

Honghuang Lin

List of Publications by Year in Descending Order

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Version: 2024-04-27

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

174
papers

8,588
citations

45
h-index

90
g-index

204
ext. papers

11,575
ext. citations

9.6
avg, IF

4.98
L-index

#	Paper	IF	Citations
174	Neck Circumference and Risk of Incident Atrial Fibrillation in the Framingham Heart Study.. <i>Journal of the American Heart Association</i> , 2022 , 11, e022340	6	0
173	Comparison of Daily Routines Between Middle-aged and Older Participants With and Those Without Diabetes in the Electronic Framingham Heart Study: Cohort Study.. <i>JMIR Diabetes</i> , 2022 , 7, e29107	2.7	0
172	Comparison of Rapid Antigen Tests' Performance between Delta (B.1.61.7; AY.X) and Omicron (B.1.1.529; BA1) Variants of SARS-CoV-2: Secondary Analysis from a Serial Home Self-Testing Study. 2022 ,		2
171	The association between social network index, atrial fibrillation, and mortality in the Framingham Heart Study.. <i>Scientific Reports</i> , 2022 , 12, 3958	4.9	0
170	Association of Mass Distribution of Rapid Antigen Tests and SARS-CoV-2 Prevalence: Results from NIH-CDC funded Say Yes! Covid Test program in Michigan. 2022 ,		1
169	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	3.1	1
168	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	7.6	
167	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	6.7	0
166	Deep learning enables genetic analysis of the human thoracic aorta. <i>Nature Genetics</i> , 2021 ,	36.3	6
165	Shared Genetic and Environmental Architecture of Cardiac Phenotypes Assessed via Echocardiography: The Framingham Heart Study. <i>Circulation Genomic and Precision Medicine</i> , 2021 , 14, e003244	5.2	0
164	Fresh frozen plasma transfusion in acute variceal haemorrhage: Results from a multicentre cohort study. <i>Liver International</i> , 2021 , 41, 1901-1908	7.9	12
163	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	7.6	5
162	Genome sequencing unveils a regulatory landscape of platelet reactivity. <i>Nature Communications</i> , 2021 , 12, 3626	17.4	6
161	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	7.6	1
160	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	6	3
159	Adherence of Mobile App-Based Surveys and Comparison With Traditional Surveys: eCohort Study. <i>Journal of Medical Internet Research</i> , 2021 , 23, e24773	7.6	3
158	New biomarkers from multiomics approaches: improving risk prediction of atrial fibrillation. <i>Cardiovascular Research</i> , 2021 , 117, 1632-1644	9.9	1

157	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	5.2	0
156	P-wave signal-averaged electrocardiography: Reference values, clinical correlates, and heritability in the Framingham Heart Study. <i>Heart Rhythm</i> , 2021 , 18, 1500-1507	6.7	0
155	The genomics of heart failure: design and rationale of the HERMES consortium. <i>ESC Heart Failure</i> , 2021 ,	3.7	1
154	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	4.3	8
153	Epigenetic Age and the Risk of Incident Atrial Fibrillation. <i>Circulation</i> , 2021 ,	16.7	2
152	Comparative trans-ethnic meta-analysis of whole exome sequencing variation for Alzheimer's disease (AD) in 18,402 individuals of the Alzheimer's Disease Sequencing Project (ADSP). <i>Alzheimer's and Dementia</i> , 2020 , 16, e041583	1.2	
151	Assessing whole genome sequencing variation for Alzheimer's disease in 4707 individuals from the Alzheimer's Disease Sequencing Project (ADSP). <i>Alzheimer's and Dementia</i> , 2020 , 16, e045548	1.2	
150	Frequency of familial Alzheimer's disease gene mutations within the Alzheimer Disease Sequencing Project (ADSP). <i>Alzheimer's and Dementia</i> , 2020 , 16, e046203	1.2	
149	Epigenetic Analyses of Human Left Atrial Tissue Identifies Gene Networks Underlying Atrial Fibrillation. <i>Circulation Genomic and Precision Medicine</i> , 2020 , 13, e003085	5.2	7
148	EDEM3 Modulates Plasma Triglyceride Level through Its Regulation of LRP1 Expression. <i>IScience</i> , 2020 , 23, 100973	6.1	4
147	Aptamer-Based Proteomic Platform Identifies Novel Protein Predictors of Incident Heart Failure and Echocardiographic Traits. <i>Circulation: Heart Failure</i> , 2020 , 13, e006749	7.6	8
146	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. <i>Nature Communications</i> , 2020 , 11, 2542	17.4	16
145	Prefrontal cortex eQTLs/mQTLs enriched in genetic variants associated with alcohol use disorder and other diseases. <i>Epigenomics</i> , 2020 , 12, 789-800	4.4	5
144	FAM13A Represses AMPK Activity and Regulates Hepatic Glucose and Lipid Metabolism. <i>IScience</i> , 2020 , 23, 100928	6.1	8
143	Protein Biomarkers and Risk of Atrial Fibrillation: The FHS. <i>Circulation: Arrhythmia and Electrophysiology</i> , 2020 , 13, e007607	6.4	12
142	Exploring the Hierarchical Influence of Cognitive Functions for Alzheimer Disease: The Framingham Heart Study. <i>Journal of Medical Internet Research</i> , 2020 , 22, e15376	7.6	2
141	Identification of digital voice biomarkers for cognitive health. <i>Exploration of Medicine</i> , 2020 , 1, 406-417	1.1	2
140	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. <i>Nature Communications</i> , 2020 , 11, 163	17.4	140

