Jennifer Allen Pacheco

List of Publications by Year
in descending order

89 papers	5,602 citations	126708 33 h-index	91712 69 g-index
97 all docs	97 docs citations	97 times ranked	8920 citing authors

#	Article	IF	Citations
1	Systematic comparison of phenome-wide association study of electronic medical record data and genome-wide association study data. Nature Biotechnology, 2013, 31, 1102-1111.	9.4	846
2	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	13.7	353
3	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.	2.2	346
4	Electronic Medical Records for Genetic Research: Results of the eMERGE Consortium. Science Translational Medicine, 2011, 3, 79re1.	5.8	302
5	PheKB: a catalog and workflow for creating electronic phenotype algorithms for transportability. Journal of the American Medical Informatics Association: JAMIA, 2016, 23, 1046-1052.	2.2	284
6	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.	2.2	270
7	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.	2.6	232
8	Portability of an algorithm to identify rheumatoid arthritis in electronic health records. Journal of the American Medical Informatics Association: JAMIA, 2012, 19, e162-e169.	2.2	201
9	Meta-Analysis of Genome-Wide Association Studies in African Americans Provides Insights into the Genetic Architecture of Type 2 Diabetes. PLoS Genetics, 2014, 10, e1004517.	1.5	191
10	Meta-Analysis of Genome-Wide Association Studies for Abdominal Aortic Aneurysm Identifies Four New Disease-Specific Risk Loci. Circulation Research, 2017, 120, 341-353.	2.0	166
11	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.	1.8	135
12	Type 2 Diabetes Variants Disrupt Function of SLC16A11 through Two Distinct Mechanisms. Cell, 2017, 170, 199-212.e20.	13.5	121
13	Desiderata for computable representations of electronic health records-driven phenotype algorithms. Journal of the American Medical Informatics Association: JAMIA, 2015, 22, 1220-1230.	2.2	110
14	GWAS and enrichment analyses of non-alcoholic fatty liver disease identify new trait-associated genes and pathways across eMERGE Network. BMC Medicine, 2019, 17, 135.	2.3	110
15	Impact of data fragmentation across healthcare centers on the accuracy of a high-throughput clinical phenotyping algorithm for specifying subjects with type 2 diabetes mellitus. Journal of the American Medical Informatics Association: JAMIA, 2012, 19, 219-224.	2.2	97
16	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.	2.6	93
17	Identification of Four Novel Loci in Asthma in European American and African American Populations. American Journal of Respiratory and Critical Care Medicine, 2017, 195, 456-463.	2.5	91
18	Genetic Architecture of Abdominal Aortic Aneurysm in the Million Veteran Program. Circulation, 2020, 142, 1633-1646.	1.6	78

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19	Adverse events after surgery for nonmalignant colon polyps areÂcommonÂand associated with increased length of stay andÂcosts. Gastrointestinal Endoscopy, 2016, 84, 296-303.e1.	0.5	71
20	Analyzing the heterogeneity and complexity of Electronic Health Record oriented phenotyping algorithms. AMIA ... Annual Symposium proceedings, 2011, 2011, 274-83.	0.2	68
21	LPA Variants Are Associated With Residual Cardiovascular Risk in Patients Receiving Statins. Circulation, 2018, 138, 1839-1849.	1.6	64
22	Design patterns for the development of electronic health record-driven phenotype extraction algorithms. Journal of Biomedical Informatics, 2014, 51, 280-286.	2.5	55
23	Trans-ethnic Meta-analysis and Functional Annotation Illuminates theÂGenetic Architecture of Fasting Glucose and Insulin. American Journal of Human Genetics, 2016, 99, 56-75.	2.6	55
24	Genetic regulation of OAS1 nonsense-mediated decay underlies association with COVID-19 hospitalization in patients of European and African ancestries. Nature Genetics, 2022, 54, 1103-1116.	9.4	54
25	Facilitating phenotype transfer using a common data model. Journal of Biomedical Informatics, 2019, 96, 103253.	2.5	49
26	Developing a FHIR-based EHR phenotyping framework: A case study for identification of patients with obesity and multiple comorbidities from discharge summaries. Journal of Biomedical Informatics, 2019, 99, 103310.	2.5	48
27	Development and validation of a trans-ancestry polygenic risk score for type 2 diabetes in diverse populations. Genome Medicine, 2022, 14, .	3.6	48
28	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.	2.6	47
29	Apolipoprotein L1 VariantsÂand Blood Pressure Traits inÂAfrican Americans. Journal of the American College of Cardiology, 2017, 69, 1564-1574.	1.2	46
30	Shared Genetic Risk Factors of Intracranial, Abdominal, and Thoracic Aneurysms. Journal of the American Heart Association, 2016, 5, .	1.6	45
31	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.	1.1	44
32	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.	1.5	42
33	A Machine Learning Algorithm for Identifying Atopic Dermatitis in Adults from Electronic Health Records. , 2017, 2017, 83-90.		42
34	Probing the Virtual Proteome to Identify Novel Disease Biomarkers. Circulation, 2018, 138, 2469-2481.	1.6	42
35	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.	1.8	40
36	Generalization of Variants Identified by Genomeâ€Wide Association Studies for Electrocardiographic Traits in African Americans. Annals of Human Genetics, 2013, 77, 321-332.	0.3	37

