Joshua C Denny

List of Publications by Year
in descending order

426	34,591	4658	5829
papers	citations	85 h-index	161 g-index

467	467	467	40487
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genetics of rheumatoid arthritis contributes to biology and drug discovery. Nature, 2014, 506, 376-381.	27.8	1,974
2	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	21.4	1,818
3	A gene-based association method for mapping traits using reference transcriptome data. Nature Genetics, 2015, 47, 1091-1098.	21.4	1,473
4	PheWAS: demonstrating the feasibility of a phenome-wide scan to discover geneâ€“disease associations. Bioinformatics, 2010, 26, 1205-1210.	4.1	966
5	The â€œAll of Usâ€•Research Program. New England Journal of Medicine, 2019, 381, 668-676.	27.0	955
6	Efficiently controlling for case-control imbalance and sample relatedness in large-scale genetic association studies. Nature Genetics, 2018, 50, 1335-1341.	21.4	896
7	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
8	The Electronic Medical Records and Genomics (eMERGE) Network: past, present, and future. Genetics in Medicine, 2013, 15, 761-771.	2.4	611
9	Multi-ethnic genome-wide association study for atrial fibrillation. Nature Genetics, 2018, 50, 1225-1233.	21.4	552
10	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	21.4	470
11	Artificial intelligence, bias and clinical safety. BMJ Quality and Safety, 2019, 28, 231-237.	3.7	469
12	MedEx: a medication information extraction system for clinical narratives. Journal of the American Medical Informatics Association: JAMIA, 2010, 17, 19-24.	4.4	427
13	Coding Variation inANGPTL4,LPL,andSVEP1and the Risk of Coronary Disease. New England Journal of Medicine, 2016, 374, 1134-1144.	27.0	427
14	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	12.8	412
15	Inactivating Mutations in NPC1L1 and Protection from Coronary Heart Disease. New England Journal of Medicine, 2014, 371, 2072-2082.	27.0	386
16	Operational Implementation of Prospective Genotyping for Personalized Medicine: The Design of the Vanderbilt PREDICT Project. Clinical Pharmacology and Therapeutics, 2012, 92, 87-95.	4.7	370
17	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
18	R PheWAS: data analysis and plotting tools for phenome-wide association studies in the R environment. Bioinformatics, 2014, 30, 2375-2376.	4.1	334

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19	Trans-ethnic association study of blood pressure determinants in over 750,000 individuals. Nature Genetics, 2019, 51, 51-62.	21.4	328
20	Mapping ICD-10 and ICD-10-CM Codes to Phecodes: Workflow Development and Initial Evaluation. JMIR Medical Informatics, 2019, 7, e14325.	2.6	323
21	Robust Replication of Genotype-Phenotype Associations across Multiple Diseases in an Electronic Medical Record. American Journal of Human Genetics, 2010, 86, 560-572.	6.2	302
22	Electronic Medical Records for Genetic Research: Results of the eMERGE Consortium. Science Translational Medicine, 2011, 3, 79re1.	12.4	302
23	PCSK9 genetic variants and risk of type 2 diabetes: a mendelian randomisation study. Lancet Diabetes and Endocrinology,the, 2017, 5, 97-105.	11.4	298
24	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	21.4	286
25	PheKB: a catalog and workflow for creating electronic phenotype algorithms for transportability. Journal of the American Medical Informatics Association: JAMIA, 2016, 23, 1046-1052.	4.4	284
26	Data from clinical notes: a perspective on the tension between structure and flexible documentation. Journal of the American Medical Informatics Association: JAMIA, 2011, 18, 181-186.	4.4	281
27	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836.	21.4	281
28	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. Nature Genetics, 2017, 49, 946-952.	21.4	279
29	Clinically Actionable Genotypes Among 10,000 Patients With Preemptive Pharmacogenomic Testing. Clinical Pharmacology and Therapeutics, 2014, 95, 423-431.	4.7	272
