic Landscape of Coronary Artery Disease Through Common and Rare Structural Variants. <i>Journal of the American Heart Association</i> , 2025, 14, .	4.0	3
5	Does Age Modify the Relation Between Genetic Predisposition to Glaucoma and Various Glaucoma Traits in the UK Biobank?. , 2025, 66, 57.		1
6	Trans-ancestral rare variant association study with machine learning-based phenotyping for metabolic dysfunction-associated steatotic liver disease. <i>Genome Biology</i> , 2025, 26, .	8.1	5
7	Rare damaging CCR2 variants are associated with lower lifetime cardiovascular risk. <i>Genome Medicine</i> , 2025, 17, .	9.6	4
8	Associations between pathophysiological traits and symptom development in retrospective analysis of V30M and V122I transthyretin amyloidosis. <i>IJC Heart and Vasculature</i> , 2025, 58, 101663.	0.7	0
9	Common-variant and rare-variant genetic architecture of heart failure across the allele-frequency spectrum. <i>Nature Genetics</i> , 2025, 57, 829-838.	25.2	13
10	Genetic analyses of eight complex diseases using predicted continuous representations of disease. <i>Cell Reports Methods</i> , 2025, 5, 101115.	3.2	2
11	Machine learning-based penetrance of genetic variants. <i>Science</i> , 2025, 389, .	36.2	6
12	Genome-Wide Polygenic Risk Score for CKD in Individuals with APOL1 High-Risk Genotypes. <i>Clinical Journal of the American Society of Nephrology: CJASN</i> , 2024, 19, 374-376.	4.2	9
13	Prediction of Venous Thromboembolism in Diverse Populations Using Machine Learning and Structured Electronic Health Records. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2024, 44, 491-504.	6.0	21
14	Genome-wide study investigating effector genes and polygenic prediction for kidney function in persons with ancestry from Africa and the Americas. <i>Cell Genomics</i> , 2024, 4, 100468.	6.8	12
15	Quantitative Prediction of Right Ventricular Size and Function From the ECG. <i>Journal of the American Heart Association</i> , 2024, 13, .	4.0	9
16	Development of a human genetics-guided priority score for 19,365 genes and 399 drug indications. <i>Nature Genetics</i> , 2024, 56, 51-59.	25.2	24
17	Muesli Intake May Protect Against Coronary Artery Disease. <i>JACC: Advances</i> , 2024, 3, 100888.	1.3	1
18	Genome-first evaluation with exome sequence and clinical data uncovers underdiagnosed genetic disorders in a large healthcare system. <i>Cell Reports Medicine</i> , 2024, 5, 101518.	6.6	6

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19	Large-scale cross-ancestry genome-wide meta-analysis of serum urate. <i>Nature Communications</i> , 2024, 15, .	13.7	26
20	The Association of Urinary Sodium Excretion with Glaucoma and Related Traits in a Large United Kingdom Population. <i>Ophthalmology Glaucoma</i> , 2024, 7, 499-511.	2.4	4
21	Exome sequence analysis identifies rare coding variants associated with a machine learning-based marker for coronary artery disease. <i>Nature Genetics</i> , 2024, 56, 1412-1419.	25.2	12
22	Association of genetic risk, lifestyle, and their interaction with obesity and obesity-related morbidities. <i>Cell Metabolism</i> , 2024, 36, 1494-1503.e3.	25.2	74
23	Use of Diagnostic Codes for Primary Open-Angle Glaucoma Polygenic Risk Score Construction in Electronic Health Record-Linked Biobanks. <i>American Journal of Ophthalmology</i> , 2024, 267, 204-212.	3.8	10
24	Comparison of blood-based liver fibrosis scores in the Mount Sinai Health System, MASLD Registry, and NHANES 2017-2020 study. <i>Hepatology Communications</i> , 2024, 8, .	4.5	5
25	Multimodal fusion learning for long QT syndrome pathogenic genotypes in a racially diverse population. <i>Npj Digital Medicine</i> , 2024, 7, .	10.4	0