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37	Accuracy of Phenotyping Chronic Rhinosinusitis in the Electronic Health Record. American Journal of Rhinology and Allergy, 2014, 28, 140-144.	1.0	37
38	Genome-wide study of resistant hypertension identified from electronic health records. PLoS ONE, 2017, 12, e0171745.	1.1	36
39	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.	1.1	34
40	A Trans-Ethnic Genome-Wide Association Study of Uterine Fibroids. Frontiers in Genetics, 2019, 10, 511.	1.1	32
41	An evaluation of the NQF Quality Data Model for representing Electronic Health Record driven phenotyping algorithms. AMIA ... Annual Symposium proceedings, 2012, 2012, 911-20.	0.2	32
42	Review and evaluation of electronic health records-driven phenotype algorithm authoring tools for clinical and translational research. Journal of the American Medical Informatics Association: JAMIA, 2015, 22, 1251-1260.	2.2	30
43	A highly specific algorithm for identifying asthma cases and controls for genome-wide association studies. AMIA ... Annual Symposium proceedings, 2009, 2009, 497-501.	0.2	30
44	A case study evaluating the portability of an executable computable phenotype algorithm across multiple institutions and electronic health record environments. Journal of the American Medical Informatics Association: JAMIA, 2018, 25, 1540-1546.	2.2	29
45	Making work visible for electronic phenotype implementation: Lessons learned from the eMERGE network. Journal of Biomedical Informatics, 2019, 99, 103293.	2.5	27
46	Pathogenic and Uncertain Genetic Variants Have Clinical Cardiac Correlates in Diverse Biobank Participants. Journal of the American Heart Association, 2020, 9, e013808.	1.6	27
47	Association of Pathogenic Variants in Hereditary Cancer Genes With Multiple Diseases. JAMA Oncology, 2022, 8, 835.	3.4	25
48	rs4771122 Predicts Multiple Measures of Long-Term Weight Loss After Bariatric Surgery. Obesity Surgery, 2015, 25, 2225-2229.	1.1	19
49	An ancillary genomics system to support the return of pharmacogenomic results. Journal of the American Medical Informatics Association: JAMIA, 2019, 26, 306-310.	2.2	18
50	Identifying gene-gene interactions that are highly associated with Body Mass Index using Quantitative Multifactor Dimensionality Reduction (QMDR). BioData Mining, 2015, 8, 41.	2.2	17
51	Factors Associated With Long-Term Weight Loss Following Bariatric Surgery Using 2 Methods for Repeated Measures Analysis. American Journal of Epidemiology, 2015, 182, 235-243.	1.6	17
52	Toward <scp>crossâ€platform</scp> electronic health record<scp>â€driven</scp> phenotyping using Clinical Quality Language. Learning Health Systems, 2020, 4, e10233.	1.1	17
53	Desiderata for the development of next-generation electronic health record phenotype libraries. GigaScience, 2021, 10, .	3.3	17
54	Admixture Mapping and Subsequent Fine-Mapping Suggests a Biologically Relevant and Novel Association on Chromosome 11 for Type 2 Diabetes in African Americans. PLoS ONE, 2014, 9, e86931.	1.1	15

