Iftikhar J Kullo

List of Publications by Year
in descending order

259	15,846	23567	22166
papers	citations	58 h-index	113 g-index

269	269	269	21406
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	A comprehensive 1000 Genomesâ€“based genome-wide association meta-analysis of coronary artery disease. Nature Genetics, 2015, 47, 1121-1130.	21.4	2,054
2	Systematic comparison of phenome-wide association study of electronic medical record data and genome-wide association study data. Nature Biotechnology, 2013, 31, 1102-1111.	17.5	846
3	The eMERGE Network: A consortium of biorepositories linked to electronic medical records data for conducting genomic studies. BMC Medical Genomics, 2011, 4, 13.	1.5	618
4	The Electronic Medical Records and Genomics (eMERGE) Network: past, present, and future. Genetics in Medicine, 2013, 15, 761-771.	2.4	611
5	Validation of electronic medical record-based phenotyping algorithms: results and lessons learned from the eMERGE network. Journal of the American Medical Informatics Association: JAMIA, 2013, 20, e147-e154.	4.4	346
6	Return of Genomic Results to Research Participants: The Floor, the Ceiling, and the Choices In Between. American Journal of Human Genetics, 2014, 94, 818-826.	6.2	342
7	Electronic Medical Records for Genetic Research: Results of the eMERGE Consortium. Science Translational Medicine, 2011, 3, 79re1.	12.4	302
8	Antibody-Based Protein Multiplex Platforms: Technical and Operational Challenges. Clinical Chemistry, 2010, 56, 186-193.	3.2	277
9	Improving reporting standards for polygenic scores in risk prediction studies. Nature, 2021, 591, 211-219.	27.8	265
10	Quality Control Procedures for Genomeâ€Wide Association Studies. Current Protocols in Human Genetics, 2011, 68, Unit1.19.	3.5	259
11	Preemptive Genotyping for Personalized Medicine: Design of the Right Drug, Right Dose, Right Timeâ€“Using Genomic Data to Individualize Treatment Protocol. Mayo Clinic Proceedings, 2014, 89, 25-33.	3.0	250
12	Sex Differences in Arterial Stiffness and Ventricular-Arterial Interactions. Journal of the American College of Cardiology, 2013, 61, 96-103.	2.8	244
13	Variants Near FOXE1 Are Associated with Hypothyroidism and Other Thyroid Conditions: Using Electronic Medical Records for Genome- and Phenome-wide Studies. American Journal of Human Genetics, 2011, 89, 529-542.	6.2	232
14	A Bivariate Genome-Wide Approach to Metabolic Syndrome. Diabetes, 2011, 60, 1329-1339.	0.6	226
15	Peripheral Artery Disease. New England Journal of Medicine, 2016, 374, 861-871.	27.0	214
16	Incorporating a Genetic Risk Score Into Coronary Heart Disease Risk Estimates. Circulation, 2016, 133, 1181-1188.	1.6	198
17	Usefulness of Red Cell Distribution Width to Predict Mortality in Patients With Peripheral Artery Disease. American Journal of Cardiology, 2011, 107, 1241-1245.	1.6	173
18	Vulnerable Plaque: Pathobiology and Clinical Implications. Annals of Internal Medicine, 1998, 129, 1050.	3.9	169

#	ARTICLE	IF	CITATIONS
19	Genome- and Phenome-Wide Analyses of Cardiac Conduction Identifies Markers of Arrhythmia Risk. Circulation, 2013, 127, 1377-1385.	1.6	167
20	Meta-Analysis of Genome-Wide Association Studies for Abdominal Aortic Aneurysm Identifies Four New Disease-Specific Risk Loci. Circulation Research, 2017, 120, 341-353.	4.5	166
21	Association of Arrhythmia-Related Genetic Variants With Phenotypes Documented in Electronic Medical Records. JAMA - Journal of the American Medical Association, 2016, 315, 47.	7.4	148
22	Association of the PHACTR1/EDN1 Genetic Locus With Spontaneous Coronary Artery Dissection. Journal of the American College of Cardiology, 2019, 73, 58-66.	2.8	147
