Vern Kerchberger

List of Publications by Year
in descending order

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85	4,115	218381	143772
papers	citations	26 h-index	57 g-index

89	89	89	6711
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	13.7	353
2	Precision Medicine, AI, and the Future of Personalized Health Care. Clinical and Translational Science, 2021, 14, 86-93.	1.5	349
3	Trans-ethnic association study of blood pressure determinants in over 750,000 individuals. Nature Genetics, 2019, 51, 51-62.	9.4	328
4	Mapping ICD-10 and ICD-10-CM Codes to Phecodes: Workflow Development and Initial Evaluation. JMIR Medical Informatics, 2019, 7, e14325.	1.3	323
5	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
6	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.	1.1	268
7	Extracting research-quality phenotypes from electronic health records to support precision medicine. Genome Medicine, 2015, 7, 41.	3.6	181
8	Phenotype risk scores identify patients with unrecognized Mendelian disease patterns. Science, 2018, 359, 1233-1239.	6.0	164
9	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.	2.2	157
10	Genome-wide Modeling of Polygenic Risk Score in Colorectal Cancer Risk. American Journal of Human Genetics, 2020, 107, 432-444.	2.6	124
11	Learning from Longitudinal Data in Electronic Health Record and Genetic Data to Improve Cardiovascular Event Prediction. Scientific Reports, 2019, 9, 717.	1.6	115
12	Use of Genetic Variants Related to Antihypertensive Drugs to Inform on Efficacy and Side Effects. Circulation, 2019, 140, 270-279.	1.6	99
13	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
14	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
15	Development and evaluation of an ensemble resource linking medications to their indications. Journal of the American Medical Informatics Association: JAMIA, 2013, 20, 954-961.	2.2	92
16	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.	3.9	81
17	LPA Variants Are Associated With Residual Cardiovascular Risk in Patients Receiving Statins. Circulation, 2018, 138, 1839-1849.	1.6	64
18	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.	0.5	57

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19	Facilitating phenotype transfer using a common data model. Journal of Biomedical Informatics, 2019, 96, 103253.	2.5	49
20	Plasma sRAGE Acts as a Genetically Regulated Causal Intermediate in Sepsis-associated Acute Respiratory Distress Syndrome. American Journal of Respiratory and Critical Care Medicine, 2020, 201, 47-56.	2.5	49
21	The Influence of Big (Clinical) Data and Genomics on Precision Medicine and Drug Development. Clinical Pharmacology and Therapeutics, 2018, 103, 409-418.	2.3	42
22	Association Between Low-Density Lipoprotein Cholesterol Levels and Risk for Sepsis Among Patients Admitted to the Hospital With Infection. JAMA Network Open, 2019, 2, e187223.	2.8	40
23	Defining Phenotypes from Clinical Data to Drive Genomic Research. Annual Review of Biomedical Data Science, 2018, 1, 69-92.	2.8	38
24	Novel Method for Noninvasive Sampling of the Distal Airspace in Acute Respiratory Distress Syndrome. American Journal of Respiratory and Critical Care Medicine, 2018, 197, 1027-1035.	2.5	35
25	Genome-wide Study Identifies Association between HLA-Bâˆ—55:01 and Self-Reported Penicillin Allergy. American Journal of Human Genetics, 2020, 107, 612-621.	2.6	34
26	Detecting time-evolving phenotypic topics via tensor factorization on electronic health records: Cardiovascular disease case study. Journal of Biomedical Informatics, 2019, 98, 103270.	2.5	32
27	PheMap: a multi-resource knowledge base for high-throughput phenotyping within electronic health records. Journal of the American Medical Informatics Association: JAMIA, 2020, 27, 1675-1687.	2.2	28
28	Making work visible for electronic phenotype implementation: Lessons learned from the eMERGE network. Journal of Biomedical Informatics, 2019, 99, 103293.	2.5	27
29	The Role of Circulating Cell-Free Hemoglobin in Sepsis-Associated Acute Kidney Injury. Seminars in Nephrology, 2020, 40, 148-159.	0.6	26
30	A Genetic Approach to the Association Between PCSK9 and Sepsis. JAMA Network Open, 2019, 2, e1911130.	2.8	25
31	Alveolar epithelial glycocalyx degradation mediates surfactant dysfunction and contributes to acute respiratory distress syndrome. JCI Insight, 2022, 7, .	2.3	24
32	Genomeâ€Wide Association and Functional Studies Reveal Novel Pharmacological Mechanisms for Allopurinol. Clinical Pharmacology and Therapeutics, 2019, 106, 623-631.	2.3	23
33	Relationship between very low low-density lipoprotein cholesterol concentrations not due to statin therapy and risk of type 2 diabetes: A US-based cross-sectional observational study using electronic health records. PLoS Medicine, 2018, 15, e1002642.	3.9	22
34	A high throughput semantic concept frequency based approach for patient identification: a case study using type 2 diabetes mellitus clinical notes. AMIA ... Annual Symposium proceedings, 2010, 2010, 857-61.	0.2	22
35	Using topic modeling via non-negative matrix factorization to identify relationships between genetic variants and disease phenotypes: A case study of Lipoprotein(a) (LPA). PLoS ONE, 2019, 14, e0212112.	1.1	20
36	Phenome-wide association analysis suggests the APOL1 linked disease spectrum primarily drives kidney-specific pathways. Kidney International, 2020, 97, 1032-1041.	2.6	20

