Lee, Ming Ta Michael

List of Publications by Year
in descending order

74 papers	7,777 citations	101543 36 h-index	85541 71 g-index
83 all docs	83 docs citations	83 times ranked	12288 citing authors

#	Article	IF	Citations
1	The landscape of cancer genes and mutational processes in breast cancer. Nature, 2012, 486, 400-404.	27.8	1,535
2	Estimation of the Warfarin Dose with Clinical and Pharmacogenetic Data. New England Journal of Medicine, 2009, 360, 753-764.	27.0	1,375
3	Clinical Pharmacogenetics Implementation Consortium Guidelines for CYP2C9 and VKORC1 Genotypes and Warfarin Dosing. Clinical Pharmacology and Therapeutics, 2011, 90, 625-629.	4.7	571
4	A novel functional VKORC1 promoter polymorphism is associated with inter-individual and inter-ethnic differences in warfarin sensitivity. Human Molecular Genetics, 2005, 14, 1745-1751.	2.9	429
5	Incorporation of Pharmacogenomics into Routine Clinical Practice: the Clinical Pharmacogenetics Implementation Consortium (CPIC) Guideline Development Process. Current Drug Metabolism, 2014, 15, 209-217.	1.2	341
6	Warfarin pharmacogenetics: a single VKORC1 polymorphism is predictive of dose across 3 racial groups. Blood, 2010, 115, 3827-3834.	1.4	331
7	Clinical Pharmacogenetics Implementation Consortium Guidelines for Human Leukocyte Antigen-B Genotype and Allopurinol Dosing. Clinical Pharmacology and Therapeutics, 2013, 93, 153-158.	4.7	199
8	CYP2D6 Genotype and Adjuvant Tamoxifen: Meta-Analysis of Heterogeneous Study Populations. Clinical Pharmacology and Therapeutics, 2014, 95, 216-227.	4.7	150
9	Use of HLA-B*58:01 genotyping to prevent allopurinol induced severe cutaneous adverse reactions in Taiwan: national prospective cohort study. BMJ, The, 2015, 351, h4848.	6.0	148
10	Variant GADL1 and Response to Lithium Therapy in Bipolar I Disorder. New England Journal of Medicine, 2014, 370, 119-128.	27.0	141
11	Prospective Study of Warfarin Dosage Requirements Based on CYP2C9 and VKORC1 Genotypes. Clinical Pharmacology and Therapeutics, 2008, 84, 83-89.	4.7	135
12	Genome-wide association study of bipolar I disorder in the Han Chinese population. Molecular Psychiatry, 2011, 16, 548-556.	7.9	134
13	Genome-wide expression profiles of subchondral bone in osteoarthritis. Arthritis Research and Therapy, 2013, 15, R190.	3.5	103
14	Clinical Pharmacogenetics Implementation Consortium (CPIC) Guideline for CYP2C9 and HLAâ€B Genotypes and Phenytoin Dosing: 2020 Update. Clinical Pharmacology and Therapeutics, 2021, 109, 302-309.	4.7	102
15	Long contiguous stretches of homozygosity in the human genome. Human Mutation, 2006, 27, 1115-1121.	2.5	101
16	A European Spectrum of Pharmacogenomic Biomarkers: Implications for Clinical Pharmacogenomics. PLoS ONE, 2016, 11, e0162866.	2.5	96
17	Pharmacogenetics of warfarin: challenges and opportunities. Journal of Human Genetics, 2013, 58, 334-338.	2.3	95
18	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

