QiPing Feng

List of Publications by Year in descending order

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51 papers	1,854 citations	430874 18 h-index	302126 39 g-index
56 all docs	56 docs citations	56 times ranked	3592 citing authors

#	Article	IF	Citations
1	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.	4.7	14
2	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
3	Radical Addition of 4-Hydroxyquinazolines and Alkylation of Quinones by the Electro-Induced Homolysis of 4-Alkyl-1,4-diÂhydropyridines. Synthesis, 2022, 54, 2696-2706.	2.3	1
4	Integrating gene expression and clinical data to identify drug repurposing candidates for hyperlipidemia and hypertension. Nature Communications, 2022, 13, 46.	12.8	19
5	Brief Report: Predicted Expression of Genes Involved in the Thiopurine Metabolic Pathway and Azathioprine Discontinuation Due to Myelotoxicity. Clinical and Translational Science, 2022, , .	3.1	3
6	Integration of Omics and Phenotypic Data for Precision Medicine. Methods in Molecular Biology, 2022, 2486, 19-35.	0.9	4
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	Loci identified by a genomeâ€wide association study of carotid artery stenosis in the eMERGE network. Genetic Epidemiology, 2021, 45, 4-15.	1.3	6
11	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
12	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.	4.3	11
13	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
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	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
18	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	27.8	353

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19	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
20	Statin-induced LDL cholesterol response and type 2 diabetes: a bidirectional two-sample Mendelian randomization study. Pharmacogenomics Journal, 2020, 20, 462-470.	2.0	18
21	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
22	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.	6.2	93
23	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
24	Phenome-wide association analysis suggests the APOL1 linked disease spectrum primarily drives kidney-specific pathways. Kidney International, 2020, 97, 1032-1041.	5.2	20
25	Combining clinical and candidate gene data into a risk score for azathioprine-associated leukopenia in routine clinical practice. Pharmacogenomics Journal, 2020, 20, 736-745.	2.0	6
26	Pleiotropy in the Genetic Predisposition to Rheumatoid Arthritis: A Phenomeâ€Wide Association Study and Inverse Varianceâ€“Weighted Metaâ€Analysis. Arthritis and Rheumatology, 2020, 72, 1483-1492.	5.6	10
27	A missense variant in Mitochondrial Amidoxime Reducing Component 1 gene and protection against liver disease. PLoS Genetics, 2020, 16, e1008629.	3.5	101
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	A Genetic Approach to the Association Between PCSK9 and Sepsis. JAMA Network Open, 2019, 2, e1911130.	5.9	25
35	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
36	Learning from Longitudinal Data in Electronic Health Record and Genetic Data to Improve Cardiovascular Event Prediction. Scientific Reports, 2019, 9, 717.	3.3	115

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37	Use of Genetic Variants Related to Antihypertensive Drugs to Inform on Efficacy and Side Effects. Circulation, 2019, 140, 270-279.	1.6	99
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	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.	4.7	13
41	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.	5.9	40
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	A study paradigm integrating prospective epidemiologic cohorts and electronic health records to identify disease biomarkers. Nature Communications, 2018, 9, 3522.	12.8	13
45	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
46	Replication and fine-mapping of genetic predictors of lipid traits in Africanâ€“Americans. Journal of Human Genetics, 2017, 62, 895-901.	2.3	9
47	Meta-analysis of genome-wide association studies of HDL cholesterol response to statins. Journal of Medical Genetics, 2016, 53, 835-845.	3.2	28
48	Pharmacogenetic meta-analysis of genome-wide association studies of LDL cholesterol response to statins. Nature Communications, 2014, 5, 5068.	12.8	216
49	Approach to Clinical and Genetic Characterization of Statin-Induced Myopathy. Methods in Molecular Biology, 2014, 1175, 67-90.	0.9	6
50	Individualized risk for statin-induced myopathy: current knowledge, emerging challenges and potential solutions. Pharmacogenomics, 2012, 13, 579-594.	1.3	57
51	A Common CNR1 (Cannabinoid Receptor 1) Haplotype Attenuates the Decrease in HDL Cholesterol That Typically Accompanies Weight Gain. PLoS ONE, 2010, 5, e15779.	2.5	12