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55	Developing a data element repository to support EHR-driven phenotype algorithm authoring and execution. Journal of Biomedical Informatics, 2016, 62, 232-242.	2.5	15
56	Mechanistic Phenotypes: An Aggregative Phenotyping Strategy to Identify Disease Mechanisms Using GWAS Data. PLoS ONE, 2013, 8, e81503.	1.1	15
57	A study paradigm integrating prospective epidemiologic cohorts and electronic health records to identify disease biomarkers. Nature Communications, 2018, 9, 3522.	5.8	13
58	Impact of CYP2C9â€Interacting Drugs on Warfarin Pharmacogenomics. Clinical and Translational Science, 2020, 13, 941-949.	1.5	13
59	A Modular Architecture for Electronic Health Record-Driven Phenotyping. AMIA Summits on Translational Science Proceedings, 2015, 2015, 147-51.	0.4	13
60	A multi-institution evaluation of clinical profile anonymization. Journal of the American Medical Informatics Association: JAMIA, 2016, 23, e131-e137.	2.2	12
61	Subphenotyping depression using machine learning and electronic health records. Learning Health Systems, 2020, 4, e10241.	1.1	12
62	Stratified Mortality Prediction of Patients with Acute Kidney Injury in Critical Care. Studies in Health Technology and Informatics, 2019, 264, 462-466.	0.2	12
63	Automatically detecting problem list omissions of type 2 diabetes cases using electronic medical records. AMIA ... Annual Symposium proceedings, 2011, 2011, 1062-9.	0.2	11
64	A Prototype for Executable and Portable Electronic Clinical Quality Measures Using the KNIME Analytics Platform. AMIA Summits on Translational Science Proceedings, 2015, 2015, 127-31.	0.4	10
65	Performance of an electronic health record-based phenotype algorithm to identify community associated methicillin-resistant Staphylococcus aureus cases and controls for genetic association studies. BMC Infectious Diseases, 2016, 16, 684.	1.3	9
66	Considerations for Improving the Portability of Electronic Health Record-Based Phenotype Algorithms. AMIA ... Annual Symposium proceedings, 2019, 2019, 755-764.	0.2	9
67	Investigating the Genetic Architecture of the PR Interval Using Clinical Phenotypes. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	8
68	Defining a Contemporary Ischemic Heart Disease Genetic Risk Profile Using Historical Data. Circulation: Cardiovascular Genetics, 2016, 9, 521-530.	5.1	7
69	Evaluation of structured data from electronic health records to identify clinical classification criteria attributes for systemic lupus erythematosus. Lupus Science and Medicine, 2021, 8, e000488.	1.1	6
70	A Validated Phenotyping Algorithm for Genetic Association Studies in Age-related Macular Degeneration. Scientific Reports, 2015, 5, 12875.	1.6	5
71	ePhenotyping for Abdominal Aortic Aneurysm in the Electronic Medical Records and Genomics (eMERGE) Network: Algorithm Development and Konstanz Information Miner Workflow. International Journal of Biomedical Data Mining, 2015, 4, .	0.1	5
72	Development of a repository of computable phenotype definitions using the clinical quality language. JAMIA Open, 2021, 4, ooab094.	1.0	5

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73	Association between triglycerides, known risk SNVs and conserved rare variation in SLC25A40 in a multi-ancestry cohort. BMC Medical Genomics, 2021, 14, 11.	0.7	4
74	A Decompositional Approach to Executing Quality Data Model Algorithms on the i2b2 Platform. AMIA Summits on Translational Science Proceedings, 2016, 2016, 167-75.	0.4	4
75	Evaluating the Portability of an NLP System for Processing Echocardiograms: A Retrospective, Multi-site Observational Study. AMIA ... Annual Symposium proceedings, 2019, 2019, 190-199.	0.2	4
76	Design and validation of a FHIR-based EHR-driven phenotyping toolbox. Journal of the American Medical Informatics Association: JAMIA, 0, , .	2.2	4
77	Characterizing Design Patterns of EHR-Driven Phenotype Extraction Algorithms. , 2018, , .		2
78	Genetic association of primary nonresponse to anti-TNFÎ± therapy in patients with inflammatory bowel disease. Pharmacogenetics and Genomics, 2022, 32, 1-9.	0.7	2
79	Prototype Development: Context-Driven Dynamic XML Ophthalmologic Data Capture Application. JMIR Medical Informatics, 2017, 5, e27.	1.3	2
80	Replication of SCN5A Associations with Electrocardiographic Traits in African Americans from Clinical and Epidemiologic Studies. Lecture Notes in Computer Science, 2014, 2014, 939-951.	1.0	2
81	Predictive Modeling of the Risk of Acute Kidney Injury in Critical Care: A Systematic Investigation of The Class Imbalance Problem. AMIA Summits on Translational Science Proceedings, 2019, 2019, 809-818.	0.4	2
82	Phenoflow: A Microservice Architecture for Portable Workflow-based Phenotype Definitions. AMIA Summits on Translational Science Proceedings, 2021, 2021, 142-151.	0.4	2
83	Practice Patterns After Return of Rare Variants Associated With Cardiomyopathy in the Electronic Medical Records and Genomics Network. Circulation: Heart Failure, 2021, 14, e008155.	1.6	1
84	CQL4NLP: Development and Integration of FHIR NLP Extensions in Clinical Quality Language for EHR-driven Phenotyping. AMIA Summits on Translational Science Proceedings, 2021, 2021, 624-633.	0.4	1
85	Under-specification as the source of ambiguity and vagueness in narrative phenotype algorithm definitions. BMC Medical Informatics and Decision Making, 2022, 22, 23.	1.5	1
86	Bone mineral density and FRAX as predictors of fracture risk in women with breast cancer.. Journal of Clinical Oncology, 2013, 31, 121-121.	0.8	0
87	1302â€…Utilization of a clinical data research network to assess systemic lupus international coordinating clinics. , 2021, , .		0
88	802â€…An electronic health record-based approach to identify and characterize patients with immune checkpoint inhibitor-associated arthritis. , 2021, 9, A838-A839.		0
89	Assessing the Concordance of Clinical Classification Criteria for Lupus Between Electronic Health Records and a Physician Curated Registry. Studies in Health Technology and Informatics, 2019, 264, 1466-1467.	0.2	0