23	PHACTR1 Is a Genetic Susceptibility Locus for Fibromuscular Dysplasia Supporting Its Complex Genetic Pattern of Inheritance. PLoS Genetics, 2016, 12, e1006367.	3.5	146
24	Associations of Serum Uric Acid With Markers of Inflammation, Metabolic Syndrome, and Subclinical Coronary Atherosclerosis. American Journal of Hypertension, 2007, 20, 83-89.	2.0	145
25	Novel Risk Factors for Atherosclerosis. Mayo Clinic Proceedings, 2000, 75, 369-380.	3.0	141
26	Leveraging informatics for genetic studies: use of the electronic medical record to enable a genome-wide association study of peripheral arterial disease. Journal of the American Medical Informatics Association: JAMIA, 2010, 17, 568-574.	4.4	136
27	A genome- and phenome-wide association study to identify genetic variants influencing platelet count and volume and their pleiotropic effects. Human Genetics, 2014, 133, 95-109.	3.8	135
28	Ethnic differences in peripheral arterial disease in the NHLBI Genetic Epidemiology Network of Arteriopathy (GENOA) study. Vascular Medicine, 2003, 8, 237-242.	1.5	132
29	Arterial Ultrasonography and Tonometry as Adjuncts to Cardiovascular Risk Stratification. Journal of the American College of Cardiology, 2007, 49, 1413-1426.	2.8	121
30	A Genome-Wide Association Study of Red Blood Cell Traits Using the Electronic Medical Record. PLoS ONE, 2010, 5, e13011.	2.5	105
31	Markers of inflammation are inversely associated with V̇o2 max in asymptomatic men. Journal of Applied Physiology, 2007, 102, 1374-1379.	2.5	101
32	Aortic Pulse Wave Velocity Is Associated With Measures of Subclinical Target Organ Damage. JACC: Cardiovascular Imaging, 2011, 4, 754-761.	5.3	99
33	Harmonizing Clinical Sequencing and Interpretation for the eMERGE III Network. American Journal of Human Genetics, 2019, 105, 588-605.	6.2	99
34	Association Between Chromosome 9p21 Variants and the Ankle-Brachial Index Identified by a Meta-Analysis of 21 Genome-Wide Association Studies. Circulation: Cardiovascular Genetics, 2012, 5, 100-112.	5.1	98
35	Rapid identification of familial hypercholesterolemia from electronic health records: The SEARCH study. Journal of Clinical Lipidology, 2016, 10, 1230-1239.	1.5	98
36	Predictive Utility of Polygenic Risk Scores for Coronary Heart Disease in Three Major Racial and Ethnic Groups. American Journal of Human Genetics, 2020, 106, 707-716.	6.2	93

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37	C-Reactive Protein Is Related to Arterial Wave Reflection and Stiffness in Asymptomatic Subjects From the Community. American Journal of Hypertension, 2005, 18, 1123-1129.	2.0	91
38	A sequence variant associated with sortilin-1 (SORT1) on 1p13.3 is independently associated with abdominal aortic aneurysm. Human Molecular Genetics, 2013, 22, 2941-2947.	2.9	88
39	Billing code algorithms to identify cases of peripheral artery disease from administrative data. Journal of the American Medical Informatics Association: JAMIA, 2013, 20, e349-e354.	4.4	85
40	Conditional Risk Factors for Atherosclerosis. Mayo Clinic Proceedings, 2005, 80, 219-230.	3.0	83
41	Aortic Pulse Wave Velocity Is Associated With the Presence and Quantity of Coronary Artery Calcium. Hypertension, 2006, 47, 174-179.	2.7	83
42	Ethical, legal, and social implications of incorporating genomic information into electronic health records. Genetics in Medicine, 2013, 15, 810-816.	2.4	80
43	eMERGEing progress in genomicsÃ¢â‚¬â€the first seven years. Frontiers in Genetics, 2014, 5, 184.	2.3	79