139	Integrative Omics Approach to Identifying Genes Associated With Atrial Fibrillation. <i>Circulation Research</i> , 2020 , 126, 350-360	15.7	21
138	Genetic correlations and genome-wide associations of cortical structure in general population samples of 22,824 adults. <i>Nature Communications</i> , 2020 , 11, 4796	17.4	16
137	Low oxygen saturation during sleep reduces CD1D and RAB20 expressions that are reversed by CPAP therapy. <i>EBioMedicine</i> , 2020 , 56, 102803	8.8	2
136	Transcriptomic Heterogeneity of Alzheimer's Disease Associated with Lipid Genetic Risk. <i>NeuroMolecular Medicine</i> , 2020 , 22, 534-541	4.6	0
135	Association of Habitual Physical Activity With Cardiovascular Disease Risk. <i>Circulation Research</i> , 2020 , 127, 1253-1260	15.7	7
134	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	3.7	3
133	Genetic Determinants of Electrocardiographic P-Wave Duration and Relation to Atrial Fibrillation. <i>Circulation Genomic and Precision Medicine</i> , 2020 , 13, 387-395	5.2	4
132	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	15.1	106
131	Novel Risk Modeling Approach of Atrial Fibrillation With Restricted Mean Survival Times: Application in the Framingham Heart Study Community-Based Cohort. <i>Circulation: Cardiovascular Quality and Outcomes</i> , 2020 , 13, e005918	5.8	9
130	Assessment of the Relationship Between Genetic Determinants of Thyroid Function and Atrial Fibrillation: A Mendelian Randomization Study. <i>JAMA Cardiology</i> , 2019 , 4, 144-152	16.2	36
129	Healthy diet is associated with gene expression in blood: the Framingham Heart Study. <i>American Journal of Clinical Nutrition</i> , 2019 , 110, 742-749	7	4
128	0021 Lower Oxygen Saturation During Sleep Is Associated With Reduced Expressions Of Cd1d And Rab20 That Is Potentially Reversed By CPAP Therapy. <i>Sleep</i> , 2019 , 42, A8-A9	1.1	
127	Proteomics Profiling and Risk of New-Onset Atrial Fibrillation: Framingham Heart Study. <i>Journal of the American Heart Association</i> , 2019 , 8, e010976	6	24
126	Network Analysis of Depression-Related Transcriptomic Profiles. <i>NeuroMolecular Medicine</i> , 2019 , 21, 143-149	4.6	3
125	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	4.3	10
124	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	6.4	13
123	Whole blood microRNA expression associated with stroke: Results from the Framingham Heart Study. <i>PLoS ONE</i> , 2019 , 14, e0219261	3.7	12
122	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	6	6