30	Use of diverse electronic medical record systems to identify genetic risk for type 2 diabetes within a genome-wide association study. Journal of the American Medical Informatics Association: JAMIA, 2012, 19, 212-218.	4.4	270
31	The phenotypic legacy of admixture between modern humans and Neandertals. Science, 2016, 351, 737-741.	12.6	269
32	Evaluating phecodes, clinical classification software, and ICD-9-CM codes for phenome-wide association studies in the electronic health record. PLoS ONE, 2017, 12, e0175508.	2.5	268
33	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
34	Computational Phenotype Discovery Using Unsupervised Feature Learning over Noisy, Sparse, and Irregular Clinical Data. PLoS ONE, 2013, 8, e66341.	2.5	226
35	A study of machine-learning-based approaches to extract clinical entities and their assertions from discharge summaries. Journal of the American Medical Informatics Association: JAMIA, 2011, 18, 601-606.	4.4	223
36	Design and Anticipated Outcomes of the eMERGE-PGx Project: A Multicenter Pilot for Preemptive Pharmacogenomics in Electronic Health Record Systems. Clinical Pharmacology and Therapeutics, 2014, 96, 482-489.	4.7	223

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37	Pharmacogenetic meta-analysis of genome-wide association studies of LDL cholesterol response to statins. Nature Communications, 2014, 5, 5068.	12.8	216
38	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated WithÂCoronary ArteryÂDisease. Journal of the American College of Cardiology, 2017, 69, 823-836.	2.8	214
39	Electronic health records-driven phenotyping: challenges, recent advances, and perspectives. Journal of the American Medical Informatics Association: JAMIA, 2013, 20, e206-e211.	4.4	213
40	Multisite Investigation of Outcomes WithÂImplementation of CYP2C19 Genotype-Guided Antiplatelet Therapy After Percutaneous Coronary Intervention. JACC: Cardiovascular Interventions, 2018, 11, 181-191.	2.9	213
41	Portability of an algorithm to identify rheumatoid arthritis in electronic health records. Journal of the American Medical Informatics Association: JAMIA, 2012, 19, e162-e169.	4.4	201
42	Phenome-Wide Association Studies as a Tool to Advance Precision Medicine. Annual Review of Genomics and Human Genetics, 2016, 17, 353-373.	6.2	193
43	Joint mouseâ€“human phenome-wide association to test gene function and disease risk. Nature Communications, 2016, 7, 10464.	12.8	190
44	The IGNITE network: a model for genomic medicine implementation and research. BMC Medical Genomics, 2015, 9, 1.	1.5	189
45	Detecting Drug Interactions From Adverse-Event Reports: Interaction Between Paroxetine and Pravastatin Increases Blood Glucose Levels. Clinical Pharmacology and Therapeutics, 2011, 90, 133-142.	4.7	183
46	Extracting research-quality phenotypes from electronic health records to support precision medicine. Genome Medicine, 2015, 7, 41.	8.2	181
47	Validating drug repurposing signals using electronic health records: a case study of metformin associated with reduced cancer mortality. Journal of the American Medical Informatics Association: JAMIA, 2015, 22, 179-191.	4.4	178
48	Optimizing Drug Outcomes Through Pharmacogenetics: A Case for Preemptive Genotyping. Clinical Pharmacology and Therapeutics, 2012, 92, 235-242.	4.7	174
49	Increased monocyte count as a cellular biomarker for poor outcomes in fibrotic diseases: a retrospective, multicentre cohort study. Lancet Respiratory Medicine,the, 2019, 7, 497-508.	10.7	168
50	Genome- and Phenome-Wide Analyses of Cardiac Conduction Identifies Markers of Arrhythmia Risk. Circulation, 2013, 127, 1377-1385.	1.6	167
51	The Pharmacogenomics Research Network Translational Pharmacogenetics Program: Overcoming Challenges of Real-World Implementation. Clinical Pharmacology and Therapeutics, 2013, 94, 207-210.	4.7	164
52	Phenotype risk scores identify patients with unrecognized Mendelian disease patterns. Science, 2018, 359, 1233-1239.	12.6	164