44	Genetic Architecture of Abdominal Aortic Aneurysm in the Million Veteran Program. Circulation, 2020, 142, 1633-1646.	1.6	78
45	Natural language processing of clinical notes for identification of critical limb ischemia. International Journal of Medical Informatics, 2018, 111, 83-89.	3.3	77
46	Sex and Ethnic Differences in 47 Candidate Proteomic Markers of Cardiovascular Disease: The Mayo Clinic Proteomic Markers of Arteriosclerosis Study. PLoS ONE, 2010, 5, e9065.	2.5	76
47	An information extraction framework for cohort identification using electronic health records. AMIA Summits on Translational Science Proceedings, 2013, 2013, 149-53.	0.4	76
48	Mining peripheral arterial disease cases from narrative clinical notes using natural language processing. Journal of Vascular Surgery, 2017, 65, 1753-1761.	1.1	75
49	Multidisciplinary model to implement pharmacogenomics at the point of care. Genetics in Medicine, 2017, 19, 421-429.	2.4	74
50	Comparison of numbers of circulating blood monocytes in men grouped by body mass index (<25, 25 to) Tj ETQq0 0 0 rgBT /Overlock 1	1.6	73
51	Pitfalls of merging GWAS data: lessons learned in the eMERGE network and quality control procedures to maintain high data quality. Genetic Epidemiology, 2011, 35, 887-898.	1.3	71
52	Survival in Patients With Poorly Compressible Leg Arteries. Journal of the American College of Cardiology, 2012, 59, 400-407.	2.8	71
53	Establishment of Specialized Clinical Cardiovascular Genetics Programs: Recognizing the Need and Meeting Standards: A Scientific Statement From the American Heart Association. Circulation Genomic and Precision Medicine, 2019, 12, e000054.	3.6	71
54	Polygenic scores in biomedical research. Nature Reviews Genetics, 2022, 23, 524-532.	16.3	69

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55	The Genetic Basis of Peripheral Arterial Disease. Circulation Research, 2015, 116, 1551-1560.	4.5	68
56	Analyzing the heterogeneity and complexity of Electronic Health Record oriented phenotyping algorithms. AMIA ... Annual Symposium proceedings, 2011, 2011, 274-83.	0.2	68
57	Phenome-wide association studies demonstrating pleiotropy of genetic variants within FTO with and without adjustment for body mass index. Frontiers in Genetics, 2014, 5, 250.	2.3	66
58	Mechanisms of Disease: the genetic basis of coronary heart disease. Nature Clinical Practice Cardiovascular Medicine, 2007, 4, 558-569.	3.3	65
59	LPA Variants Are Associated With Residual Cardiovascular Risk in Patients Receiving Statins. Circulation, 2018, 138, 1839-1849.	1.6	64
60	Mayo Genome Consortia: A Genotype-Phenotype Resource for Genome-Wide Association Studies With an Application to the Analysis of Circulating Bilirubin Levels. Mayo Clinic Proceedings, 2011, 86, 606-614.	3.0	63
61	A collaborative approach to developing an electronic health record phenotyping algorithm for drug-induced liver injury. Journal of the American Medical Informatics Association: JAMIA, 2013, 20, e243-e252.	4.4	63
62	The eMERGE genotype set of 83,717 subjects imputed to ~40â€‰million variants genome wide and association with the herpes zoster medical record phenotype. Genetic Epidemiology, 2019, 43, 63-81.	1.3	63
63	Frequency of genomic secondaryÂfindings among 21,915 eMERGE network participants. Genetics in Medicine, 2020, 22, 1470-1477.	2.4	61
64	Enhanced Endothelium-Dependent Relaxations After Gene Transfer of Recombinant Endothelial Nitric Oxide Synthase to Rabbit Carotid Arteries. Hypertension, 1997, 30, 314-320.	2.7	61
65	Longitudinal low density lipoprotein cholesterol goal achievement and cardiovascular outcomes among adult patients with familial hypercholesterolemia: The CASCADE FH registry. Atherosclerosis, 2019, 289, 85-93.	0.8	60
