

# Honghuang Lin

## List of Publications by Year in descending order

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Version: 2024-02-01

173  
papers

13,689  
citations

36271

51  
h-index

27389

106  
g-index

204  
all docs

204  
docs citations

204  
times ranked

23688  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic meta-analysis of diagnosed Alzheimer's disease identifies new risk loci and implicates A $\beta$ , tau, immunity and lipid processing. <i>Nature Genetics</i> , 2019, 51, 414-430.	9.4	1,962
2	Rare coding variants in PLCG2, ABI3, and TREM2 implicate microglial-mediated innate immunity in Alzheimer's disease. <i>Nature Genetics</i> , 2017, 49, 1373-1384.	9.4	783
3	Multi-ethnic genome-wide association study for atrial fibrillation. <i>Nature Genetics</i> , 2018, 50, 1225-1233.	9.4	552
4	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017, 542, 186-190.	13.7	544
5	Meta-analysis identifies six new susceptibility loci for atrial fibrillation. <i>Nature Genetics</i> , 2012, 44, 670-675.	9.4	533
6	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. <i>Nature Communications</i> , 2020, 11, 163.	5.8	466
7	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. <i>Nature Communications</i> , 2016, 7, 10023.	5.8	412
8	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. <i>Nature Genetics</i> , 2016, 48, 1171-1184.	9.4	362
9	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. <i>American Journal of Human Genetics</i> , 2018, 103, 691-706.	2.6	326
10	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. <i>Nature Genetics</i> , 2018, 50, 26-41.	9.4	286
11	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. <i>Nature Genetics</i> , 2017, 49, 946-952.	9.4	279
12	PROFEAT: a web server for computing structural and physicochemical features of proteins and peptides from amino acid sequence. <i>Nucleic Acids Research</i> , 2006, 34, W32-W37.	6.5	270
13	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. <i>Nature Genetics</i> , 2016, 48, 1151-1161.	9.4	261
14	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. <i>Genome Biology</i> , 2016, 17, 255.	3.8	251
15	Atrial Fibrillation. <i>Circulation</i> , 2011, 124, 1982-1993.	1.6	225
16	Evaluation of MHC class I peptide binding prediction servers: Applications for vaccine research. <i>BMC Immunology</i> , 2008, 9, 8.	0.9	207
17	Genetic Predisposition, Clinical Risk Factor Burden, and Lifetime Risk of Atrial Fibrillation. <i>Circulation</i> , 2018, 137, 1027-1038.	1.6	196
18	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.	2.6	193