121	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	5.5	5
120	Sparse Relevance Kernel Machine-Based Performance Dependency Analysis of Analog and Mixed-Signal Circuits 2019 , 423-447		
119	Genetic meta-analysis of diagnosed Alzheimer's disease identifies new risk loci and implicates A β tau, immunity and lipid processing. <i>Nature Genetics</i> , 2019 , 51, 414-430	36.3	917
118	Integrated Multiomics Approach to Identify Genetic Underpinnings of Heart Failure and Its Echocardiographic Precursors: Framingham Heart Study. <i>Circulation Genomic and Precision Medicine</i> , 2019 , 12, e002489	5.2	12
117	Genetic architecture of subcortical brain structures in 38,851 individuals. <i>Nature Genetics</i> , 2019 , 51, 1624-1636	36.3	81
116	ROBO4 variants predispose individuals to bicuspid aortic valve and thoracic aortic aneurysm. <i>Nature Genetics</i> , 2019 , 51, 42-50	36.3	56
115	Association of Methylation Signals With Incident Coronary Heart Disease in an Epigenome-Wide Assessment of Circulating Tumor Necrosis Factor α <i>JAMA Cardiology</i> , 2018 , 3, 463-472	16.2	17
114	Familial clustering of hypertensive target organ damage in the community. <i>Journal of Hypertension</i> , 2018 , 36, 1086-1093	1.9	6
113	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	16.7	5
112	Tissue-specific Network Analysis of Genetic Variants Associated with Coronary Artery Disease. <i>Scientific Reports</i> , 2018 , 8, 11492	4.9	6
111	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	5.6	8
110	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. <i>Nature Communications</i> , 2018 , 9, 2904	17.4	39
109	Exome-chip meta-analysis identifies novel loci associated with cardiac conduction, including ADAMTS6. <i>Genome Biology</i> , 2018 , 19, 87	18.3	25
108	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	4.3	18
107	Multi-ethnic genome-wide association study for atrial fibrillation. <i>Nature Genetics</i> , 2018 , 50, 1225-1233	36.3	277
106	Genetic Reduction in Left Ventricular Protein Kinase C- β and Adverse Ventricular Remodeling in Human Subjects. <i>Circulation Genomic and Precision Medicine</i> , 2018 , 11, e001901	5.2	4
105	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	36.3	186
104	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	6.4	36

103	Genetic Predisposition, Clinical Risk Factor Burden, and Lifetime Risk of Atrial Fibrillation. <i>Circulation</i> , 2018 , 137, 1027-1038	16.7	133
102	Association Between Titin Loss-of-Function Variants and Early-Onset Atrial Fibrillation. <i>JAMA - Journal of the American Medical Association</i> , 2018 , 320, 2354-2364	27.4	75
101	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	5.2	14
100	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	11	151
99	Recent exposure to particle radioactivity and biomarkers of oxidative stress and inflammation: The Framingham Heart Study. <i>Environment International</i> , 2018 , 121, 1210-1216	12.9	21
98	Common and Rare Coding Genetic Variation Underlying the Electrocardiographic PR Interval. <i>Circulation Genomic and Precision Medicine</i> , 2018 , 11, e002037	5.2	11
97	Common Coding Variants in Are Associated With the Nav1.8 Late Current and Cardiac Conduction. <i>Circulation Genomic and Precision Medicine</i> , 2018 , 11, e001663	5.2	14
96	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017 , 542, 186-190	50.4	412
95	Methylome-wide Association Study of Atrial Fibrillation in Framingham Heart Study. <i>Scientific Reports</i> , 2017 , 7, 40377	4.9	33
94	TANTIGEN: a comprehensive database of tumor T cell antigens. <i>Cancer Immunology, Immunotherapy</i> , 2017 , 66, 731-735	7.4	37
93	Genetic invalidation of Lp-PLA as a therapeutic target: Large-scale study of five functional Lp-PLA-lowering alleles. <i>European Journal of Preventive Cardiology</i> , 2017 , 24, 492-504	3.9	16
92	Discovery of novel heart rate-associated loci using the Exome Chip. <i>Human Molecular Genetics</i> , 2017 , 26, 2346-2363	5.6	17
91	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. <i>Nature Genetics</i> , 2017 , 49, 946-952	36.3	176
90	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	9.9	12
89	Genetic Obesity and the Risk of Atrial Fibrillation: Causal Estimates from Mendelian Randomization. <i>Circulation</i> , 2017 , 135, 741-754	16.7	62
88	Diminished Expression Is Associated With Increased Risk of Atrial Fibrillation and Shortening of the Cardiac Action Potential. <i>Circulation: Cardiovascular Genetics</i> , 2017 , 10,		20
87	Validation of Polygenic Scores for QT Interval in Clinical Populations. <i>Circulation: Cardiovascular Genetics</i> , 2017 , 10,		8
86	MicroRNA Signature of Cigarette Smoking and Evidence for a Putative Causal Role of MicroRNAs in Smoking-Related Inflammation and Target Organ Damage. <i>Circulation: Cardiovascular Genetics</i> , 2017 , 10,		28