66	Measurement and Quality Control Issues in Multiplex Protein Assays: A Case Study. Clinical Chemistry, 2009, 55, 1092-1099.	3.2	59
67	Genetics of Peripheral Artery Disease. Circulation, 2012, 125, 3220-3228.	1.6	59
68	Early identification of cardiovascular risk using genomics and proteomics. Nature Reviews Cardiology, 2010, 7, 309-317.	13.7	56
69	Brachial artery diameter and vasodilator response to nitroglycerine, but not flow-mediated dilatation, are associated with the presence and quantity of coronary artery calcium in asymptomatic adults. Clinical Science, 2007, 112, 175-182.	4.3	55
70	Complement Receptor 1 Gene Variants Are Associated with Erythrocyte Sedimentation Rate. American Journal of Human Genetics, 2011, 89, 131-138.	6.2	55
71	Measures of arterial stiffness and wave reflection are associated with walking distance in patients with peripheral arterial disease. Atherosclerosis, 2007, 191, 384-390.	0.8	49
72	Disease Location Is Associated With Survival in Patients With Peripheral Arterial Disease. Journal of the American Heart Association, 2013, 2, e000304.	3.7	49

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73	Precision Cardiovascular Medicine: State of Genetic Testing. Mayo Clinic Proceedings, 2017, 92, 642-662.	3.0	49
74	Facilitating phenotype transfer using a common data model. Journal of Biomedical Informatics, 2019, 96, 103253.	4.3	49
75	Vascular Gene Transfer. Arteriosclerosis, Thrombosis, and Vascular Biology, 1999, 19, 196-207.	2.4	48
76	A genome-wide linkage scan for ankleâ€“brachial index in African American and non-Hispanic white subjects participating in the GENOA study. Atherosclerosis, 2006, 187, 433-438.	0.8	48
77	Genome-wide polygenic score to predict chronic kidney disease across ancestries. Nature Medicine, 2022, 28, 1412-1420.	30.7	48
78	Relation of low cardiorespiratory fitness to the metabolic syndrome in middle-aged men. American Journal of Cardiology, 2002, 90, 795-797.	1.6	47
79	Geographic differences in allele frequencies of susceptibility SNPs for cardiovascular disease. BMC Medical Genetics, 2011, 12, 55.	2.1	47
80	Penetrance of Hemochromatosis in HFE Genotypes Resulting in p.Cys282Tyr and p.[Cys282Tyr];[His63Asp] in the eMERGE Network. American Journal of Human Genetics, 2015, 97, 512-520.	6.2	47
81	Aortic Augmentation Index Is Inversely Associated With Cardiorespiratory Fitness in Men Without Known Coronary Heart Disease. American Journal of Hypertension, 2006, 19, 1019-1024.	2.0	46
82	Leveraging the electronic health record to implement genomic medicine. Genetics in Medicine, 2013, 15, 270-271.	2.4	46
83	Interleukin-6 Receptor Signaling and Abdominal Aortic Aneurysm Growth Rates. Circulation Genomic and Precision Medicine, 2019, 12, e002413.	3.6	46
84	Genome-Wide Association Studies for Atherosclerotic Vascular Disease and Its Risk Factors. Circulation: Cardiovascular Genetics, 2009, 2, 63-72.	5.1	44
85	Arterial dysfunction and functional performance in patients with peripheral artery disease: A review. Vascular Medicine, 2011, 16, 203-211.	1.5	44
86	Ethical Considerations Related to Return of Results from Genomic Medicine Projects: The eMERGE Network (Phase III) Experience. Journal of Personalized Medicine, 2018, 8, 2.	2.5	44
87	Genetic Loci Implicated in Erythroid Differentiation and Cell Cycle Regulation Are Associated With Red Blood Cell Traits. Mayo Clinic Proceedings, 2012, 87, 461-474.	3.0	43
