

# Wei-Qi Wei

## List of Publications by Year in descending order

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Version: 2024-02-01

57  
papers

3,700  
citations

279487

23  
h-index

197535

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. <i>Clinical Pharmacology and Therapeutics</i> , 2022, 111, 435-443.	2.3	4
2	Integrating gene expression and clinical data to identify drug repurposing candidates for hyperlipidemia and hypertension. <i>Nature Communications</i> , 2022, 13, 46.	5.8	19
3	Arrhythmia Variant Associations and Reclassifications in the eMERGE-III Sequencing Study. <i>Circulation</i> , 2022, 145, 877-891.	1.6	18
4	Integration of Omics and Phenotypic Data for Precision Medicine. <i>Methods in Molecular Biology</i> , 2022, 2486, 19-35.	0.4	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). <i>Journal of Allergy and Clinical Immunology: in Practice</i> , 2022, , .	2.0	2
6	Psychiatric manifestations of rare variation in medically actionable genes: a PheWAS approach. <i>BMC Genomics</i> , 2022, 23, 385.	1.2	1
7	Race, Genotype, and Azathioprine Discontinuation. <i>Annals of Internal Medicine</i> , 2022, 175, 1092-1099.	2.0	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. <i>Journal of Biomedical Informatics</i> , 2021, 113, 103657.	2.5	20
9	Association of Genetic Variation With Cirrhosis: A Multi-Trait Genome-Wide Association and Gene-Environment Interaction Study. <i>Gastroenterology</i> , 2021, 160, 1620-1633.e13.	0.6	68
10	DDIWAS: High-throughput electronic health record-based screening of drug-drug interactions. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2021, 28, 1421-1430.	2.2	10
11	Phenotyping coronavirus disease 2019 during a global health pandemic: Lessons learned from the characterization of an early cohort. <i>Journal of Biomedical Informatics</i> , 2021, 117, 103777.	2.5	11
12	Pleiotropy of systemic lupus erythematosus risk alleles and cardiometabolic disorders: A phenome-wide association study and inverse-variance weighted meta-analysis. <i>Lupus</i> , 2021, 30, 1264-1272.	0.8	2
13	Genomic considerations for FHIR®; eMERGE implementation lessons. <i>Journal of Biomedical Informatics</i> , 2021, 118, 103795.	2.5	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. <i>JAMA Network Open</i> , 2021, 4, e2112820.	2.8	16
15	High-throughput framework for genetic analyses of adverse drug reactions using electronic health records. <i>PLoS Genetics</i> , 2021, 17, e1009593.	1.5	5
16	A unified framework identifies new links between plasma lipids and diseases from electronic medical records across large-scale cohorts. <i>Nature Genetics</i> , 2021, 53, 972-981.	9.4	17
17	Quantitative disease risk scores from EHR with applications to clinical risk stratification and genetic studies. <i>Npj Digital Medicine</i> , 2021, 4, 116.	5.7	7
18	Associations of Genetically Predicted Lp(a) (Lipoprotein [a]) Levels With Cardiovascular Traits in Individuals of European and African Ancestry. <i>Circulation Genomic and Precision Medicine</i> , 2021, 14, e003354.	1.6	21