53	Genetic variation among 82 pharmacogenes: The PGRNseq data from the eMERGE network. Clinical Pharmacology and Therapeutics, 2016, 100, 160-169.	4.7	163
54	Precision medicine in 2030â€”seven ways to transform healthcare. Cell, 2021, 184, 1415-1419.	28.9	161

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55	The Emerging Role of Electronic Medical Records in Pharmacogenomics. Clinical Pharmacology and Therapeutics, 2011, 89, 379-386.	4.7	157
56	Combining billing codes, clinical notes, and medications from electronic health records provides superior phenotyping performance. Journal of the American Medical Informatics Association: JAMIA, 2016, 23, e20-e27.	4.4	157
57	Chapter 13: Mining Electronic Health Records in the Genomics Era. PLoS Computational Biology, 2012, 8, e1002823.	3.2	148
58	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
59	Big Data Science: Opportunities and Challenges to Address Minority Health and Health Disparities in the 21st Century. Ethnicity and Disease, 2017, 27, 95.	2.3	141
60	Understanding patientâ€provider communication entered via a patient portal system. Proceedings of the American Society for Information Science and Technology, 2012, 49, 1-4.	0.2	140
61	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
62	SJS/TEN 2017: Building Multidisciplinary Networks to Drive Science and Translation. Journal of Allergy and Clinical Immunology: in Practice, 2018, 6, 38-69.	3.8	134
63	Genome-wide Association Studies Identify Genetic Loci Associated With Albuminuria in Diabetes. Diabetes, 2016, 65, 803-817.	0.6	131
64	Diversity and inclusion for the All of Us research program: A scoping review. PLoS ONE, 2020, 15, e0234962.	2.5	128
65	Limestone: High-throughput candidate phenotype generation via tensor factorization. Journal of Biomedical Informatics, 2014, 52, 199-211.	4.3	121
66	TYK2 Protein-Coding Variants Protect against Rheumatoid Arthritis and Autoimmunity, with No Evidence of Major Pleiotropic Effects on Non-Autoimmune Complex Traits. PLoS ONE, 2015, 10, e0122271.	2.5	120
67	Biobanks and Electronic Medical Records: Enabling Cost-Effective Research. Science Translational Medicine, 2014, 6, 234cm3.	12.4	118
68	Identification of Genomic Predictors of Atrioventricular Conduction. Circulation, 2010, 122, 2016-2021.	1.6	117
69	Learning from Longitudinal Data in Electronic Health Record and Genetic Data to Improve Cardiovascular Event Prediction. Scientific Reports, 2019, 9, 717.	3.3	115
70	The disclosure of diagnosis codes can breach research participants' privacy. Journal of the American Medical Informatics Association: JAMIA, 2010, 17, 322-327.	4.4	112
71	Desiderata for computable representations of electronic health records-driven phenotype algorithms. Journal of the American Medical Informatics Association: JAMIA, 2015, 22, 1220-1230.	4.4	110
72	Research Directions in the Clinical Implementation of Pharmacogenomics: An Overview of US Programs and Projects. Clinical Pharmacology and Therapeutics, 2018, 103, 778-786.	4.7	110

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73	Rubik. , 2015, 2015, 1265-1274.		108
74	Evaluation of a Method to Identify and Categorize Section Headers in Clinical Documents. Journal of the American Medical Informatics Association: JAMIA, 2009, 16, 806-815.	4.4	106
75	Importance of multi-modal approaches to effectively identify cataract cases from electronic health records. Journal of the American Medical Informatics Association: JAMIA, 2012, 19, 225-234.	4.4	106
76	Phenome-wide scanning identifies multiple diseases and disease severity phenotypes associated with HLA variants. Science Translational Medicine, 2017, 9, .	12.4	105
77	Genetics of glucocorticoid-associated osteonecrosis in children with acute lymphoblastic leukemia. Blood, 2015, 126, 1770-1776.	1.4	102
78	A missense variant in Mitochondrial Amidoxime Reducing Component 1 gene and protection against liver disease. PLoS Genetics, 2020, 16, e1008629.	3.5	101