85	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	7	9
84	Whole blood gene expression and white matter Hyperintensities. <i>Molecular Neurodegeneration</i> , 2017 , 12, 67	19	4
83	Rare coding variants in <i>PLCG2</i> , <i>ABI3</i> , and <i>TREM2</i> implicate microglial-mediated innate immunity in Alzheimer's disease. <i>Nature Genetics</i> , 2017 , 49, 1373-1384	36.3	508
82	Novel Mutation in (Filamin C) Causes Familial Restrictive Cardiomyopathy. <i>Circulation: Cardiovascular Genetics</i> , 2017 , 10,		43
81	Gain-of-function mutations in <i>GATA6</i> lead to atrial fibrillation. <i>Heart Rhythm</i> , 2017 , 14, 284-291	6.7	15
80	Large-scale genome-wide analysis identifies genetic variants associated with cardiac structure and function. <i>Journal of Clinical Investigation</i> , 2017 , 127, 1798-1812	15.9	68
79	Transcriptome-wide association study of inflammatory biologic age. <i>Aging</i> , 2017 , 9, 2288-2301	5.6	5
78	A whole-blood transcriptome meta-analysis identifies gene expression signatures of cigarette smoking. <i>Human Molecular Genetics</i> , 2016 , 25, 4611-4623	5.6	58
77	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. <i>Nature Genetics</i> , 2016 , 48, 1151-1161	36.3	181
76	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	36.3	251
75	Gene-gene Interaction Analyses for Atrial Fibrillation. <i>Scientific Reports</i> , 2016 , 6, 35371	4.9	11
74	Variants in angiotensin-converting enzyme 2 (<i>ANGPT2</i>) contribute to variation in nocturnal oxyhaemoglobin saturation level. <i>Human Molecular Genetics</i> , 2016 , 25, 5244-5253	5.6	15
73	Association of genetic variations and gene expression in a family-based study. <i>BMC Proceedings</i> , 2016 , 10, 109-112	2.3	
72	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. <i>Nature Communications</i> , 2016 , 7, 10023	17.4	295
71	Shared genetic susceptibility of vascular-related biomarkers with ischemic and recurrent stroke. <i>Neurology</i> , 2016 , 86, 351-9	6.5	26
70	Whole Exome Sequencing in Atrial Fibrillation. <i>PLoS Genetics</i> , 2016 , 12, e1006284	6	24
69	Mutation of a common amino acid in <i>NKX2.5</i> results in dilated cardiomyopathy in two large families. <i>BMC Medical Genetics</i> , 2016 , 17, 83	2.1	12
68	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. <i>Genome Biology</i> , 2016 , 17, 255	18.3	171