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19	Genetic architecture of subcortical brain structures in 38,851 individuals. <i>Nature Genetics</i> , 2019, 51, 1624-1636.	9.4	192
20	Whole exome sequencing study identifies novel rare and common Alzheimer's-Associated variants involved in immune response and transcriptional regulation. <i>Molecular Psychiatry</i> , 2020, 25, 1859-1875.	4.1	191
21	Evaluation of MHC-II peptide binding prediction servers: applications for vaccine research. <i>BMC Bioinformatics</i> , 2008, 9, S22.	1.2	187
22	Integrating Genetic, Transcriptional, and Functional Analyses to Identify 5 Novel Genes for Atrial Fibrillation. <i>Circulation</i> , 2014, 130, 1225-1235.	1.6	183
23	Association Between Titin Loss-of-Function Variants and Early-Onset Atrial Fibrillation. <i>JAMA - Journal of the American Medical Association</i> , 2018, 320, 2354.	3.8	144
24	Higher dietary anthocyanin and flavonol intakes are associated with anti-inflammatory effects in a population of US adults. <i>American Journal of Clinical Nutrition</i> , 2015, 102, 172-181.	2.2	143
25	Loci influencing blood pressure identified using a cardiovascular gene-centric array. <i>Human Molecular Genetics</i> , 2013, 22, 1663-1678.	1.4	141
26	Novel Genetic Markers Associate With Atrial Fibrillation Risk in Europeans and Japanese. <i>Journal of the American College of Cardiology</i> , 2014, 63, 1200-1210.	1.2	127
27	Short-Term Exposure to Air Pollution and Biomarkers of Oxidative Stress: The Framingham Heart Study. <i>Journal of the American Heart Association</i> , 2016, 5, .	1.6	109
28	Pleiotropic genes for metabolic syndrome and inflammation. <i>Molecular Genetics and Metabolism</i> , 2014, 112, 317-338.	0.5	107
29	Large-scale genome-wide analysis identifies genetic variants associated with cardiac structure and function. <i>Journal of Clinical Investigation</i> , 2017, 127, 1798-1812.	3.9	106
30	Plasma microRNAs are associated with atrial fibrillation and change after catheter ablation (the Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 30	0.3	101
31	ROBO4 variants predispose individuals to bicuspid aortic valve and thoracic aortic aneurysm. <i>Nature Genetics</i> , 2019, 51, 42-50.	9.4	101
32	Common genetic variation at the IL1RL1 locus regulates IL-33/ST2 signaling. <i>Journal of Clinical Investigation</i> , 2013, 123, 4208-4218.	3.9	101
33	Genetic Obesity and the Risk of Atrial Fibrillation. <i>Circulation</i> , 2017, 135, 741-754.	1.6	96
34	Deep learning enables genetic analysis of the human thoracic aorta. <i>Nature Genetics</i> , 2022, 54, 40-51.	9.4	90
35	Relations between circulating microRNAs and atrial fibrillation: Data from the Framingham Offspring Study. <i>Heart Rhythm</i> , 2014, 11, 663-669.	0.3	80
36	A support vector machines approach for virtual screening of active compounds of single and multiple mechanisms from large libraries at an improved hit-rate and enrichment factor. <i>Journal of Molecular Graphics and Modelling</i> , 2008, 26, 1276-1286.	1.3	76

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37	A Whole-Blood Transcriptome Meta-Analysis Identifies Gene Expression Signatures of Cigarette Smoking. <i>Human Molecular Genetics</i> , 2016, 25, ddw288.	1.4	76
38	Recent progresses in the application of machine learning approach for predicting protein functional class independent of sequence similarity. <i>Proteomics</i> , 2006, 6, 4023-4037.	1.3	72
39	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. <i>Nature Communications</i> , 2018, 9, 2904.	5.8	71
40	Support vector machines approach for predicting druggable proteins: recent progress in its exploration and investigation of its usefulness. <i>Drug Discovery Today</i> , 2007, 12, 304-313.	3.2	69
41	Efficacy of different protein descriptors in predicting protein functional families. <i>BMC Bioinformatics</i> , 2007, 8, 300.	1.2	66
42	TANTIGEN: a comprehensive database of tumor T cell antigens. <i>Cancer Immunology, Immunotherapy</i> , 2017, 66, 731-735.	2.0	66
43	PEARLS: A Program for Energetic Analysis of Receptor-Ligand System. <i>Journal of Chemical Information and Modeling</i> , 2006, 46, 445-450.	2.5	64
44	Assessment of the Relationship Between Genetic Determinants of Thyroid Function and Atrial Fibrillation. <i>JAMA Cardiology</i> , 2019, 4, 144.	3.0	64
45	Novel Mutation in <i>FLNC</i> (Filamin C) Causes Familial Restrictive Cardiomyopathy. <i>Circulation: Cardiovascular Genetics</i> , 2017, 10, .	5.1	62
46	Prediction of transporter family from protein sequence by support vector machine approach. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 62, 218-231.	1.5	61
47	Genetic correlations and genome-wide associations of cortical structure in general population samples of 22,824 adults. <i>Nature Communications</i> , 2020, 11, 4796.	5.8	61
48	Prediction of MHC-binding peptides of flexible lengths from sequence-derived structural and physicochemical properties. <i>Molecular Immunology</i> , 2007, 44, 866-877.	1.0	60
49	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. <i>Nature Communications</i> , 2020, 11, 2542.	5.8	59
50	Measures of Biologic Age in a Community Sample Predict Mortality and Age-Related Disease: The Framingham Offspring Study. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2018, 73, 757-762.	1.7	59
51	Computer prediction of drug resistance mutations in proteins. <i>Drug Discovery Today</i> , 2005, 10, 521-529.	3.2	58
52	Prediction of the functional class of metal-binding proteins from sequence derived physicochemical properties by support vector machine approach. <i>BMC Bioinformatics</i> , 2006, 7, S13.	1.2	58
53	Next Steps in Cardiovascular Disease Genomic Research—Sequencing, Epigenetics, and Transcriptomics. <i>Clinical Chemistry</i> , 2012, 58, 113-126.	1.5	55
54	Machine learning approaches for predicting compounds that interact with therapeutic and ADMET related proteins. <i>Journal of Pharmaceutical Sciences</i> , 2007, 96, 2838-2860.	1.6	54