79	A hybrid system for temporal information extraction from clinical text. Journal of the American Medical Informatics Association: JAMIA, 2013, 20, 828-835.	4.4	99
80	Challenges and strategies for implementing genomic services in diverse settings: experiences from the Implementing GeNomics In pracTicE (IGNITE) network. BMC Medical Genomics, 2017, 10, 35.	1.5	99
81	Harmonizing Clinical Sequencing and Interpretation for the eMERGE III Network. American Journal of Human Genetics, 2019, 105, 588-605.	6.2	99
82	Use of Genetic Variants Related to Antihypertensive Drugs to Inform on Efficacy and Side Effects. Circulation, 2019, 140, 270-279.	1.6	99
83	"Understanding" Medical School Curriculum Content Using KnowledgeMap. Journal of the American Medical Informatics Association: JAMIA, 2003, 10, 351-362.	4.4	96
84	A study of active learning methods for named entity recognition in clinical text. Journal of Biomedical Informatics, 2015, 58, 11-18.	4.3	95
85	Assessing the accuracy of observer-reported ancestry in a biorepository linked to electronic medical records. Genetics in Medicine, 2010, 12, 648-650.	2.4	94
86	Return of individual research results from genome-wide association studies: experience of the Electronic Medical Records and Genomics (eMERGE) Network. Genetics in Medicine, 2012, 14, 424-431.	2.4	94
87	Development and evaluation of an ensemble resource linking medications to their indications. Journal of the American Medical Informatics Association: JAMIA, 2013, 20, 954-961.	4.4	92
88	Predicting warfarin dosage in Europeanâ€“Americans and Africanâ€“Americans using DNA samples linked to an electronic health record. Pharmacogenomics, 2012, 13, 407-418.	1.3	90
89	The use of a DNA biobank linked to electronic medical records to characterize pharmacogenomic predictors of tacrolimus dose requirement in kidney transplant recipients. Pharmacogenetics and Genomics, 2012, 22, 32-42.	1.5	89
90	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	21.4	89

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91	Predicting Clopidogrel Response Using DNA Samples Linked to an Electronic Health Record. Clinical Pharmacology and Therapeutics, 2012, 91, 257-263.	4.7	88
92	Single-trait and multi-trait genome-wide association analyses identify novel loci for blood pressure in African-ancestry populations. PLoS Genetics, 2017, 13, e1006728.	3.5	88
93	Electronic health record design and implementation for pharmacogenomics: a local perspective. Genetics in Medicine, 2013, 15, 833-841.	2.4	87
94	Applying active learning to high-throughput phenotyping algorithms for electronic health records data. Journal of the American Medical Informatics Association: JAMIA, 2013, 20, e253-e259.	4.4	85
95	Associations of autoantibodies, autoimmune risk alleles, and clinical diagnoses from the electronic medical records in rheumatoid arthritis cases and nonâ€“rheumatoid arthritis controls. Arthritis and Rheumatism, 2013, 65, 571-581.	6.7	84
96	Clinical phenotyping in selected national networks: demonstrating the need for high-throughput, portable, and computational methods. Artificial Intelligence in Medicine, 2016, 71, 57-61.	6.5	84
97	Mining 100 million notes to find homelessness and adverse childhood experiences: 2 case studies of rare and severe social determinants of health in electronic health records. Journal of the American Medical Informatics Association: JAMIA, 2018, 25, 61-71.	4.4	81
98	Genetically determined serum urate levels and cardiovascular and other diseases in UK Biobank cohort: A phenome-wide mendelian randomization study. PLoS Medicine, 2019, 16, e1002937.	8.4	81
99	Development of Inpatient Risk Stratification Models of Acute Kidney Injury for Use in Electronic Health Records. Medical Decision Making, 2010, 30, 639-650.	2.4	80
100	eMERGEing progress in genomicsÃ¢â‚¬â€the first seven years. Frontiers in Genetics, 2014, 5, 184.	2.3	79