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19	Polygenic Risk Score to Identify Subclinical Coronary Heart Disease Risk in Young Adults. <i>Circulation Genomic and Precision Medicine</i> , 2021, 14, e003341.	1.6	12
20	Mapping the Read2/CTV3 controlled clinical terminologies to Phecodes in UK Biobank primary care electronic health records: implementation and evaluation.. <i>AMIA ... Annual Symposium proceedings</i> , 2021, 2021, 362-371.	0.2	0
21	Association of Genetic Risk of Obesity with Postoperative Complications Using Mendelian Randomization. <i>World Journal of Surgery</i> , 2020, 44, 84-94.	0.8	4
22	PheMap: a multi-resource knowledge base for high-throughput phenotyping within electronic health records. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2020, 27, 1675-1687.	2.2	28
23	Readiness for PENicillin allergy testing: Perception of Allergy Label (PEN-PAL) survey. <i>Journal of Allergy and Clinical Immunology: in Practice</i> , 2020, 8, 3180-3182.e4.	2.0	11
24	Minority-centric meta-analyses of blood lipid levels identify novel loci in the Population Architecture using Genomics and Epidemiology (PAGE) study. <i>PLoS Genetics</i> , 2020, 16, e1008684.	1.5	17
25	Novel and known morbidities of leukodystrophies identified using a phenome-wide association study. <i>Neurology: Clinical Practice</i> , 2020, 10, 406-414.	0.8	5
26	A missense variant in Mitochondrial Amidoxime Reducing Component 1 gene and protection against liver disease. <i>PLoS Genetics</i> , 2020, 16, e1008629.	1.5	101
27	Genome-wide Study Identifies Association between HLA-B*55:01 and Self-Reported Penicillin Allergy. <i>American Journal of Human Genetics</i> , 2020, 107, 612-621.	2.6	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. <i>BMC Medicine</i> , 2019, 17, 135.	2.3	110
35	Harmonizing Clinical Sequencing and Interpretation for the eMERGE III Network. <i>American Journal of Human Genetics</i> , 2019, 105, 588-605.	2.6	99
36	Detecting time-evolving phenotypic topics via tensor factorization on electronic health records: Cardiovascular disease case study. <i>Journal of Biomedical Informatics</i> , 2019, 98, 103270.	2.5	32

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37	Learning from Longitudinal Data in Electronic Health Record and Genetic Data to Improve Cardiovascular Event Prediction. <i>Scientific Reports</i> , 2019, 9, 717.	1.6	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). <i>PLoS ONE</i> , 2019, 14, e0212112.	1.1	20
39	A phenome-wide association study to discover pleiotropic effects of PCSK9, APOB, and LDLR. <i>Npj Genomic Medicine</i> , 2019, 4, 3.	1.7	26
40	Mapping ICD-10 and ICD-10-CM Codes to Phecodes: Workflow Development and Initial Evaluation. <i>JMIR Medical Informatics</i> , 2019, 7, e14325.	1.3	323
41	MR-PheWAS: exploring the causal effect of SUA level on multiple disease outcomes by using genetic instruments in UK Biobank. <i>Annals of the Rheumatic Diseases</i> , 2018, 77, 1039-1047.	0.5	57
42	<i>LPA</i> Variants Are Associated With Residual Cardiovascular Risk in Patients Receiving Statins. <i>Circulation</i> , 2018, 138, 1839-1849.	1.6	64
43	Phenotype risk scores identify patients with unrecognized Mendelian disease patterns. <i>Science</i> , 2018, 359, 1233-1239.	6.0	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. <i>PLoS Medicine</i> , 2018, 15, e1002642.	3.9	22
45	Defining Phenotypes from Clinical Data to Drive Genomic Research. <i>Annual Review of Biomedical Data Science</i> , 2018, 1, 69-92.	2.8	38
46	Efficiently controlling for case-control imbalance and sample relatedness in large-scale genetic association studies. <i>Nature Genetics</i> , 2018, 50, 1335-1341.	9.4	896
47	Identification of susceptibility pathways for the role of chromosome 15q25.1 in modifying lung cancer risk. <i>Nature Communications</i> , 2018, 9, 3221.	5.8	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 African&quot;Americans. <i>Journal of Human Genetics</i> , 2017, 62, 895-901.	1.1	9
50	Evaluating electronic health record data sources and algorithmic approaches to identify hypertensive individuals. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2017, 24, 162-171.	2.2	74
51	Evaluating phecodes, clinical classification software, and ICD-9-CM codes for phenome-wide association studies in the electronic health record. <i>PLoS ONE</i> , 2017, 12, e0175508.	1.1	268
52	Combining billing codes, clinical notes, and medications from electronic health records provides superior phenotyping performance. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2016, 23, e20-e27.	2.2	157
53	Extracting research-quality phenotypes from electronic health records to support precision medicine. <i>Genome Medicine</i> , 2015, 7, 41.	3.6	181
54	The absence of longitudinal data limits the accuracy of high-throughput clinical phenotyping for identifying type 2 diabetes mellitus subjects. <i>International Journal of Medical Informatics</i> , 2013, 82, 239-247.	1.6	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.	2.2	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.	2.2	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.	2.2	270