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55	A Global Characterization and Identification of Multifunctional Enzymes. PLoS ONE, 2012, 7, e38979.	1.1	53
56	Gene expression and genetic variation in human atria. Heart Rhythm, 2014, 11, 266-271.	0.3	48
57	Methylome-wide Association Study of Atrial Fibrillation in Framingham Heart Study. Scientific Reports, 2017, 7, 40377.	1.6	48
58	Exome-chip meta-analysis identifies novel loci associated with cardiac conduction, including ADAMTS6. Genome Biology, 2018, 19, 87.	3.8	47
59	Genome-Wide Association Study of Cardiac Structure and Systolic Function in African Americans. Circulation: Cardiovascular Genetics, 2013, 6, 37-46.	5.1	46
60	MicroRNA Signature of Cigarette Smoking and Evidence for a Putative Causal Role of MicroRNAs in Smoking-Related Inflammation and Target Organ Damage. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	45
61	Fresh frozen plasma transfusion in acute variceal haemorrhage: Results from a multicentre cohort study. Liver International, 2021, 41, 1901-1908.	1.9	45
62	Proteomics Profiling and Risk of New-Onset Atrial Fibrillation: Framingham Heart Study. Journal of the American Heart Association, 2019, 8, e010976.	1.6	42
63	Integrative Omics Approach to Identifying Genes Associated With Atrial Fibrillation. Circulation Research, 2020, 126, 350-360.	2.0	41
64	Prediction of the functional class of lipid binding proteins from sequence-derived properties irrespective of sequence similarity. Journal of Lipid Research, 2006, 47, 824-831.	2.0	40
65	Association of exome sequences with plasma C-reactive protein levels in >9000 participants. Human Molecular Genetics, 2015, 24, 559-571.	1.4	36
66	Association of Habitual Physical Activity With Cardiovascular Disease Risk. Circulation Research, 2020, 127, 1253-1260.	2.0	36
67	Epigenetic Age and the Risk of Incident Atrial Fibrillation. Circulation, 2021, 144, 1899-1911.	1.6	35
68	Whole Exome Sequencing in Atrial Fibrillation. PLoS Genetics, 2016, 12, e1006284.	1.5	35
69	Genetic analysis of right heart structure and function in 40,000 people. Nature Genetics, 2022, 54, 792-803.	9.4	34
70	Shared genetic susceptibility of vascular-related biomarkers with ischemic and recurrent stroke. Neurology, 2016, 86, 351-359.	1.5	33
71	Diminished <i>PRRX1</i> Expression Is Associated With Increased Risk of Atrial Fibrillation and Shortening of the Cardiac Action Potential. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	33
72	Association of Methylation Signals With Incident Coronary Heart Disease in an Epigenome-Wide Assessment of Circulating Tumor Necrosis Factor $\pm$ . JAMA Cardiology, 2018, 3, 463.	3.0	33