26	Integration of observational and causal evidence for the association between adiposity and 17 gastrointestinal outcomes: An umbrella review and meta-analysis. <i>Obesity Reviews</i> , 2024, 25, .	7.5	4
27	Rare variant contribution to the heritability of coronary artery disease. <i>Nature Communications</i> , 2024, 15, .	13.7	9
28	Expanding drug targets for 112 chronic diseases using a machine learning-assisted genetic priority score. <i>Nature Communications</i> , 2024, 15, .	13.7	7
29	Ensemble and consensus approaches to prediction of recessive inheritance for missense variants in human disease. <i>Cell Reports Methods</i> , 2024, 4, 100914.	3.2	6
30	Cannabis Use and CKD: Epidemiological Associations and Mendelian Randomization. <i>Kidney Medicine</i> , 2023, 5, 100582.	2.7	5
31	Machine learning-based marker for coronary artery disease: derivation and validation in two longitudinal cohorts. <i>Lancet, The</i> , 2023, 401, 215-225.	62.3	133
32	The Association of Alcohol Consumption with Glaucoma and Related Traits. <i>Ophthalmology Glaucoma</i> , 2023, 6, 366-379.	2.4	38
33	Genetic Associations Between Smoking- and Glaucoma-Related Traits. <i>Translational Vision Science and Technology</i> , 2023, 12, 20.	2.2	8
34	Clinical Trial Design for Triglyceride-Rich Lipoprotein-Lowering Therapies. <i>Journal of the American College of Cardiology</i> , 2023, 81, 1646-1658.	2.3	29
35	Causal effect of adiposity on the risk of 19 gastrointestinal diseases: a Mendelian randomization study. <i>Obesity</i> , 2023, 31, 1436-1444.	4.0	31
36	Machine Learning Identifies Plasma Metabolites Associated With Heart Failure in Underrepresented Populations With the TTR V122I Variant. <i>Journal of the American Heart Association</i> , 2023, 12, .	4.0	2

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37	A machine learning model identifies patients in need of autoimmune disease testing using electronic health records. <i>Nature Communications</i> , 2023, 14, .	13.7	25
38	Cholesterol Contributes to Risk, Severity, and Machine Learning-Driven Diagnosis of Lyme Disease. <i>Clinical Infectious Diseases</i> , 2023, 77, 839-847.	5.2	8
39	Polygenic prediction of preeclampsia and gestational hypertension. <i>Nature Medicine</i> , 2023, 29, 1540-1549.	33.0	101
40	Genome-wide association study of thoracic aortic aneurysm and dissection in the Million Veteran Program. <i>Nature Genetics</i> , 2023, 55, 1106-1115.	25.2	53
41	An atlas of associations between 14 micronutrients and 22 cancer outcomes: Mendelian randomization analyses. <i>BMC Medicine</i> , 2023, 21, .	7.1	35
42	Prioritization of therapeutic targets for dyslipidemia using integrative multi-omics and multi-trait analysis. <i>Cell Reports Medicine</i> , 2023, 4, 101112.	6.6	20
43	Severe hypertriglyceridemia: Existing and emerging therapies. , 2023, 251, 108544.		31
44	Whole-genome sequencing uncovers two loci for coronary artery calcification and identifies ARSE as a regulator of vascular calcification. <i>Nature Cardiovascular Research</i> , 2023, 2, 1159-1172.	8.4	17
45	Whole-Genome Sequencing Association Analyses of Stroke and Its Subtypes in Ancestrally Diverse Populations From Trans-Omics for Precision Medicine Project. <i>Stroke</i> , 2022, 53, 875-885.	6.0	33
46	Overcoming constraints on the detection of recessive selection in human genes from population frequency data. <i>American Journal of Human Genetics</i> , 2022, 109, 33-49.	6.5	18
47	Population-Based Penetrance of Deleterious Clinical Variants. <i>JAMA - Journal of the American Medical Association</i> , 2022, 327, 350.	16.6	95