67	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,	6	81
66	Metabolomic Profiling in Relation to New-Onset Atrial Fibrillation (from the Framingham Heart Study). <i>American Journal of Cardiology</i> , 2016 , 118, 1493-1496	3	17
65	Relevance vector and feature machine for statistical analog circuit characterization and built-in self-test optimization 2016 ,		4
64	Genome-wide association analysis of plasma B-type natriuretic peptide in blacks: the Jackson Heart Study. <i>Circulation: Cardiovascular Genetics</i> , 2015 , 8, 122-30		26
63	Gene expression markers of age-related inflammation in two human cohorts. <i>Experimental Gerontology</i> , 2015 , 70, 37-45	4-5	17
62	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, 131-40		22
61	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, 172-81	7	116
60	. <i>IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems</i> , 2015 , 34, 1467-1480	2.5	9
59	Plasma microRNAs are associated with atrial fibrillation and change after catheter ablation (the miRhythm study). <i>Heart Rhythm</i> , 2015 , 12, 3-10	6.7	78
58	Association of exome sequences with plasma C-reactive protein levels in >9000 participants. <i>Human Molecular Genetics</i> , 2015 , 24, 559-71	5.6	31
57	Genome-wide association study for endothelial growth factors. <i>Circulation: Cardiovascular Genetics</i> , 2015 , 8, 389-97		10
56	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	15.1	102
55	Whole-exome sequencing identifies rare and low-frequency coding variants associated with LDL cholesterol. <i>American Journal of Human Genetics</i> , 2014 , 94, 233-45	11	170
54	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, 452-7	6.7	18
53	Integrating genetic, transcriptional, and functional analyses to identify 5 novel genes for atrial fibrillation. <i>Circulation</i> , 2014 , 130, 1225-35	16.7	143
52	Rare genetic variant analysis on blood pressure in related samples. <i>BMC Proceedings</i> , 2014 , 8, S35	2.3	4
51	A comparison of whole genome sequencing with exome sequencing for family-based association studies. <i>BMC Proceedings</i> , 2014 , 8, S38	2.3	12
50	Strategies to design and analyze targeted sequencing data: cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium Targeted Sequencing Study. <i>Circulation: Cardiovascular Genetics</i> , 2014 , 7, 335-43		15

49	Sequencing of SCN5A 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, 365-73		7
48	Relations between circulating microRNAs and atrial fibrillation: data from the Framingham Offspring Study. <i>Heart Rhythm</i> , 2014 , 11, 663-9	6.7	71
47	Gene expression and genetic variation in human atria. <i>Heart Rhythm</i> , 2014 , 11, 266-71	6.7	42
46	Whole blood gene expression and atrial fibrillation: the Framingham Heart Study. <i>PLoS ONE</i> , 2014 , 9, e96794	3.7	18
45	Sequencing of 2 subclinical atherosclerosis candidate regions in 3669 individuals: Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) Consortium Targeted Sequencing Study. <i>Circulation: Cardiovascular Genetics</i> , 2014 , 7, 359-64		11
44	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	8.4	2
43	Whole blood gene expression and interleukin-6 levels. <i>Genomics</i> , 2014 , 104, 490-5	4.3	19
42	A low-frequency variant in MAPK14 provides mechanistic evidence of a link with myeloperoxidase: a prognostic cardiovascular risk marker. <i>Journal of the American Heart Association</i> , 2014 , 3,	6	6
41	Pleiotropic genes for metabolic syndrome and inflammation. <i>Molecular Genetics and Metabolism</i> , 2014 , 112, 317-38	3.7	81
40	The 2010 Dietary Guidelines for Americans food groups associated with decreased inflammation (370.3). <i>FASEB Journal</i> , 2014 , 28, 370.3	0.9	
39	Loci influencing blood pressure identified using a cardiovascular gene-centric array. <i>Human Molecular Genetics</i> , 2013 , 22, 1663-78	5.6	119
38	Genome-wide association study of cardiac structure and systolic function in African Americans: the Candidate Gene Association Resource (CARE) study. <i>Circulation: Cardiovascular Genetics</i> , 2013 , 6, 37-46		40
37	Common genetic variation at the IL1RL1 locus regulates IL-33/ST2 signaling. <i>Journal of Clinical Investigation</i> , 2013 , 123, 4208-18	15.9	87
36	2010 Dietary Guidelines for Americans and decreased inflammation. <i>FASEB Journal</i> , 2013 , 27, lb397	0.9	
35	Comparing Bowtie and BWA to Align Short Reads from a RNA-Seq Experiment. <i>Advances in Intelligent and Soft Computing</i> , 2012 , 197-207		1
34	Next steps in cardiovascular disease genomic research--sequencing, epigenetics, and transcriptomics. <i>Clinical Chemistry</i> , 2012 , 58, 113-26	5.5	49
33	A global characterization and identification of multifunctional enzymes. <i>PLoS ONE</i> , 2012 , 7, e38979	3.7	46
32	Functional analysis of HapMap SNPs. <i>Gene</i> , 2012 , 511, 358-63	3.8	5