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73	Dana-Farber repository for machine learning in immunology. <i>Journal of Immunological Methods</i> , 2011, 374, 18-25.	0.6	32
74	Genome-Wide Association Analysis of Plasma B $\beta$ -Type Natriuretic Peptide in Blacks. <i>Circulation: Cardiovascular Genetics</i> , 2015, 8, 122-130.	5.1	32
75	Protein Biomarkers and Risk of Atrial Fibrillation. <i>Circulation: Arrhythmia and Electrophysiology</i> , 2020, 13, e007607.	2.1	31
76	Discovery of novel heart rate-associated loci using the Exome Chip. <i>Human Molecular Genetics</i> , 2017, 26, 2346-2363.	1.4	29
77	Genome sequencing unveils a regulatory landscape of platelet reactivity. <i>Nature Communications</i> , 2021, 12, 3626.	5.8	29
78	Prediction of factor Xa inhibitors by machine learning methods. <i>Journal of Molecular Graphics and Modelling</i> , 2007, 26, 505-518.	1.3	28
79	Whole blood gene expression and white matter Hyperintensities. <i>Molecular Neurodegeneration</i> , 2017, 12, 67.	4.4	28
80	MHC-BPS: MHC-binder prediction server for identifying peptides of flexible lengths from sequence-derived physicochemical properties. <i>Immunogenetics</i> , 2006, 58, 607-613.	1.2	27
81	Metabolomic Profiling in Relation to New-Onset Atrial Fibrillation (from the Framingham Heart) <a href="#">Tj ETQq1 1 0.784314.rgBT /Overlock I</a>	0.7	27
82	ExomeChip-Wide Analysis of 95 626 Individuals Identifies 10 Novel Loci Associated With QT and JT Intervals. <i>Circulation Genomic and Precision Medicine</i> , 2018, 11, e001758.	1.6	27
83	Recent exposure to particle radioactivity and biomarkers of oxidative stress and inflammation: The Framingham Heart Study. <i>Environment International</i> , 2018, 121, 1210-1216.	4.8	27
84	Common Coding Variants in <i>SCN10A</i> Are Associated With the Nav1.8 Late Current and Cardiac Conduction. <i>Circulation Genomic and Precision Medicine</i> , 2018, 11, e001663.	1.6	26
85	Quality control and integration of genotypes from two calling pipelines for whole genome sequence data in the Alzheimer's disease sequencing project. <i>Genomics</i> , 2019, 111, 808-818.	1.3	26
86	Aptamer-Based Proteomic Platform Identifies Novel Protein Predictors of Incident Heart Failure and Echocardiographic Traits. <i>Circulation: Heart Failure</i> , 2020, 13, e006749.	1.6	26
87	Derivation of Stable Microarray Cancer-Differentiating Signatures Using Consensus Scoring of Multiple Random Sampling and Gene-Ranking Consistency Evaluation. <i>Cancer Research</i> , 2007, 67, 9996-10003.	0.4	25
88	Assessment of the Mid-Life Demographic and Lifestyle Risk Factors of Dementia Using Data from the Framingham Heart Study Offspring Cohort. <i>Journal of Alzheimer's Disease</i> , 2018, 63, 1119-1127.	1.2	25
89	Whole blood gene expression and interleukin-6 levels. <i>Genomics</i> , 2014, 104, 490-495.	1.3	24
90	Targeted sequencing in candidate genes for atrial fibrillation: The Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Targeted Sequencing Study. <i>Heart Rhythm</i> , 2014, 11, 452-457.	0.3	24