101	Analysis of predicted loss-of-function variants in UK Biobank identifies variants protective for disease. Nature Communications, 2018, 9, 1613.	12.8	78
102	Genetic Architecture of Abdominal Aortic Aneurysm in the Million Veteran Program. Circulation, 2020, 142, 1633-1646.	1.6	78
103	Benefit of Preemptive Pharmacogenetic Information on Clinical Outcome. Clinical Pharmacology and Therapeutics, 2018, 103, 787-794.	4.7	77
104	Evaluating the Utility of Polygenic Risk Scores in Identifying High-Risk Individuals for Eight Common Cancers. JNCI Cancer Spectrum, 2020, 4, pkaa021.	2.9	75
105	Facilitating pharmacogenetic studies using electronic health records and natural-language processing: a case study of warfarin. Journal of the American Medical Informatics Association: JAMIA, 2011, 18, 387-391.	4.4	74
106	Four Susceptibility Loci for Gallstone Disease Identified in a Meta-analysis of Genome-Wide Association Studies. Gastroenterology, 2016, 151, 351-363.e28.	1.3	74
107	Evaluating electronic health record data sources and algorithmic approaches to identify hypertensive individuals. Journal of the American Medical Informatics Association: JAMIA, 2017, 24, 162-171.	4.4	74
108	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. Nature Communications, 2018, 9, 2904.	12.8	71

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109	Phenome-wide association study (PheWAS) in EMR-linked pediatric cohorts, genetically links PLCL1 to speech language development and IL5-IL13 to Eosinophilic Esophagitis. Frontiers in Genetics, 2014, 5, 401.	2.3	70
110	Association of Genetic Variation With Cirrhosis: A Multi-Trait Genome-Wide Association and Geneâ€“Environment Interaction Study. Gastroenterology, 2021, 160, 1620-1633.e13.	1.3	68
111	Analyzing the heterogeneity and complexity of Electronic Health Record oriented phenotyping algorithms. AMIA ... Annual Symposium proceedings, 2011, 2011, 274-83.	0.2	68
112	Integrating existing natural language processing tools for medication extraction from discharge summaries. Journal of the American Medical Informatics Association: JAMIA, 2010, 17, 528-531.	4.4	67
113	Identifying lupus patients in electronic health records: Development and validation of machine learning algorithms and application of rule-based algorithms. Seminars in Arthritis and Rheumatism, 2019, 49, 84-90.	3.4	67
114	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
115	Attitudes of clinicians following large-scale pharmacogenomics implementation. Pharmacogenomics Journal, 2016, 16, 393-398.	2.0	66
116	NaÃ¯ve Electronic Health Record phenotype identification for Rheumatoid arthritis. AMIA ... Annual Symposium proceedings, 2011, 2011, 189-96.	0.2	66
117	Extracting timing and status descriptors for colonoscopy testing from electronic medical records. Journal of the American Medical Informatics Association: JAMIA, 2010, 17, 383-388.	4.4	65
118	Comparative analysis of pharmacovigilance methods in the detection of adverse drug reactions using electronic medical records. Journal of the American Medical Informatics Association: JAMIA, 2013, 20, 420-426.	4.4	64
119	LPA Variants Are Associated With Residual Cardiovascular Risk in Patients Receiving Statins. Circulation, 2018, 138, 1839-1849.	1.6	64
120	Natural Language Processing Improves Identification of Colorectal Cancer Testing in the Electronic Medical Record. Medical Decision Making, 2012, 32, 188-197.	2.4	63
121	Opportunities for genomic clinical decision support interventions. Genetics in Medicine, 2013, 15, 817-823.	2.4	63
122	Automatic identification of methotrexate-induced liver toxicity in patients with rheumatoid arthritis from the electronic medical record. Journal of the American Medical Informatics Association: JAMIA, 2015, 22, e151-e161.	4.4	63
123	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
124	Platelet Inhibitors Reduce Rupture in a Mouse Model of Established Abdominal Aortic Aneurysm. Arteriosclerosis, Thrombosis, and Vascular Biology, 2015, 35, 2032-2041.	2.4	61