48	Coronary Risk Estimation Based on Clinical Data in Electronic Health Records. <i>Journal of the American College of Cardiology</i> , 2022, 79, 1155-1166.	2.3	40
49	Whole-genome sequencing reveals host factors underlying critical COVID-19. <i>Nature</i> , 2022, 607, 97-103.	37.9	298
50	Genetic and phenotypic profiling of supranormal ejection fraction reveals decreased survival and underdiagnosed heart failure. <i>European Journal of Heart Failure</i> , 2022, 24, 2118-2127.	7.4	41
51	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential. <i>Science Advances</i> , 2022, 8, .	10.9	73
52	The Association between Serum Lipids and Intraocular Pressure in 2 Large United Kingdom Cohorts. <i>Ophthalmology</i> , 2022, 129, 986-996.	7.8	33
53	Statin Use in Relation to Intraocular Pressure, Glaucoma, and Ocular Coherence Tomography Parameters in the UK Biobank. , 2022, 63, 31.		10
54	Genome-Wide Epistatic Interaction between DEF1B and APOL1 High-Risk Genotypes for Chronic Kidney Disease. <i>Clinical Journal of the American Society of Nephrology: CJASN</i> , 2022, 17, 1522-1525.	4.2	6

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55	A tissue-level phenome-wide network map of colocalized genes and phenotypes in the UK Biobank. <i>Communications Biology</i> , 2022, 5, .	4.4	3
56	Large-scale genome-wide association study of coronary artery disease in genetically diverse populations. <i>Nature Medicine</i> , 2022, 28, 1679-1692.	33.0	302
57	Cross-Ancestry Investigation of Venous Thromboembolism Genomic Predictors. <i>Circulation</i> , 2022, 146, 1225-1242.	18.1	87
58	A framework for detecting noncoding rare-variant associations of large-scale whole-genome sequencing studies. <i>Nature Methods</i> , 2022, 19, 1599-1611.	24.6	99
59	Genome-wide association and multi-trait analyses characterize the common genetic architecture of heart failure. <i>Nature Communications</i> , 2022, 13, .	13.7	129
60	Transethnic Transferability of a Genome-Wide Polygenic Score for Coronary Artery Disease. <i>Circulation Genomic and Precision Medicine</i> , 2021, 14, .	2.9	37
61	A genotype-first approach to exploring Mendelian cardiovascular traits with clear external manifestations. <i>Genetics in Medicine</i> , 2021, 23, 94-102.	4.2	38
62	Intraocular Pressure, Glaucoma, and Dietary Caffeine Consumption. <i>Ophthalmology</i> , 2021, 128, 866-876.	7.8	71
63	Exploiting the GTEx resources to decipher the mechanisms at GWAS loci. <i>Genome Biology</i> , 2021, 22, .	8.1	266
64	An integrative multiomic network model links lipid metabolism to glucose regulation in coronary artery disease. <i>Nature Communications</i> , 2021, 12, .	13.7	46
65	Exome-wide evaluation of rare coding variants using electronic health records identifies new gene-phenotype associations. <i>Nature Medicine</i> , 2021, 27, 66-72.	33.0	62
66	Probing the aggregated effects of purifying selection per individual on 1,380 medical phenotypes in the UK Biobank. <i>PLoS Genetics</i> , 2021, 17, e1009337.	3.2	4
67	Genome-wide polygenic risk score for retinopathy of type 2 diabetes. <i>Human Molecular Genetics</i> , 2021, 30, 952-960.	2.9	24
68	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. <i>Nature Communications</i> , 2021, 12, .	13.7	24
69	Genetic pleiotropy of ERCC6 loss-of-function and deleterious missense variants links retinal dystrophy, arrhythmia, and immunodeficiency in diverse ancestries. <i>Human Mutation</i> , 2021, 42, 969-977.	4.5	3
70	Non-invasive ventilation versus mechanical ventilation in hypoxemic patients with COVID-19. <i>Infection</i> , 2021, 49, 989-997.	2.9	23
71	Mapping the human genetic architecture of COVID-19. <i>Nature</i> , 2021, 600, 472-477.	37.9	871