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91	Genome-Wide Meta-Analyses of Plasma Renin Activity and Concentration Reveal Association With the Kininogen 1 and Prekallikrein Genes. <i>Circulation: Cardiovascular Genetics</i> , 2015, 8, 131-140.	5.1	24
92	Gain-of-function mutations in GATA6 lead to atrial fibrillation. <i>Heart Rhythm</i> , 2017, 14, 284-291.	0.3	24
93	Whole Blood Gene Expression and Atrial Fibrillation: The Framingham Heart Study. <i>PLoS ONE</i> , 2014, 9, e96794.	1.1	23
94	Gene expression markers of age-related inflammation in two human cohorts. <i>Experimental Gerontology</i> , 2015, 70, 37-45.	1.2	23
95	Genetic invalidation of Lp-PLA2 as a therapeutic target: Large-scale study of five functional Lp-PLA2-lowering alleles. <i>European Journal of Preventive Cardiology</i> , 2017, 24, 492-504.	0.8	22
96	Variants in angiotensin-converting enzyme 2 ( <i>ANGPT2</i> ) contribute to variation in nocturnal oxyhaemoglobin saturation level. <i>Human Molecular Genetics</i> , 2016, 25, ddw324.	1.4	21
97	Homology-Free Prediction of Functional Class of Proteins and Peptides by Support Vector Machines. <i>Current Protein and Peptide Science</i> , 2008, 9, 70-95.	0.7	19
98	Common and Rare Coding Genetic Variation Underlying the Electrocardiographic PR Interval. <i>Circulation Genomic and Precision Medicine</i> , 2018, 11, e002037.	1.6	19
99	Whole Blood Gene Expression Associated With Clinical Biological Age. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2019, 74, 81-88.	1.7	19
100	Whole blood microRNA expression associated with stroke: Results from the Framingham Heart Study. <i>PLoS ONE</i> , 2019, 14, e0219261.	1.1	19
101	An Artificial Intelligence-Assisted Method for Dementia Detection Using Images from the Clock Drawing Test. <i>Journal of Alzheimer's Disease</i> , 2021, 83, 581-589.	1.2	19
102	Identification of digital voice biomarkers for cognitive health. <i>Exploration of Medicine</i> , 2020, 1, 406-417.	1.5	19
103	Sequencing of 2 Subclinical Atherosclerosis Candidate Regions in 3669 Individuals. <i>Circulation: Cardiovascular Genetics</i> , 2014, 7, 359-364.	5.1	18
104	Strategies to Design and Analyze Targeted Sequencing Data. <i>Circulation: Cardiovascular Genetics</i> , 2014, 7, 335-343.	5.1	18
105	Integrated Multiomics Approach to Identify Genetic Underpinnings of Heart Failure and Its Echocardiographic Precursors. <i>Circulation Genomic and Precision Medicine</i> , 2019, 12, e002489.	1.6	18
106	Validation of Polygenic Scores for QT Interval in Clinical Populations. <i>Circulation: Cardiovascular Genetics</i> , 2017, 10, .	5.1	17
107	Genetic Determinants of Electrocardiographic P-Wave Duration and Relation to Atrial Fibrillation. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, 387-395.	1.6	16
108	FAM13A Represses AMPK Activity and Regulates Hepatic Glucose and Lipid Metabolism. <i>IScience</i> , 2020, 23, 100928.	1.9	16

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109	Association Between the Digital Clock Drawing Test and Neuropsychological Test Performance: Large Community-Based Prospective Cohort (Framingham Heart Study). <i>Journal of Medical Internet Research</i> , 2021, 23, e27407.	2.1	16
110	Comparison of On-Site Versus Remote Mobile Device Support in the Framingham Heart Study Using the Health eHeart Study for Digital Follow-up: Randomized Pilot Study Set Within an Observational Study Design. <i>JMIR MHealth and UHealth</i> , 2019, 7, e13238.	1.8	16
111	Gene-gene Interaction Analyses for Atrial Fibrillation. <i>Scientific Reports</i> , 2016, 6, 35371.	1.6	15
112	Prefrontal cortex eQTLs/mQTLs enriched in genetic variants associated with alcohol use disorder and other diseases. <i>Epigenomics</i> , 2020, 12, 789-800.	1.0	15
113	MoViES: molecular vibrations evaluation server for analysis of fluctuational dynamics of proteins and nucleic acids. <i>Nucleic Acids Research</i> , 2004, 32, W679-W685.	6.5	14
114	Mutation of a common amino acid in NKX2.5 results in dilated cardiomyopathy in two large families. <i>BMC Medical Genetics</i> , 2016, 17, 83.	2.1	14
115	Epigenetic Analyses of Human Left Atrial Tissue Identifies Gene Networks Underlying Atrial Fibrillation. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, e003085.	1.6	14
116	Novel Risk Modeling Approach of Atrial Fibrillation With Restricted Mean Survival Times. <i>Circulation: Cardiovascular Quality and Outcomes</i> , 2020, 13, e005918.	0.9	14
117	Proteomic Signatures of Lifestyle Risk Factors for Cardiovascular Disease: A Cross-sectional Analysis of the Plasma Proteome in the Framingham Heart Study. <i>Journal of the American Heart Association</i> , 2021, 10, e018020.	1.6	14
118	Prediction of functional class of novel plant proteins by a statistical learning method. <i>New Phytologist</i> , 2005, 168, 109-121.	3.5	13
119	Circuit Performance Classification With Active Learning Guided Sampling for Support Vector Machines. <i>IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems</i> , 2015, 34, 1467-1480.	1.9	13
120	Cross-sectional relations of whole blood miRNA expression levels and hand grip strength in a community sample. <i>Aging Cell</i> , 2017, 16, 888-894.	3.0	13
121	Adherence of Mobile App-Based Surveys and Comparison With Traditional Surveys: eCohort Study. <i>Journal of Medical Internet Research</i> , 2021, 23, e24773.	2.1	13
122	A comparison of whole genome sequencing with exome sequencing for family-based association studies. <i>BMC Proceedings</i> , 2014, 8, S38.	1.8	12
123	Sequencing of <i>SCN5A</i> Identifies Rare and Common Variants Associated With Cardiac Conduction: Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium. <i>Circulation: Cardiovascular Genetics</i> , 2014, 7, 365-373.	5.1	12
124	Using data science to diagnose and characterize heterogeneity of Alzheimer's disease. <i>Alzheimer's and Dementia: Translational Research and Clinical Interventions</i> , 2019, 5, 264-271.	1.8	12
125	New biomarkers from multiomics approaches: improving risk prediction of atrial fibrillation. <i>Cardiovascular Research</i> , 2021, 117, 1632-1644.	1.8	12
126	Transcriptome-wide association study of inflammatory biologic age. <i>Aging</i> , 2017, 9, 2288-2301.	1.4	12