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37	A retrospective approach to evaluating potential adverse outcomes associated with delay of procedures for cardiovascular and cancer-related diagnoses in the context of COVID-19. Journal of Biomedical Informatics, 2021, 113, 103657.	2.5	20
38	Haptoglobin-2 variant increases susceptibility to acute respiratory distress syndrome during sepsis. JCI Insight, 2019, 4, .	2.3	20
39	Integrating gene expression and clinical data to identify drug repurposing candidates for hyperlipidemia and hypertension. Nature Communications, 2022, 13, 46.	5.8	19
40	Arrhythmia Variant Associations and Reclassifications in the eMERGE-III Sequencing Study. Circulation, 2022, 145, 877-891.	1.6	18
41	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.	1.5	17
42	A Mendelian Randomization Approach Using 3-HMG-Coenzyme-A Reductase Gene Variation to Evaluate the Association of Statin-Induced Low-Density Lipoprotein Cholesterol Lowering With Noncardiovascular Disease Phenotypes. JAMA Network Open, 2021, 4, e2112820.	2.8	16
43	Assessing the role of a medication-indication resource in the treatment relation extraction from clinical text. Journal of the American Medical Informatics Association: JAMIA, 2015, 22, e162-e176.	2.2	15
44	TPMT and NUDT15 Variants Predict Discontinuation of Azathioprine for Myelotoxicity in Patients with Inflammatory Disease: Realâ€World Clinical Results. Clinical Pharmacology and Therapeutics, 2022, 111, 263-271.	2.3	14
45	Race, Genotype, and Azathioprine Discontinuation. Annals of Internal Medicine, 2022, 175, 1092-1099.	2.0	14
46	A study paradigm integrating prospective epidemiologic cohorts and electronic health records to identify disease biomarkers. Nature Communications, 2018, 9, 3522.	5.8	13
47	Coâ€Prescription of Strong <scp>CYP</scp>1A2 Inhibitors and the Risk of Tizanidineâ€Associated Hypotension: A Retrospective Cohort Study. Clinical Pharmacology and Therapeutics, 2019, 105, 703-709.	2.3	13
48	Polygenic Risk Score to Identify Subclinical Coronary Heart Disease Risk in Young Adults. Circulation Genomic and Precision Medicine, 2021, 14, e003341.	1.6	12
49	Readiness for PENicillin allergy testing: Perception of Allergy Label (PEN-PAL) survey. Journal of Allergy and Clinical Immunology: in Practice, 2020, 8, 3180-3182.e4.	2.0	11
50	ConceptWAS: A high-throughput method for early identification of COVID-19 presenting symptoms and characteristics from clinical notes. Journal of Biomedical Informatics, 2021, 117, 103748.	2.5	11
51	Phenotyping coronavirus disease 2019 during a global health pandemic: Lessons learned from the characterization of an early cohort. Journal of Biomedical Informatics, 2021, 117, 103777.	2.5	11
52	Standardization of methods for sampling the distal airspace in mechanically ventilated patients using heat moisture exchange filter fluid. American Journal of Physiology - Lung Cellular and Molecular Physiology, 2021, 320, L785-L790.	1.3	11
53	Penicillin allergy labels drive perioperative prophylactic antibiotic selection in orthopedic procedures. Journal of Allergy and Clinical Immunology: in Practice, 2020, 8, 3634-3636.e1.	2.0	10
54	DDIWAS: High-throughput electronic health record-based screening of drug-drug interactions. Journal of the American Medical Informatics Association: JAMIA, 2021, 28, 1421-1430.	2.2	10