88	Discovering peripheral arterial disease cases from radiology notes using natural language processing. AMIA ... Annual Symposium proceedings, 2010, 2010, 722-6.	0.2	43
89	High Density GWAS for LDL Cholesterol in African Americans Using Electronic Medical Records Reveals a Strong Protective Variant in APOE. Clinical and Translational Science, 2012, 5, 394-399.	3.1	42
90	Practical considerations in genomic decision support: The eMERGE experience. Journal of Pathology Informatics, 2015, 6, 50.	1.7	42

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91	Aortic augmentation index is associated with the ankle-brachial index: A community-based study. Atherosclerosis, 2007, 195, 248-253.	0.8	41
92	Hypertension in pregnancy is a risk factor for peripheral arterial disease decades after pregnancy. Atherosclerosis, 2013, 229, 212-216.	0.8	40
93	Return of results in the genomic medicine projects of the eMERGE network. Frontiers in Genetics, 2014, 5, 50.	2.3	40
94	The ATXN2-SH2B3 locus is associated with peripheral arterial disease: an electronic medical record-based genome-wide association study. Frontiers in Genetics, 2014, 5, 166.	2.3	40
95	Molecular population genetics of PCSK9: a signature of recent positive selection. Pharmacogenetics and Genomics, 2008, 18, 169-179.	1.5	39
96	Complexity in the genetic architecture of leukoaraiosis in hypertensive sibships from the GENOA Study. BMC Medical Genomics, 2009, 2, 16.	1.5	39
97	Gene expression profiling of peripheral blood mononuclear cells in the setting of peripheral arterial disease. Journal of Clinical Bioinformatics, 2012, 2, 6.	1.2	39
98	New Case Detection by Cascade Testing in Familial Hypercholesterolemia. Circulation Genomic and Precision Medicine, 2019, 12, e002723.	3.6	39
99	Returning Results in the Genomic Era: Initial Experiences of the eMERGE Network. Journal of Personalized Medicine, 2020, 10, 30.	2.5	39
100	Early-onset peripheral arterial occlusive disease: clinical features and determinants of disease severity and location. Vascular Medicine, 2003, 8, 95-100.	1.5	37
101	Genome-wide study of resistant hypertension identified from electronic health records. PLoS ONE, 2017, 12, e0171745.	2.5	36
102	Forearm Vascular Reactivity and Arterial Stiffness in Asymptomatic Adults From the Community. Hypertension, 2008, 51, 1512-1518.	2.7	35
103	Evolutionary Genetics of Coronary Heart Disease. Circulation, 2009, 119, 459-467.	1.6	35
104	Brachial-ankle pulse wave velocity is associated with walking distance in patients referred for peripheral arterial disease evaluation. Atherosclerosis, 2009, 206, 173-178.	0.8	35
105	My Approach to the Patient With Familial Hypercholesterolemia. Mayo Clinic Proceedings, 2016, 91, 770-786.	3.0	35
106	Genetic Variants Associated with Serum Thyroid Stimulating Hormone (TSH) Levels in European Americans and African Americans from the eMERGE Network. PLoS ONE, 2014, 9, e111301.	2.5	34
107	Sex Differences in the Associations of Hemodynamic Load With Left Ventricular Hypertrophy and Concentric Remodeling. American Journal of Hypertension, 2016, 29, 73-80.	2.0	34
108	Genetic investigation of fibromuscular dysplasia identifies risk loci and shared genetics with common cardiovascular diseases. Nature Communications, 2021, 12, 6031.	12.8	34

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109	Patterns of population differentiation of candidate genes for cardiovascular disease. BMC Genetics, 2007, 8, 48.	2.7	33
110	Genotype-informed estimation of risk of coronary heart disease based on genome-wide association data linked to the electronic medical record. BMC Cardiovascular Disorders, 2011, 11, 66.	1.7	33