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127	Genome-Wide Association Study for Endothelial Growth Factors. <i>Circulation: Cardiovascular Genetics</i> , 2015, 8, 389-397.	5.1	11
128	Whole exome sequencing in the Framingham Heart Study identifies rare variation in <i>HYAL2</i> that influences platelet aggregation. <i>Thrombosis and Haemostasis</i> , 2017, 117, 1083-1092.	1.8	11
129	Epigenome-Wide Association Study of Soluble Tumor Necrosis Factor Receptor 2 Levels in the Framingham Heart Study. <i>Frontiers in Pharmacology</i> , 2018, 9, 207.	1.6	11
130	Healthy diet is associated with gene expression in blood: the Framingham Heart Study. <i>American Journal of Clinical Nutrition</i> , 2019, 110, 742-749.	2.2	11
131	The genomics of heart failure: design and rationale of the HERMES consortium. <i>ESC Heart Failure</i> , 2021, 8, 5531-5541.	1.4	11
132	Genetic Reduction in Left Ventricular Protein Kinase C $\beta$ and Adverse Ventricular Remodeling in Human Subjects. <i>Circulation Genomic and Precision Medicine</i> , 2018, 11, e001901.	1.6	10
133	Relations between plasma microRNAs, echocardiographic markers of atrial remodeling, and atrial fibrillation: Data from the Framingham Offspring study. <i>PLoS ONE</i> , 2020, 15, e0236960.	1.1	10
134	Automatic synchronization and distribution of biological databases and software over low-bandwidth networks among developing countries. <i>Bioinformatics</i> , 2008, 24, 299-301.	1.8	9
135	Association of Habitual Physical Activity With Home Blood Pressure in the Electronic Framingham Heart Study (eFHS): Cross-sectional Study. <i>Journal of Medical Internet Research</i> , 2021, 23, e25591.	2.1	9
136	EDEM3 Modulates Plasma Triglyceride Level through Its Regulation of LRP1 Expression. <i>IScience</i> , 2020, 23, 100973.	1.9	8
137	Advances in Exploration of Machine Learning Methods for Predicting Functional Class and Interaction Profiles of Proteins and Peptides Irrespective of Sequence Homology. <i>Current Bioinformatics</i> , 2007, 2, 95-112.	0.7	7
138	A Low-Frequency Variant in <i>MAPK14</i> Provides Mechanistic Evidence of a Link With Myeloperoxidase: A Prognostic Cardiovascular Risk Marker. <i>Journal of the American Heart Association</i> , 2014, 3, .	1.6	7
139	Low oxygen saturation during sleep reduces <i>CD1D</i> and <i>RAB20</i> expressions that are reversed by CPAP therapy. <i>EBioMedicine</i> , 2020, 56, 102803.	2.7	7
140	Rare Coding Variants Associated With Electrocardiographic Intervals Identify Monogenic Arrhythmia Susceptibility Genes: A Multi-Ancestry Analysis. <i>Circulation Genomic and Precision Medicine</i> , 2021, 14, e003300.	1.6	7
141	Identifying Blood Biomarkers for Dementia Using Machine Learning Methods in the Framingham Heart Study. <i>Cells</i> , 2022, 11, 1506.	1.8	7
142	Design and Preliminary Findings of Adherence to the Self-Testing for Our Protection From COVID-19 (STOP COVID-19) Risk-Based Testing Protocol: Prospective Digital Study. <i>JMIR Formative Research</i> , 2022, 6, e38113.	0.7	7
143	Familial clustering of hypertensive target organ damage in the community. <i>Journal of Hypertension</i> , 2018, 36, 1086-1093.	0.3	6
144	Tissue-specific Network Analysis of Genetic Variants Associated with Coronary Artery Disease. <i>Scientific Reports</i> , 2018, 8, 11492.	1.6	6