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55	Replication and fine-mapping of genetic predictors of lipid traits in Africanâ€“Americans. Journal of Human Genetics, 2017, 62, 895-901.	1.1	9
56	Genomeâ€Wide Approach to Measure Variantâ€Based Heritability of Drug Outcome Phenotypes. Clinical Pharmacology and Therapeutics, 2021, 110, 714-722.	2.3	7
57	Combining clinical and candidate gene data into a risk score for azathioprine-associated leukopenia in routine clinical practice. Pharmacogenomics Journal, 2020, 20, 736-745.	0.9	6
58	Clinical and Genetic Contributors to New-Onset Atrial Fibrillation in Critically Ill Adults*. Critical Care Medicine, 2020, 48, 22-30.	0.4	5
59	Pharmacogenetics of hypoglycemia associated with sulfonylurea therapy in usual clinical care. Pharmacogenomics Journal, 2020, 20, 831-839.	0.9	5
60	Novel and known morbidities of leukodystrophies identified using a phenome-wide association study. Neurology: Clinical Practice, 2020, 10, 406-414.	0.8	5
61	Response to Li and Hopper. American Journal of Human Genetics, 2021, 108, 527-529.	2.6	5
62	High-throughput framework forÂgenetic analyses of adverse drug reactions using electronic health records. PLoS Genetics, 2021, 17, e1009593.	1.5	5
63	Impact of Clinician Recognition of Acute Respiratory Distress Syndrome on Evidenced-Based Interventions in the Medical ICU. , 2021, 3, e0457.		5
64	Association of Genetic Risk of Obesity with Postoperative Complications Using Mendelian Randomization. World Journal of Surgery, 2020, 44, 84-94.	0.8	4
65	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
66	Racial disparity in taxaneâ€induced neutropenia among cancer patients. Cancer Medicine, 2021, 10, 6767-6776.	1.3	4
67	Integration of Omics and Phenotypic Data for Precision Medicine. Methods in Molecular Biology, 2022, 2486, 19-35.	0.4	4
68	Neptune: an environment for the delivery of genomic medicine. Genetics in Medicine, 2021, 23, 1838-1846.	1.1	3
69	An updated, computable MEDication-Indication resource for biomedical research. Scientific Reports, 2021, 11, 18953.	1.6	3
70	Brief Report: Predicted Expression of Genes Involved in the Thiopurine Metabolic Pathway and Azathioprine Discontinuation Due to Myelotoxicity. Clinical and Translational Science, 2022, , .	1.5	3
71	Machine Learning Challenges in Pharmacogenomic Research. Clinical Pharmacology and Therapeutics, 2021, 110, 552-554.	2.3	2
72	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

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73	Novel Analysis Methods to Mine Immune-Mediated Phenotypes and Find Genetic Variation Within the Electronic Health Record (Roadmap for Phenotype to Genotype: Immunogenomics). Journal of Allergy and Clinical Immunology: in Practice, 2022, , .	2.0	2
74	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
75	Psychiatric manifestations of rare variation in medically actionable genes: a PheWAS approach. BMC Genomics, 2022, 23, 385.	1.2	1
76	Mendelian randomization analysis of plasma levels of CD209 and MICB proteins and the risk of varicose veins of lower extremities. PLoS ONE, 2022, 17, e0268725.	1.1	1
77	Using a gene-environment interaction study to evaluate risk for lung cancer.. Journal of Clinical Oncology, 2016, 34, 1524-1524.	0.8	0
78	Title is missing!. , 2020, 16, e1008684.		0
79	Title is missing!. , 2020, 16, e1008684.		0
80	Title is missing!. , 2020, 16, e1008684.		0
81	Title is missing!. , 2020, 16, e1008684.		0
82	Title is missing!. , 2020, 16, e1008684.		0
83	Title is missing!. , 2020, 16, e1008684.		0
84	Mapping the Read2/CTV3 controlled clinical terminologies to Phecodes in UK Biobank primary care electronic health records: implementation and evaluation.. AMIA ... Annual Symposium proceedings, 2021, 2021, 362-371.	0.2	0
85	Pulmonary Vasculopathy in COVID-19 ARDS: A Step Closer to the Full Picture. American Journal of Respiratory and Critical Care Medicine, 0, , .	2.5	0