125	Developing Electronic Health Record Algorithms That Accurately Identify Patients With Systemic Lupus Erythematosus. Arthritis Care and Research, 2017, 69, 687-693.	3.4	61
126	Phenome-wide Mendelian-randomization study of genetically determined vitamin D on multiple health outcomes using the UK Biobank study. International Journal of Epidemiology, 2019, 48, 1425-1434.	1.9	61

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127	Frequency of genomic secondaryÂfindings among 21,915 eMERGE network participants. Genetics in Medicine, 2020, 22, 1470-1477.	2.4	61
128	Knowledge-Driven Multi-Locus Analysis Reveals Gene-Gene Interactions Influencing HDL Cholesterol Level in Two Independent EMR-Linked Biobanks. PLoS ONE, 2011, 6, e19586.	2.5	60
129	Predicting changes in hypertension control using electronic health records from a chronic disease management program. Journal of the American Medical Informatics Association: JAMIA, 2014, 21, 337-344.	4.4	60
130	A comparison of rule-based and machine learning approaches for classifying patient portal messages. International Journal of Medical Informatics, 2017, 105, 110-120.	3.3	60
131	Electronic Health Record Based Algorithm to Identify Patients with Autism Spectrum Disorder. PLoS ONE, 2016, 11, e0159621.	2.5	59
132	Genetic variation in the HLA region is associated with susceptibility to herpes zoster. Genes and Immunity, 2015, 16, 1-7.	4.1	58
133	Comparison of HLA allelic imputation programs. PLoS ONE, 2017, 12, e0172444.	2.5	58
134	Transcription factor ETV1 is essential for rapid conduction in the heart. Journal of Clinical Investigation, 2016, 126, 4444-4459.	8.2	58
135	MR-PheWAS: exploring the causal effect of SUA level on multiple disease outcomes by using genetic instruments in UK Biobank. Annals of the Rheumatic Diseases, 2018, 77, 1039-1047.	0.9	57
136	Complement Receptor 1 Gene Variants Are Associated with Erythrocyte Sedimentation Rate. American Journal of Human Genetics, 2011, 89, 131-138.	6.2	55
137	Design patterns for the development of electronic health record-driven phenotype extraction algorithms. Journal of Biomedical Informatics, 2014, 51, 280-286.	4.3	55
138	Genome-wide association and pathway analysis of left ventricular function after anthracycline exposure in adults. Pharmacogenetics and Genomics, 2017, 27, 247-254.	1.5	54
139	New data and an old puzzle: the negative association between schizophrenia and rheumatoid arthritis. International Journal of Epidemiology, 2015, 44, 1706-1721.	1.9	53
140	Modulators of normal electrocardiographic intervals identified in a large electronic medical record. Heart Rhythm, 2011, 8, 271-277.	0.7	52
141	Genotype and risk of major bleeding during warfarin treatment. Pharmacogenomics, 2014, 15, 1973-1983.	1.3	50
142	CTNNA3 and SEMA3D: Promising loci for asthma exacerbation identified through multiple genome-wide association studies. Journal of Allergy and Clinical Immunology, 2015, 136, 1503-1510.	2.9	50
143	Large-Scale Exome-wide Association Analysis Identifies Loci for White Blood Cell Traits and Pleiotropy with Immune-Mediated Diseases. American Journal of Human Genetics, 2016, 99, 22-39.	6.2	50
144	A genome-wide association study of heparin-induced thrombocyto - penia using an electronic medical record. Thrombosis and Haemostasis, 2015, 113, 772-781.	3.4	49

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145	Facilitating phenotype transfer using a common data model. Journal of Biomedical Informatics, 2019, 96, 103253.	4.3	49
146	Evaluation of a Prediction Model for the Development of Atrial Fibrillation in a Repository of Electronic Medical Records. JAMA Cardiology, 2016, 1, 1007.	6.1	48
147	An Atlas of Genetic Variation Linking Pathogen-Induced Cellular Traits to Human Disease. Cell Host and Microbe, 2018, 24, 308-323.e6.	11.0	48
148	Electronic Medical Records as a Tool in Clinical Pharmacology: Opportunities and Challenges. Clinical Pharmacology and Therapeutics, 2012, 91, 1083-1086.	4.7	47