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145	Network Analysis of Depression-Related Transcriptomic Profiles. <i>NeuroMolecular Medicine</i> , 2019, 21, 143-149.	1.8	6
146	P-wave signal-averaged electrocardiography: Reference values, clinical correlates, and heritability in the Framingham Heart Study. <i>Heart Rhythm</i> , 2021, 18, 1500-1507.	0.3	6
147	Functional analysis of HapMap SNPs. <i>Gene</i> , 2012, 511, 358-363.	1.0	5
148	Rare genetic variant analysis on blood pressure in related samples. <i>BMC Proceedings</i> , 2014, 8, S35.	1.8	5
149	Relevance vector and feature machine for statistical analog circuit characterization and built-in self-test optimization. , 2016, , .		5
150	Association of Genetic Variation in Coronary Artery Disease-Related Loci With the Risk of Heart Failure With Preserved Versus Reduced Ejection Fraction. <i>Circulation</i> , 2018, 137, 1290-1292.	1.6	5
151	Exploring the Hierarchical Influence of Cognitive Functions for Alzheimer Disease: The Framingham Heart Study. <i>Journal of Medical Internet Research</i> , 2020, 22, e15376.	2.1	5
152	Neck Circumference and Risk of Incident Atrial Fibrillation in the Framingham Heart Study. <i>Journal of the American Heart Association</i> , 2022, 11, e022340.	1.6	5
153	Lymphocyte activation gene-3-associated protein networks are associated with HDL-cholesterol and mortality in the Trans-omics for Precision Medicine program. <i>Communications Biology</i> , 2022, 5, 362.	2.0	5
154	Transcriptomic Heterogeneity of Alzheimer's Disease Associated with Lipid Genetic Risk. <i>NeuroMolecular Medicine</i> , 2020, 22, 534-541.	1.8	4
155	Human Leukocyte Antigen Typing Using a Knowledge Base Coupled with a High-Throughput Oligonucleotide Probe Array Analysis. <i>Frontiers in Immunology</i> , 2014, 5, 597.	2.2	3
156	Relations Between BMI Trajectories and Habitual Physical Activity Measured by a Smartwatch in the Electronic Cohort of the Framingham Heart Study: Cohort Study. <i>JMIR Cardio</i> , 2022, 6, e32348.	0.7	3
157	Associations Between the Digital Clock Drawing Test and Brain Volume: Large Community-Based Prospective Cohort (Framingham Heart Study). <i>Journal of Medical Internet Research</i> , 2022, 24, e34513.	2.1	3
158	Comparing Bowtie and BWA to Align Short Reads from a RNA-Seq Experiment. <i>Advances in Intelligent and Soft Computing</i> , 2012, , 197-207.	0.2	2
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