72	Whole-genome association analyses of sleep-disordered breathing phenotypes in the NHLBI TOPMed program. <i>Genome Medicine</i> , 2021, 13, .	9.6	28

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73	Derivation and Validation of Genome-Wide Polygenic Score for Ischemic Heart Failure. <i>Journal of the American Heart Association</i> , 2021, 10, .	4.0	9
74	SARS-CoV-2 susceptibility and COVID-19 disease severity are associated with genetic variants affecting gene expression in a variety of tissues. <i>Cell Reports</i> , 2021, 37, 110020.	6.3	37
75	Tissue-specific genetic features inform prediction of drug side effects in clinical trials. <i>Science Advances</i> , 2020, 6, .	10.9	58
76	Limitations of Contemporary Guidelines for Managing Patients at High Genetic Risk of Coronary Artery Disease. <i>Journal of the American College of Cardiology</i> , 2020, 75, 2769-2780.	2.3	119
77	Derivation and validation of genome-wide polygenic score for urinary tract stone diagnosis. <i>Kidney International</i> , 2020, 98, 1323-1330.	5.3	18
78	Minority-centric meta-analyses of blood lipid levels identify novel loci in the Population Architecture using Genomics and Epidemiology (PAGE) study. <i>PLoS Genetics</i> , 2020, 16, e1008684.	3.2	32
79	De novo mutations across 1,465 diverse genomes reveal mutational insights and reductions in the Amish founder population. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 2560-2569.	7.5	105
80	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. <i>International Journal of Medical Informatics</i> , 2019, 129, 334-341.	3.3	56
81	HOPS: a quantitative score reveals pervasive horizontal pleiotropy in human genetic variation is driven by extreme polygenicity of human traits and diseases. <i>Genome Biology</i> , 2019, 20, .	8.1	70
82	Whole Genome Sequencing Identifies CRISPLD2 as a Lung Function Gene in Children With Asthma. <i>Chest</i> , 2019, 156, 1068-1079.	1.0	6
83	Genetic analyses of diverse populations improves discovery for complex traits. <i>Nature</i> , 2019, 570, 514-518.	37.9	973
84	Estimation of metabolic syndrome heritability in three large populations including full pedigree and genomic information. <i>Human Genetics</i> , 2019, 138, 739-748.	2.9	5
85	Association of the V122I Hereditary Transthyretin Amyloidosis Genetic Variant With Heart Failure Among Individuals of African or Hispanic/Latino Ancestry. <i>JAMA - Journal of the American Medical Association</i> , 2019, 322, 2191.	16.6	143
86	No causal effects of serum urate levels on the risk of chronic kidney disease: A Mendelian randomization study. <i>PLoS Medicine</i> , 2019, 16, e1002725.	8.1	126
87	Detection of widespread horizontal pleiotropy in causal relationships inferred from Mendelian randomization between complex traits and diseases. <i>Nature Genetics</i> , 2018, 50, 693-698.	25.2	7,419
88	Using Full Genomic Information to Predict Disease: Breaking Down the Barriers Between Complex and Mendelian Diseases. <i>Annual Review of Genomics and Human Genetics</i> , 2018, 19, 289-301.	6.7	13
89	Plasma biomarkers are associated with renal outcomes in individuals with APOL1 risk variants. <i>Kidney International</i> , 2018, 93, 1409-1416.	5.3	29
90	The Genetic Landscape of Diamond-Blackfan Anemia. <i>American Journal of Human Genetics</i> , 2018, 103, 930-947.	6.5	236

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91	Deep coverage whole genome sequences and plasma lipoprotein(a) in individuals of European and African ancestries. <i>Nature Communications</i> , 2018, 9, .	13.7	105
92	Deep-coverage whole genome sequences and blood lipids among 16,324 individuals. <i>Nature Communications</i> , 2018, 9, .	13.7	163