31	Meta-analysis identifies six new susceptibility loci for atrial fibrillation. <i>Nature Genetics</i> , 2012 , 44, 670-5	36.3	429
30	Atrial fibrillation: current knowledge and future directions in epidemiology and genomics. <i>Circulation</i> , 2011 , 124, 1982-93	16.7	197
29	Dana-Farber repository for machine learning in immunology. <i>Journal of Immunological Methods</i> , 2011 , 374, 18-25	2.5	24
28	Microarray data analysis of gene expression evolution. <i>Gene Regulation and Systems Biology</i> , 2009 , 3, 211-4	2	
27	Evaluation of MHC-II peptide binding prediction servers: applications for vaccine research. <i>BMC Bioinformatics</i> , 2008 , 9 Suppl 12, S22	3.6	158
26	Evaluation of MHC class I peptide binding prediction servers: applications for vaccine research. <i>BMC Immunology</i> , 2008 , 9, 8	3.7	179
25	Prediction of antibiotic resistance proteins from sequence-derived properties irrespective of sequence similarity. <i>International Journal of Antimicrobial Agents</i> , 2008 , 32, 221-6	14.3	1
24	Automatic synchronization and distribution of biological databases and software over low-bandwidth networks among developing countries. <i>Bioinformatics</i> , 2008 , 24, 299-301	7.2	7
23	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	2.8	16
22	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, 1276-86	2.8	66
21	Machine learning approaches for predicting compounds that interact with therapeutic and ADMET related proteins. <i>Journal of Pharmaceutical Sciences</i> , 2007 , 96, 2838-60	3.9	44
20	Prediction of factor Xa inhibitors by machine learning methods. <i>Journal of Molecular Graphics and Modelling</i> , 2007 , 26, 505-18	2.8	23
19	Efficacy of different protein descriptors in predicting protein functional families. <i>BMC Bioinformatics</i> , 2007 , 8, 300	3.6	50
18	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, 304-13	8.8	58
17	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	10.1	22
16	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	4.7	7
15	Prediction of MHC-binding peptides of flexible lengths from sequence-derived structural and physicochemical properties. <i>Molecular Immunology</i> , 2007 , 44, 866-77	4.3	54
14	MHC-BPS: MHC-binder prediction server for identifying peptides of flexible lengths from sequence-derived physicochemical properties. <i>Immunogenetics</i> , 2006 , 58, 607-13	3.2	20

13	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 Suppl 5, S13	3.6	44
12	Prediction of the functional class of lipid binding proteins from sequence-derived properties irrespective of sequence similarity. <i>Journal of Lipid Research</i> , 2006 , 47, 824-31	6.3	28
11	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, W32-7	20.1	222
10	PEARLS: program for energetic analysis of receptor-ligand system. <i>Journal of Chemical Information and Modeling</i> , 2006 , 46, 445-50	6.1	60
9	Recent progresses in the application of machine learning approach for predicting protein functional class independent of sequence similarity. <i>Proteomics</i> , 2006 , 6, 4023-37	4.8	60
8	Prediction of transporter family from protein sequence by support vector machine approach. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 62, 218-31	4.2	48
7	Prediction of functional class of novel plant proteins by a statistical learning method. <i>New Phytologist</i> , 2005 , 168, 109-21	9.8	11
6	Computer prediction of drug resistance mutations in proteins. <i>Drug Discovery Today</i> , 2005 , 10, 521-9	8.8	46
5	MoViES: molecular vibrations evaluation server for analysis of fluctuational dynamics of proteins and nucleic acids. <i>Nucleic Acids Research</i> , 2004 , 32, W679-85	20.1	13
4	Discovering patterns of pleiotropy in genome-wide association studies		1
3	Genome-wide association study provides new insights into the genetic architecture and pathogenesis of heart failure		2
2	Deep learning enables genetic analysis of the human thoracic aorta		6
1	Atrial Fibrillation Genetic Risk Differentiates Cardioembolic Stroke from other Stroke Subtypes		1