111	Plasma Osteopontin Levels and Adverse Cardiovascular Outcomes in the PEACE Trial. PLoS ONE, 2016, 11, e0156965.	2.5	33
112	Genetic Variants That Confer Resistance to Malaria Are Associated with Red Blood Cell Traits in African-Americans: An Electronic Medical Record-based Genome-Wide Association Study. G3: Genes, Genomes, Genetics, 2013, 3, 1061-1068.	1.8	32
113	Association of polymorphisms in NOS3 with the ankle-brachial index in hypertensive adults. Atherosclerosis, 2008, 196, 905-912.	0.8	31
114	Associations of Candidate Biomarkers of Vascular Disease with the Ankle-Brachial Index and Peripheral Arterial Disease. American Journal of Hypertension, 2013, 26, 495-502.	2.0	31
115	Arterial stiffness is associated with increase in blood pressure over time in treated hypertensives. Journal of the American Society of Hypertension, 2014, 8, 414-421.	2.3	30
116	Association of Plasma Homocysteine With Coronary Artery Calcification in Different Categories of Coronary Heart Disease Risk. Mayo Clinic Proceedings, 2006, 81, 177-182.	3.0	29
117	The Return of Actionable Variants Empirical (RAVE) Study, a Mayo Clinic Genomic Medicine Implementation Study: Design and Initial Results. Mayo Clinic Proceedings, 2018, 93, 1600-1610.	3.0	29
118	Integrating pharmacogenomics into the electronic health record by implementing genomic indicators. Journal of the American Medical Informatics Association: JAMIA, 2020, 27, 154-158.	4.4	29
119	Association of Novel Risk Factors With the Ankle Brachial Index in African American and Non-Hispanic White Populations. Mayo Clinic Proceedings, 2007, 82, 709-716.	3.0	28
120	Methods for the selection of tagging SNPs: a comparison of tagging efficiency and performance. European Journal of Human Genetics, 2007, 15, 228-236.	2.8	28
121	Implementation of preemptive DNA sequenceâ€“based pharmacogenomics testing across a large academic medical center: The Mayo-Baylor RIGHT 10K Study. Genetics in Medicine, 2022, 24, 1062-1072.	2.4	28
122	Pleiotropic genetic effects contribute to the correlation between HDL cholesterol, triglycerides, and LDL particle size in hypertensive sibships. American Journal of Hypertension, 2005, 18, 99-103.	2.0	27
123	Association of Novel Risk Factors With the Ankle Brachial Index in African American and Non-Hispanic White Populations. Mayo Clinic Proceedings, 2007, 82, 709-716.	3.0	27
124	Making work visible for electronic phenotype implementation: Lessons learned from the eMERGE network. Journal of Biomedical Informatics, 2019, 99, 103293.	4.3	27
125	A phenome-wide association study to discover pleiotropic effects of PCSK9, APOB, and LDLR. Npj Genomic Medicine, 2019, 4, 3.	3.8	26
126	A Perspective on the New American College of Cardiology/American Heart Association Guidelines for Cardiovascular Risk Assessment. Mayo Clinic Proceedings, 2014, 89, 1244-1256.	3.0	25

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127	Effect of Disclosing Genetic Risk for Coronary Heart Disease on Information Seeking and Sharing. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	25
128	Participant choices for return of genomic results in the eMERGE Network. Genetics in Medicine, 2020, 22, 1821-1829.	2.4	25
129	Family History as a Risk Factor for Peripheral Arterial Disease. American Journal of Cardiology, 2014, 114, 928-932.	1.6	24
130	Genome-Wide Association Study of Peripheral Artery Disease. Circulation Genomic and Precision Medicine, 2021, 14, e002862.	3.6	24
131	Lack of Association Between Lipoprotein(a) and Coronary Artery Calcification in the Genetic Epidemiology Network of Arteriopathy (GENOA) Study. Mayo Clinic Proceedings, 2004, 79, 1258-1263.	3.0	23