149	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
150	Physician response to implementation of genotypeâ€tailored antiplatelet therapy. Clinical Pharmacology and Therapeutics, 2016, 100, 67-74.	4.7	47
151	A genome-wide association study identifies variants in KCNIP4 associated with ACE inhibitor-induced cough. Pharmacogenomics Journal, 2016, 16, 231-237.	2.0	47
152	Apolipoprotein L1 VariantsÂand Blood Pressure Traits inÂAfrican Americans. Journal of the American College of Cardiology, 2017, 69, 1564-1574.	2.8	46
153	Automated extraction of clinical traits of multiple sclerosis in electronic medical records. Journal of the American Medical Informatics Association: JAMIA, 2013, 20, e334-e340.	4.4	45
154	A long journey to short abbreviations: developing an open-source framework for clinical abbreviation recognition and disambiguation (CARD). Journal of the American Medical Informatics Association: JAMIA, 2017, 24, e79-e86.	4.4	45
155	Role of carotid bodies in control of the neuroendocrine response to exercise. American Journal of Physiology - Endocrinology and Metabolism, 2001, 281, E742-E748.	3.5	44
156	A Robust e-Epidemiology Tool in Phenotyping Heart Failure with Differentiation for Preserved and Reduced Ejection Fraction: the Electronic Medical Records and Genomics (eMERGE) Network. Journal of Cardiovascular Translational Research, 2015, 8, 475-483.	2.4	44
157	Extracting and integrating data from entire electronic health records for detecting colorectal cancer cases. AMIA ... Annual Symposium proceedings, 2011, 2011, 1564-72.	0.2	44
158	Teaching evidence-based medicine: Impact on studentsâ€™ literature use and inpatient clinical documentation. Medical Teacher, 2011, 33, e306-e312.	1.8	43
159	Identifying QT prolongation from ECG impressions using a general-purpose Natural Language Processor. International Journal of Medical Informatics, 2009, 78, S34-S42.	3.3	42
160	Generating Clinical Notes for Electronic Health Record Systems. Applied Clinical Informatics, 2010, 01, 232-243.	1.7	42
161	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
162	Building bridges across electronic health record systems through inferred phenotypic topics. Journal of Biomedical Informatics, 2015, 55, 82-93.	4.3	42

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163	The Influence of Big (Clinical) Data and Genomics on Precision Medicine and Drug Development. Clinical Pharmacology and Therapeutics, 2018, 103, 409-418.	4.7	42
164	Probing the Virtual Proteome to Identify Novel Disease Biomarkers. Circulation, 2018, 138, 2469-2481.	1.6	42
165	Practical considerations in genomic decision support: The eMERGE experience. Journal of Pathology Informatics, 2015, 6, 50.	1.7	42
166	The KnowledgeMap project: development of a concept-based medical school curriculum database. AMIA ... Annual Symposium proceedings, 2003, , 195-9.	0.2	41
167	Phenome-Wide Association Studies. JAMA - Journal of the American Medical Association, 2022, 327, 75.	7.4	41
168	A Polygenic and Phenotypic Risk Prediction for Polycystic Ovary Syndrome Evaluated by Phenome-Wide Association Studies. Journal of Clinical Endocrinology and Metabolism, 2020, 105, 1918-1936.	3.6	40
169	Developing an Algorithm to Detect Early Childhood Obesity in Two Tertiary Pediatric Medical Centers. Applied Clinical Informatics, 2016, 07, 693-706.	1.7	39
170	SOS2 and ACP1 Loci Identified through Large-Scale Exome Chip Analysis Regulate Kidney Development and Function. Journal of the American Society of Nephrology: JASN, 2017, 28, 981-994.	6.1	39
171	A multi-stage genome-wide association study of uterine fibroids in African Americans. Human Genetics, 2017, 136, 1363-1373.	3.8	39
172	Medical records-based chronic kidney disease phenotype for clinical care and â€œbig dataâ€•observational and genetic studies. Npj Digital Medicine, 2021, 4, 70.	10.9	39
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