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19	Transcriptional upregulation of DDR2 by ATF4 facilitates osteoblastic differentiation through p38 MAPK-mediated Runx2 activation. Journal of Bone and Mineral Research, 2010, 25, 2489-2503.	2.8	74
20	PharmVar GeneFocus: CYP2C19. Clinical Pharmacology and Therapeutics, 2021, 109, 352-366.	4.7	72
21	Genetic determinants of warfarin dosing in the Han-Chinese population. Pharmacogenomics, 2009, 10, 1905-1913.	1.3	70
22	Pharmacogenomics of adverse drug reactions: implementing personalized medicine. Human Molecular Genetics, 2012, 21, R58-R65.	2.9	70
23	Definition of the minimal viral components required for the initiation of unprimed RNA synthesis by influenza virus RNA polymerase. Nucleic Acids Research, 2002, 30, 429-438.	14.5	69
24	Frequent somatic transfer of mitochondrial DNA into the nuclear genome of human cancer cells. Genome Research, 2015, 25, 814-824.	5.5	69
25	Pharmacogenomic polygenic response score predicts ischaemic events and cardiovascular mortality in clopidogrel-treated patients. European Heart Journal - Cardiovascular Pharmacotherapy, 2020, 6, 203-210.	3.0	69
26	LPA Variants Are Associated With Residual Cardiovascular Risk in Patients Receiving Statins. Circulation, 2018, 138, 1839-1849.	1.6	64
27	Impact of the CYP4F2 p.V433M Polymorphism on Coumarin Dose Requirement: Systematic Review and Meta-Analysis. Clinical Pharmacology and Therapeutics, 2012, 92, 746-756.	4.7	56
28	Genome-Wide Association Study of Treatment Refractory Schizophrenia in Han Chinese. PLoS ONE, 2012, 7, e33598.	2.5	55
29	Human-Disease Phenotype Map Derived from PheWAS across 38,682 Individuals. American Journal of Human Genetics, 2019, 104, 55-64.	6.2	54
30	A genome-wide association study identifies a novel susceptibility locus for the immunogenicity of polyethylene glycol. Nature Communications, 2017, 8, 522.	12.8	50
31	A genome-wide association study of polycystic ovary syndrome identified from electronic health records. American Journal of Obstetrics and Gynecology, 2020, 223, 559.e1-559.e21.	1.3	49
32	R1193Q of SCN5A, a Brugada and long QT mutation, is a common polymorphism in Han Chinese. Journal of Medical Genetics, 2005, 42, e7-e7.	3.2	48
33	Contribution of VKORC1 and CYP2C9 polymorphisms in the interethnic variability of warfarin dose in Malaysian populations. Annals of Hematology, 2011, 90, 635-641.	1.8	41
34	Deciphering next-generation pharmacogenomics: an information technology perspective. Open Biology, 2014, 4, 140071.	3.6	41
35	Success stories in genomic medicine from resource-limited countries. Human Genomics, 2015, 9, 11.	2.9	41
36	SNP (â€“617C>A) in ARE-Like Loci of the NRF2 Gene: A New Biomarker for Prognosis of Lung Adenocarcinoma in Japanese Non-Smoking Women. PLoS ONE, 2013, 8, e73794.	2.5	40

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37	Test Pricing and Reimbursement in Genomic Medicine: Towards a General Strategy. Public Health Genomics, 2016, 19, 352-363.	1.0	37
38	Genome-wide DNA methylation profile implicates potential cartilage regeneration at the late stage of knee osteoarthritis. Osteoarthritis and Cartilage, 2016, 24, 835-843.	1.3	37
39	Chromatin accessibility landscape of articular knee cartilage reveals aberrant enhancer regulation in osteoarthritis. Scientific Reports, 2018, 8, 15499.	3.3	37
40	Identification of susceptibility gene associated with female primary SjÃ¶grenâ€™s syndrome in Han Chinese by genome-wide association study. Human Genetics, 2016, 135, 1287-1294.	3.8	36
41	Identification of DNA methylation changes associated with disease progression in subchondral bone with site-matched cartilage in knee osteoarthritis. Scientific Reports, 2016, 6, 34460.	3.3	33
42	Genome-wide association and replication study of anti-tuberculosis drugs-induced liver toxicity. BMC Genomics, 2016, 17, 755.	2.8	32
43	Pharmacogenetic dosing of warfarin in the Han-Chinese population: a randomized trial. Pharmacogenomics, 2017, 18, 245-253.	1.3	32
44	Genomewide Association Study of Platelet Reactivity and Cardiovascular Response in Patients Treated With Clopidogrel: A Study by the International Clopidogrel Pharmacogenomics Consortium. Clinical Pharmacology and Therapeutics, 2020, 108, 1067-1077.	4.7	32
45	Genome-wide association study in NSAID-induced acute urticaria/angioedema in Spanish and Han Chinese populations. Pharmacogenomics, 2013, 14, 1857-1869.	1.3	31
46	Genome-wide and candidate gene approaches of clopidogrel efficacy using pharmacodynamic and clinical end pointsâ€"Rationale and design of the International Clopidogrel Pharmacogenomics Consortium (ICPC). American Heart Journal, 2018, 198, 152-159.	2.7	24
47	Effect of <scp>CYP</scp>4F2,<scp>VKORC</scp>1, and <scp>CYP</scp>2C9 in Influencing Coumarin Dose: A Singleâ€Patient Data Metaâ€Analysis in More Than 15,000 Individuals. Clinical Pharmacology and Therapeutics, 2019, 105, 1477-1491.	4.7	23
48	Genome-Wide Meta-analysis Identifies Genetic Variants Associated With Glycemic Response to Sulfonylureas. Diabetes Care, 2021, 44, 2673-2682.	8.6	23
49	Bridging genomics research between developed and developing countries: the Genomic Medicine Alliance. Personalized Medicine, 2014, 11, 615-623.	1.5	22
50	Identification of PTCSC3 as a Novel Locus for Largeâ€Vessel Ischemic Stroke: A Genomeâ€Wide Association Study. Journal of the American Heart Association, 2016, 5, e003003.	3.7	22
51	Clinical Application of Pharmacogenomics: The Example of HLA-Based Drug-Induced Toxicity. Public Health Genomics, 2014, 17, 248-255.	1.0	18
52	Pharmacogenetics of toxic epidermal necrolysis. Expert Opinion on Pharmacotherapy, 2010, 11, 2153-2162.	1.8	17
53	A genome-wide association study links small-vessel ischemic stroke to autophagy. Scientific Reports, 2017, 7, 15229.	3.3	17
54	Determinants of the Over-Anticoagulation Response during Warfarin Initiation Therapy in Asian Patients Based on Population Pharmacokinetic-Pharmacodynamic Analyses. PLoS ONE, 2014, 9, e105891.	2.5	17