132	Increased Serum N-Terminal Proâ€“B-Type Natriuretic Peptide Levels in Patients With Medial Arterial Calcification and Poorly Compressible Leg Arteries. Arteriosclerosis, Thrombosis, and Vascular Biology, 2011, 31, 197-202.	2.4	23
133	Enhancing the Power of Genetic Association Studies through the Use of Silver Standard Cases Derived from Electronic Medical Records. PLoS ONE, 2013, 8, e63481.	2.5	23
134	Leveraging the Electronic Health Record to Create an Automated Realâ€Time Prognostic Tool for Peripheral Arterial Disease. Journal of the American Heart Association, 2018, 7, e009680.	3.7	23
135	Adenovirus-Mediated Gene Transfer of Macrophage Colony Stimulating Factor to the Arterial Wall In Vivo. Arteriosclerosis, Thrombosis, and Vascular Biology, 1998, 18, 1157-1163.	2.4	22
136	Novel Genomic Loci Influencing Plasma Homocysteine Levels. Stroke, 2006, 37, 1703-1709.	2.0	22
137	Shared Decision-Making following Disclosure of Coronary Heart Disease Genetic Risk: Results from a Randomized Clinical Trial. Journal of Investigative Medicine, 2017, 65, 681-688.	1.6	22
138	Genetic basis of hypercholesterolemia in adults. Npj Genomic Medicine, 2021, 6, 28.	3.8	22
139	Comparative and evolutionary pharmacogenetics of ABCB1: complex signatures of positive selection on coding and regulatory regions. Pharmacogenetics and Genomics, 2007, 17, 667-678.	1.5	21
140	Biomarkers Associated With Pulse Pressure in African-Americans and Non-Hispanic Whites. American Journal of Hypertension, 2012, 25, 145-151.	2.0	21
141	Whole Exome Sequencing Implicates an INO80D Mutation in a Syndrome of Aortic Hypoplasia, Premature Atherosclerosis, and Arterial Stiffness. Circulation: Cardiovascular Genetics, 2014, 7, 607-614.	5.1	21
142	Association of Ankle-Brachial Indices With Limb Revascularization or Amputation in Patients With Peripheral Artery Disease. JAMA Network Open, 2018, 1, e185547.	5.9	21
143	Empowering genomic medicine by establishing critical sequencing result data flows: the eMERGE example. Journal of the American Medical Informatics Association: JAMIA, 2018, 25, 1375-1381.	4.4	21
144	Returning genomic results in a Federally Qualified Health Center: the intersection of precision medicine and social determinants of health. Genetics in Medicine, 2020, 22, 1552-1559.	2.4	21

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145	Associations of Genetically Predicted Lp(a) (Lipoprotein [a]) Levels With Cardiovascular Traits in Individuals of European and African Ancestry. Circulation Genomic and Precision Medicine, 2021, 14, e003354.	3.6	21
146	Association of Cardiovascular Risk Factors with Microvascular and Conduit Artery Function in Hypertensive Subjects. American Journal of Hypertension, 2007, 20, 735-742.	2.0	20
147	Investigating the complex genetic architecture of ankle-brachial index, a measure of peripheral arterial disease, in non-Hispanic whites. BMC Medical Genomics, 2008, 1, 16.	1.5	20
148	Plasma Midregional Pro-atrial Natriuretic Peptide Is Associated With Blood Pressure Indices and Hypertension Severity in Adults With Hypertension. American Journal of Hypertension, 2009, 22, 425-431.	2.0	20
149	Should pretest genetic counselling be required for patients pursuing genomic sequencing? Results from a survey of participants in a large genomic implementation study. Journal of Medical Genetics, 2019, 56, 317-324.	3.2	20
150	Developing a Process for Returning Medically Actionable Genomic Variants to Latino Patients in a Federally Qualified Health Center. Public Health Genomics, 2018, 21, 77-84.	1.0	19
