# QiPing Feng

## List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/5369635/publications.pdf

Version: 2024-02-01

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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 | The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679. | 27.8 | 353 |
| 2 | Pharmacogenetic meta-analysis of genome-wide association studies of LDL cholesterol response to statins. Nature Communications, 2014, 5, 5068. | 12.8 | 216 |
| 3 | Phenotype risk scores identify patients with unrecognized Mendelian disease patterns. Science, 2018, 359, 1233-1239. | 12.6 | 164 |
| 4 | Learning from Longitudinal Data in Electronic Health Record and Genetic Data to Improve Cardiovascular Event Prediction. Scientific Reports, 2019, 9, 717. | 3.3 | 115 |
| 5 | A missense variant in Mitochondrial Amidoxime Reducing Component 1 gene and protection against liver disease. PLoS Genetics, 2020, 16, e1008629. | 3.5 | 101 |
| 6 | Use of Genetic Variants Related to Antihypertensive Drugs to Inform on Efficacy and Side Effects. Circulation, 2019, 140, 270-279. | 1.6 | 99 |
| 7 | 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 |
| 8 | 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 |
| 9 | LPA Variants Are Associated With Residual Cardiovascular Risk in Patients Receiving Statins. Circulation, 2018, 138, 1839-1849. | 1.6 | 64 |
| 10 | Individualized risk for statin-induced myopathy: current knowledge, emerging challenges and potential solutions. Pharmacogenomics, 2012, 13, 579-594. | 1.3 | 57 |
| 11 | 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 |
| 12 | 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 |
| 13 | Meta-analysis of genome-wide association studies of HDL cholesterol response to statins. Journal of Medical Genetics, 2016, 53, 835-845. | 3.2 | 28 |
| 14 | 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 |
| 15 | A phenome-wide association study to discover pleiotropic effects of PCSK9, APOB, and LDLR. Npj Genomic Medicine, 2019, 4, 3. | 3.8 | 26 |
| 16 | A Genetic Approach to the Association Between PCSK9 and Sepsis. JAMA Network Open, 2019, 2, e1911130. | 5.9 | 25 |
| 17 | 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 |
| 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 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | 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 |
| 20 | Phenome-wide association analysis suggests the APOL1 linked disease spectrum primarily drives kidney-specific pathways. Kidney International, 2020, 97, 1032-1041. | 5.2 | 20 |
| 21 | 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 |
| 22 | Integrating gene expression and clinical data to identify drug repurposing candidates for hyperlipidemia and hypertension. Nature Communications, 2022, 13, 46. | 12.8 | 19 |
| 23 | 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 |
| 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 | 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 |
| 26 | 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 |
| 27 | 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 |
| 28 | Race, Genotype, and Azathioprine Discontinuation. Annals of Internal Medicine, 2022, 175, 1092-1099. | 3.9 | 14 |
| 29 | A study paradigm integrating prospective epidemiologic cohorts and electronic health records to identify disease biomarkers. Nature Communications, 2018, 9, 3522. | 12.8 | 13 |
| 30 | 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 |
| 31 | 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 |
| 32 | 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 |
| 33 | 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 |
| 34 | 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 |
| 35 | Replication and fine-mapping of genetic predictors of lipid traits in Africanâ€"Americans. Journal of Human Genetics, 2017, 62, 895-901. | 2.3 | 9 |
| 36 | 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 |

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|---|---|---|---|
| 37 | 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 |
| 38 | Approach to Clinical and Genetic Characterization of Statin-Induced Myopathy. Methods in Molecular Biology, 2014, 1175, 67-90. | 0.9 | 6 |
| 39 | High-throughput framework forÂgenetic analyses of adverse drug reactions using electronic health records. PLoS Genetics, 2021, 17, e1009593. | 3.5 | 5 |
| 40 | 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 |
| 41 | Integration of Omics and Phenotypic Data for Precision Medicine. Methods in Molecular Biology, 2022, 2486, 19-35. | 0.9 | 4 |
| 42 | 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 |
| 43 | 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 |
| 44 | 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 |
| 45 | Title is missing!. , 2020, 16, e1008684. | | 0 |
| 46 | Title is missing!. , 2020, 16, e1008684. | | 0 |
| 47 | Title is missing!. , 2020, 16, e1008684. | | 0 |
| 48 | Title is missing!. , 2020, 16, e1008684. | | 0 |
| 49 | Title is missing!. , 2020, 16, e1008684. | | 0 |
| 50 | Title is missing!. , 2020, 16, e1008684. | | 0 |
| 51 | 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 |