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55	Intragenic microdeletion of RUNX2 is a novel mechanism for cleidocranial dysplasia. Genomic Medicine, 2008, 2, 45-49.	0.3	16
56	VKORC1 haplotypes in five East-Asian populations and Indians. Pharmacogenomics, 2009, 10, 1609-1616.	1.3	16
57	Research Directions in Genetic Predispositions to Stevensâ€“Johnson Syndrome / Toxic Epidermal Necrolysis. Clinical Pharmacology and Therapeutics, 2018, 103, 390-394.	4.7	15
58	A largeâ€scale replication study for the association of rs17039192 in HIFâ€2Î± with knee osteoarthritis. Journal of Orthopaedic Research, 2012, 30, 1244-1248.	2.3	14
59	Dissecting genetic factors affecting phenylephrine infusion rates during anesthesia: a genome-wide association study employing EHR data. BMC Medicine, 2019, 17, 168.	5.5	14
60	Pharmacogenetics of lithium effects on glomerular function in bipolar disorder patients under chronic lithium treatment: a pilot study. Neuroscience Letters, 2017, 638, 1-4.	2.1	13
61	Genome-Wide Association and Replication Study of Hepatotoxicity Induced by Antiretrovirals Alone or with Concomitant Anti-Tuberculosis Drugs. OMICS A Journal of Integrative Biology, 2017, 21, 207-216.	2.0	12
62	Differences in Warfarin Pharmacodynamics and Predictors of Response Among Three Racial Populations. Clinical Pharmacokinetics, 2019, 58, 1077-1089.	3.5	12
63	Genetic Architecture Associated With Familial Short Stature. Journal of Clinical Endocrinology and Metabolism, 2020, 105, 1801-1813.	3.6	12
64	Polycystic Ovary Syndrome Susceptibility Loci Inform Disease Etiological Heterogeneity. Journal of Clinical Medicine, 2021, 10, 2688.	2.4	10
65	Genome-wide Association Analysis Across 16,956 Patients Identifies a Novel Genetic Association Between BMP6, NIPAL1, CNGA1 and Spondylosis. Spine, 2021, 46, E625-E631.	2.0	8
66	A Mutation in Cartilage Oligomeric Matrix Protein (COMP) Causes Early-Onset Osteoarthritis in a Large Kindred Study. Annals of Human Genetics, 2011, 75, 575-583.	0.8	7
67	GSTM1 Copy Number Is Not Associated With Risk of Kidney Failure in a Large Cohort. Frontiers in Genetics, 2019, 10, 765.	2.3	4
68	Deep Ensemble Network for Quantification and Severity Assessment of Knee Osteoarthritis. , 2019, , .		4
69	PPARGC1B Is Associated with Nontraumatic Osteonecrosis of the Femoral Head. Journal of Bone and Joint Surgery - Series A, 2020, 102, 1628-1636.	3.0	4
70	Variants at the MHC Region Associate With Susceptibility to Clostridioides difficile Infection: A Genome-Wide Association Study Using Comprehensive Electronic Health Records. Frontiers in Immunology, 2021, 12, 638913.	4.8	4
71	Polymorphic analysis of CYP2C9 gene in Vietnamese population. Molecular Biology Reports, 2018, 45, 893-900.	2.3	1
72	. Genomic Medicine in Taiwan: Research and Developments. , 2012, , 874-886.		1

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73	Correlations between the enantio- and regio-selective metabolisms of warfarin. Pharmacogenomics, 2017, 18, 133-142.	1.3	0
74	Response to Comment on Dawed et al. Genome-Wide Meta-analysis Identifies Genetic Variants Associated With Glycemic Response to Sulfonylureas. Diabetes Care 2021;44:2673â€“2682. Diabetes Care, 2022, 45, e82-e83.	8.6	0