151	A Clinical Decision Support Tool for Familial Hypercholesterolemia Based on Physician Input. Mayo Clinic Proceedings Innovations, Quality & Outcomes, 2018, 2, 103-112.	2.4	19
152	Evaluation of the MC4R gene across eMERGE network identifies many unreported obesity-associated variants. International Journal of Obesity, 2021, 45, 155-169.	3.4	19
153	Genome-Wide Association Study of Serum Creatinine Levels during Vancomycin Therapy. PLoS ONE, 2015, 10, e0127791.	2.5	19
154	An electronic medical record-linked biorepository to identify novel biomarkers for atherosclerotic cardiovascular disease. Global Cardiology Science & Practice, 2013, 2013, 10.	0.4	18
155	Higher plasma leptin levels are associated with reduced left ventricular mass and left ventricular diastolic stiffness in black women: insights from the Genetic Epidemiology Network of Arteriopathy (GENOA) study. Hypertension Research, 2018, 41, 629-638.	2.7	18
156	Evidence for Positive Selection in the C-terminal Domain of the Cholesterol Metabolism Gene PCSK9 Based on Phylogenetic Analysis in 14 Primate Species. PLoS ONE, 2007, 2, e1098.	2.5	18
157	Arrhythmia Variant Associations and Reclassifications in the eMERGE-III Sequencing Study. Circulation, 2022, 145, 877-891.	1.6	18
158	Associations of Alterations in Pulsatile Arterial Load With Left Ventricular Longitudinal Strain. American Journal of Hypertension, 2015, 28, 1325-1331.	2.0	17
159	Risk Factors for Polyvascular Involvement in Patients With Peripheral Artery Disease: A Mendelian Randomization Study. Journal of the American Heart Association, 2020, 9, e017740.	3.7	17
160	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
161	A unified framework identifies new links between plasma lipids and diseases from electronic medical records across large-scale cohorts. Nature Genetics, 2021, 53, 972-981.	21.4	17
162	Leveraging the Electronic Health Record to Address the COVID-19 Pandemic. Mayo Clinic Proceedings, 2021, 96, 1592-1608.	3.0	17

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163	Identifying Abdominal Aortic Aneurysm Cases and Controls using Natural Language Processing of Radiology Reports. AMIA Summits on Translational Science Proceedings, 2013, 2013, 249-53.	0.4	17
164	A Novel Quantitative Trait Locus on Chromosome 1 with Pleiotropic Effects on HDL-Cholesterol and LDL Particle Size in Hypertensive Sibships. American Journal of Hypertension, 2005, 18, 1084-1090.	2.0	16
165	C-reactive protein among community-dwelling hypertensives on single-agent antihypertensive treatment. Journal of the American Society of Hypertension, 2009, 3, 260-266.	2.3	16
166	Identifying peripheral arterial disease cases using natural language processing of clinical notes. , 2016, 2016, 126-131.		16
167	Relation of Plasma Midregional Proatrial Natriuretic Peptide to Target Organ Damage in Adults With Systemic Hypertension. American Journal of Cardiology, 2009, 103, 1255-1260.	1.6	15
168	Design of a randomized controlled trial of disclosing genomic risk of coronary heart disease: the Myocardial Infarction Genes (MI-GENES) study. BMC Medical Genomics, 2015, 8, 51.	1.5	15
169	An Implementation Science Framework to Develop a Clinical Decision Support Tool for Familial Hypercholesterolemia. Journal of Personalized Medicine, 2020, 10, 67.	2.5	15
170	Understanding the Return of Genomic Sequencing Results Process: Content Review of Participant Summary Letters in the eMERGE Research Network. Journal of Personalized Medicine, 2020, 10, 38.	2.5	15
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