93	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated With Coronary Artery Disease. <i>Journal of the American College of Cardiology</i> , 2017, 69, 823-836.	2.3	243
94	Human knockouts and phenotypic analysis in a cohort with a high rate of consanguinity. <i>Nature</i> , 2017, 544, 235-239.	37.9	347
95	Loss of Cardioprotective Effects at the ADAMTS7 Locus as a Result of Gene-Smoking Interactions. <i>Circulation</i> , 2017, 135, 2336-2353.	18.1	59
96	Fifteen new risk loci for coronary artery disease highlight arterial-wall-specific mechanisms. <i>Nature Genetics</i> , 2017, 49, 1113-1119.	25.2	306
97	Association of Triglyceride-Related Genetic Variants With Mitral Annular Calcification. <i>Journal of the American College of Cardiology</i> , 2017, 69, 2941-2948.	2.3	31
98	What can we learn about lipoprotein metabolism and coronary heart disease from studying rare variants?. <i>Current Opinion in Lipidology</i> , 2016, 27, 99-104.	4.0	5
99	Coding Variation in ANGPTL4, LPL, and SVEP1 and the Risk of Coronary Disease. <i>New England Journal of Medicine</i> , 2016, 374, 1134-1144.	34.6	481
100	Insight into rheumatological cause and effect through the use of Mendelian randomization. <i>Nature Reviews Rheumatology</i> , 2016, 12, 486-496.	25.5	55
101	Analysis of protein-coding genetic variation in 60,706 humans. <i>Nature</i> , 2016, 536, 285-291.	37.9	9,849
102	No Association of Coronary Artery Disease with X-Chromosomal Variants in Comprehensive International Meta-Analysis. <i>Scientific Reports</i> , 2016, 6, .	3.4	30
103	Systematic Functional Dissection of Common Genetic Variation Affecting Red Blood Cell Traits. <i>Cell</i> , 2016, 165, 1530-1545.	33.7	350
104	Rare variant in scavenger receptor BI raises HDL cholesterol and increases risk of coronary heart disease. <i>Science</i> , 2016, 351, 1166-1171.	36.2	506
105	Whole-exome sequencing of over 4100 men of African ancestry and prostate cancer risk. <i>Human Molecular Genetics</i> , 2016, 25, 371-381.	2.9	28
106	Dominance of Deleterious Alleles Controls the Response to a Population Bottleneck. <i>PLoS Genetics</i> , 2015, 11, e1005436.	3.2	90
107	Disproportionate Contributions of Select Genomic Compartments and Cell Types to Genetic Risk for Coronary Artery Disease. <i>PLoS Genetics</i> , 2015, 11, e1005622.	3.2	85
108	No evidence that selection has been less effective at removing deleterious mutations in Europeans than in Africans. <i>Nature Genetics</i> , 2015, 47, 126-131.	25.2	221

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109	Myocardial Infarction-associated SNP at 6p24 Interferes With MEF2 Binding and Associates With PHACTR1 Expression Levels in Human Coronary Arteries. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2015, 35, 1472-1479.	6.0	87
110	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. <i>American Journal of Human Genetics</i> , 2015, 97, 576-592.	6.5	1,332
111	Searching for missing heritability: Designing rare variant association studies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, .	7.5	622
112	Association of Low-Density Lipoprotein Cholesterol-related Genetic Variants With Aortic Valve Calcium and Incident Aortic Stenosis. <i>JAMA - Journal of the American Medical Association</i> , 2014, 312, 1764.	16.6	217
113	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. <i>American Journal of Human Genetics</i> , 2014, 94, 233-245.	6.5	205
114	Inactivating Mutations in NPC1L1 and Protection from Coronary Heart Disease. <i>New England Journal of Medicine</i> , 2014, 371, 2072-2082.	34.6	405
115	Loss-of-Function Mutations in APOC3, Triglycerides, and Coronary Disease. <i>New England Journal of Medicine</i> , 2014, 371, 22-31.	34.6	1,054
