Wei-Qi Wei

List of Publications by Year
in descending order

57 papers	3,700 citations	279798 23 h-index	197818 49 g-index
62 all docs	62 docs citations	62 times ranked	7591 citing authors

#	Article	IF	Citations
1	Identifying Potential Therapeutic Applications and Diagnostic Harms of Increased Bilirubin Concentrations: A Clinical and Genetic Approach. Clinical Pharmacology and Therapeutics, 2022, 111, 435-443.	4.7	4
2	Integrating gene expression and clinical data to identify drug repurposing candidates for hyperlipidemia and hypertension. Nature Communications, 2022, 13, 46.	12.8	19
3	Arrhythmia Variant Associations and Reclassifications in the eMERGE-III Sequencing Study. Circulation, 2022, 145, 877-891.	1.6	18
4	Integration of Omics and Phenotypic Data for Precision Medicine. Methods in Molecular Biology, 2022, 2486, 19-35.	0.9	4
5	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, , .	3.8	2
6	Psychiatric manifestations of rare variation in medically actionable genes: a PheWAS approach. BMC Genomics, 2022, 23, 385.	2.8	1
7	Race, Genotype, and Azathioprine Discontinuation. Annals of Internal Medicine, 2022, 175, 1092-1099.	3.9	14
8	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.	4.3	20
9	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
10	DDIWAS: High-throughput electronic health record-based screening of drug-drug interactions. Journal of the American Medical Informatics Association: JAMIA, 2021, 28, 1421-1430.	4.4	10
11	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.	4.3	11
12	Pleiotropy of systemic lupus erythematosus risk alleles and cardiometabolic disorders: A phenome-wide association study and inverse-variance weighted meta-analysis. Lupus, 2021, 30, 1264-1272.	1.6	2
13	Genomic considerations for FHIRÂ®; eMERGE implementation lessons. Journal of Biomedical Informatics, 2021, 118, 103795.	4.3	15
14	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.	5.9	16
15	High-throughput framework forÂgenetic analyses of adverse drug reactions using electronic health records. PLoS Genetics, 2021, 17, e1009593.	3.5	5
16	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
17	Quantitative disease risk scores from EHR with applications to clinical risk stratification and genetic studies. Npj Digital Medicine, 2021, 4, 116.	10.9	7
18	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

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19	Polygenic Risk Score to Identify Subclinical Coronary Heart Disease Risk in Young Adults. Circulation Genomic and Precision Medicine, 2021, 14, e003341.	3.6	12
20	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
21	Association of Genetic Risk of Obesity with Postoperative Complications Using Mendelian Randomization. World Journal of Surgery, 2020, 44, 84-94.	1.6	4
22	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.	4.4	28
23	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.	3.8	11
24	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
25	Novel and known morbidities of leukodystrophies identified using a phenome-wide association study. Neurology: Clinical Practice, 2020, 10, 406-414.	1.6	5
26	A missense variant in Mitochondrial Amidoxime Reducing Component 1 gene and protection against liver disease. PLoS Genetics, 2020, 16, e1008629.	3.5	101
27	Genome-wide Study Identifies Association between HLA-Bâˆ—55:01 and Self-Reported Penicillin Allergy. American Journal of Human Genetics, 2020, 107, 612-621.	6.2	34
28	Title is missing!. , 2020, 16, e1008684.		0
29	Title is missing!. , 2020, 16, e1008684.		0
30	Title is missing!. , 2020, 16, e1008684.		0
31	Title is missing!. , 2020, 16, e1008684.		0
32	Title is missing!. , 2020, 16, e1008684.		0
33	Title is missing!. , 2020, 16, e1008684.		0
34	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.	5.5	110
35	Harmonizing Clinical Sequencing and Interpretation for the eMERGE III Network. American Journal of Human Genetics, 2019, 105, 588-605.	6.2	99
36	Detecting time-evolving phenotypic topics via tensor factorization on electronic health records: Cardiovascular disease case study. Journal of Biomedical Informatics, 2019, 98, 103270.	4.3	32

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37	Learning from Longitudinal Data in Electronic Health Record and Genetic Data to Improve Cardiovascular Event Prediction. Scientific Reports, 2019, 9, 717.	3.3	115
38	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.	2.5	20
39	A phenome-wide association study to discover pleiotropic effects of PCSK9, APOB, and LDLR. Npj Genomic Medicine, 2019, 4, 3.	3.8	26
40	Mapping ICD-10 and ICD-10-CM Codes to Phecodes: Workflow Development and Initial Evaluation. JMIR Medical Informatics, 2019, 7, e14325.	2.6	323
41	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
42	LPA Variants Are Associated With Residual Cardiovascular Risk in Patients Receiving Statins. Circulation, 2018, 138, 1839-1849.	1.6	64
43	Phenotype risk scores identify patients with unrecognized Mendelian disease patterns. Science, 2018, 359, 1233-1239.	12.6	164
44	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.	8.4	22
45	Defining Phenotypes from Clinical Data to Drive Genomic Research. Annual Review of Biomedical Data Science, 2018, 1, 69-92.	6.5	38
46	Efficiently controlling for case-control imbalance and sample relatedness in large-scale genetic association studies. Nature Genetics, 2018, 50, 1335-1341.	21.4	896
47	Identification of susceptibility pathways for the role of chromosome 15q25.1 in modifying lung cancer risk. Nature Communications, 2018, 9, 3221.	12.8	60
48	Detecting potential pleiotropy across cardiovascular and neurological diseases using univariate, bivariate, and multivariate methods on 43,870 individuals from the eMERGE network. , 2018, , .		6
49	Replication and fine-mapping of genetic predictors of lipid traits in Africanâ€“Americans. Journal of Human Genetics, 2017, 62, 895-901.	2.3	9
50	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
51	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
52	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
53	Extracting research-quality phenotypes from electronic health records to support precision medicine. Genome Medicine, 2015, 7, 41.	8.2	181
54	The absence of longitudinal data limits the accuracy of high-throughput clinical phenotyping for identifying type 2 diabetes mellitus subjects. International Journal of Medical Informatics, 2013, 82, 239-247.	3.3	42

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55	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
56	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.	4.4	97
57	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