116	Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction. <i>Nature</i> , 2014, 518, 102-106.	37.9	623
117	Discovery and refinement of loci associated with lipid levels. <i>Nature Genetics</i> , 2013, 45, 1274-1283.	25.2	2,993
118	Common variants associated with plasma triglycerides and risk for coronary artery disease. <i>Nature Genetics</i> , 2013, 45, 1345-1352.	25.2	833
119	Exome sequencing and complex disease: practical aspects of rare variant association studies. <i>Human Molecular Genetics</i> , 2012, 21, R1-R9.	2.9	115
120	Advances in genetics show the need for extending screening strategies for autosomal dominant hypercholesterolaemia. <i>European Heart Journal</i> , 2012, 33, 1360-1366.	2.2	84
121	Plasma HDL cholesterol and risk of myocardial infarction: a mendelian randomisation study. <i>Lancet</i> , The, 2012, 380, 572-580.	62.3	2,112
122	Bayesian inference analyses of the polygenic architecture of rheumatoid arthritis. <i>Nature Genetics</i> , 2012, 44, 483-489.	25.2	412
123	A High-Coverage Genome Sequence from an Archaic Denisovan Individual. <i>Science</i> , 2012, 338, 222-226.	36.2	1,927
124	Evolution and Functional Impact of Rare Coding Variation from Deep Sequencing of Human Exomes. <i>Science</i> , 2012, 337, 64-69.	36.2	1,620
125	Large-scale association analysis identifies new risk loci for coronary artery disease. <i>Nature Genetics</i> , 2012, 45, 25-33.	25.2	1,557
126	Large-scale association analysis identifies 13 new susceptibility loci for coronary artery disease. <i>Nature Genetics</i> , 2011, 43, 333-338.	25.2	1,812

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127	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.	8.1	81
128	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.	3.8	7
129	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.	6.2	35
130	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.	2.3	86
131	Exome Sequencing, ANGPTL3 Mutations, and Familial Combined Hypolipidemia. New England Journal of Medicine, 2010, 363, 2220-2227.	34.6	717
132	Genetic Variation at the Proprotein Convertase Subtilisin/Kexin Type 5 Gene Modulates High-Density Lipoprotein Cholesterol Levels. Circulation: Cardiovascular Genetics, 2009, 2, 467-475.	3.8	33
133	Genome-wide association of early-onset myocardial infarction with single nucleotide polymorphisms and copy number variants. Nature Genetics, 2009, 41, 334-341.	25.2	1,024
134	K45R variant of squalene synthase increases total cholesterol levels in two study samples from a French Canadian population. Human Mutation, 2008, 29, 689-694.	4.5	5
135	Phenome-wide Mendelian randomization study of plasma triglyceride levels and 2600 disease traits. ELife, 0, 12, .	1.6	5
136	Pyruvate and related energetic metabolites modulate resilience against high genetic risk for glaucoma. ELife, 0, 14, .	1.6	6
137	Pyruvate and related energetic metabolites modulate resilience against high genetic risk for glaucoma. ELife, 0, 14, .	1.6	0
138	Gene therapy and genome editing for lipoprotein disorders. European Heart Journal, 0, 46, 3420-3433.	2.2	11
139	Development of a genetic priority score to predict drug side effects using human genetic evidence. Nature Communications, 0, 16, .	13.7	1
140	Genetic evidence informs the direction of therapeutic modulation in drug development. , 0, 2, .		2
141	Genomics of drug target prioritization for complex diseases. Nature Reviews Genetics, 0, , .	47.0	1
142	Genomic and transcriptomic analyses of aortic stenosis enhance therapeutic target discovery and disease prediction. Nature Genetics, 0, 58, 57-66.	25.2	1