Tim Wiltshire

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Insights and lessons learned from a prospective clinical pharmacology study in allogeneic hematopoietic stem cell transplant during the COVIDâ€19 pandemic. Clinical and Translational Science, 2022, 15, 583-587.	3.1	2
2	The feasibility and potential of pharmacogenetics to reduce adverse drug events in nursing home residents. Journal of the American Geriatrics Society, 2022, 70, 1573-1578.	2.6	0
3	Modelâ€Based Prediction of Irinotecanâ€Induced Grade 4 Neutropenia in Advanced Cancer Patients: Influence of Demographic and Clinical Factors. Clinical Pharmacology and Therapeutics, 2022, 112, 316-326.	4.7	3
4	Evaluation of the performance of a prior tacrolimus population pharmacokinetic kidney transplant model among adult allogeneic hematopoietic stem cell transplant patients. Clinical and Translational Science, 2021, 14, 908-918.	3.1	4
5	North Carolina's multi-institutional pharmacogenomics efforts with the North Carolina Precision Health Collaborative. Pharmacogenomics, 2021, 22, 73-80.	1.3	1
6	Cost-Effectiveness of Multigene Pharmacogenetic Testing in Patients With Acute Coronary Syndrome After Percutaneous Coronary Intervention. Value in Health, 2020, 23, 61-73.	0.3	30
7	Projected impact of pharmacogenomic testing on medications beyond antiplatelet therapy in percutaneous coronary intervention patients. Pharmacogenomics, 2020, 21, 431-441.	1.3	7
8	Influence of Germline Genetics on Tacrolimus Pharmacokinetics and Pharmacodynamics in Allogeneic Hematopoietic Stem Cell Transplant Patients. International Journal of Molecular Sciences, 2020, 21, 858.	4.1	16
9	Characterizing the pharmacogenome using molecular inversion probes for targeted next-generation sequencing. Pharmacogenomics, 2019, 20, 1005-1020.	1.3	9
10	Denisovan, modern human and mouse TNFAIP3 alleles tune A20 phosphorylation and immunity. Nature Immunology, 2019, 20, 1299-1310.	14.5	53
11	The NIEHS TaRGET II Consortium and environmental epigenomics. Nature Biotechnology, 2018, 36, 225-227.	17.5	79
12	Clinical pharmacogenetics: how do we ensure a favorable future for patients?. Pharmacogenomics, 2018, 19, 553-562.	1.3	5
13	Pharmacogenetic Analysis of the Modelâ€Based Pharmacokinetics of Five Antiâ€HIV Drugs: How Does This Influence the Effect of Aging?. Clinical and Translational Science, 2018, 11, 226-236.	3.1	7
14	Challenges and Solutions for Future Pharmacy Practice in the Era of Precision Medicine. American Journal of Pharmaceutical Education, 2018, 82, 6652.	2.1	4
15	Implementing Clinical Pharmacogenomics in the Classroom: Student Pharmacist Impressions of an Educational Intervention Including Personal Genotyping. Pharmacy (Basel, Switzerland), 2018, 6, 115.	1.6	18
16	Human carbonic anhydrase-8 AAV8 gene therapy inhibits nerve growth factor signaling producing prolonged analgesia and anti-hyperalgesia in mice. Gene Therapy, 2018, 25, 297-311.	4.5	6
17	Projected impact of a multigene pharmacogenetic test to optimize medication prescribing in cardiovascular patients. Pharmacogenomics, 2018, 19, 771-782.	1.3	13
18	Car8 dorsal root ganglion expression and genetic regulation of analgesic responses are associated with a cis-eQTL in mice. Mammalian Genome, 2017, 28, 407-415.	2.2	7

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19	Advancing precision medicine in healthcare: addressing implementation challenges to increase pharmacogenetic testing in the clinical setting. Physiological Genomics, 2017, 49, 346-354.	2.3	8
20	Candidate Risk Factors and Mechanisms for Tolvaptan-Induced Liver Injury Are Identified Using a Collaborative Cross Approach. Toxicological Sciences, 2017, 156, kfw269.	3.1	46
21	Precision Dosing: Public Health Need, Proposed Framework, and Anticipated Impact. Clinical and Translational Science, 2017, 10, 443-454.	3.1	55
22	Transitioning Pharmacogenomics into the Clinical Setting: Training Future Pharmacists. Frontiers in Pharmacology, 2016, 7, 241.	3.5	36
23	Determinants of host susceptibility to murine respiratory syncytial virus (RSV) disease identify a role for the innate immunity scavenger receptor MARCO gene in human infants. EBioMedicine, 2016, 11, 73-84.	6.1	24
24	Gulp1 is associated with the pharmacokinetics of PEGylated liposomal doxorubicin (PLD) in inbred mouse strains. Nanomedicine: Nanotechnology, Biology, and Medicine, 2016, 12, 2007-2017.	3.3	13
25	Molecular genetic mechanisms of allelic specific regulation of murine Comt expression. Pain, 2015, 156, 1965-1977.	4.2	8
26	Immune cell-based screening assay for response to anticancer agents: applications in pharmacogenomics. Pharmacogenomics and Personalized Medicine, 2015, 8, 81.	0.7	10
27	Carbonic Anhydrase-8 Regulates Inflammatory Pain by Inhibiting the ITPR1-Cytosolic Free Calcium Pathway. PLoS ONE, 2015, 10, e0118273.	2.5	30
28	Identifying genes that mediate anthracyline toxicity in immune cells. Frontiers in Pharmacology, 2015, 6, 62.	3.5	4
29	Mst1 Directs Myosin IIa Partitioning of Low and Higher Affinity Integrins during T Cell Migration. PLoS ONE, 2014, 9, e105561.	2.5	16
30	Genomeâ€wide association mapping of acute lung injury in neonatal inbred mice. FASEB Journal, 2014, 28, 2538-2550.	0.5	20
31	A cellular genetics approach identifies gene-drug interactions and pinpoints drug toxicity pathway nodes. Frontiers in Genetics, 2014, 5, 272.	2.3	5
32	Characterization of Highper, an ENU-induced mouse mutant with abnormal psychostimulant and stress responses. Psychopharmacology, 2013, 225, 407-419.	3.1	1
33	In Vitro and In Vivo Mouse Models for Pharmacogenetic Studies. Methods in Molecular Biology, 2013, 1015, 263-278.	0.9	8
34	The intramembrane protease Sppl2a is required for B cell and DC development and survival via cleavage of the invariant chain. Journal of Experimental Medicine, 2013, 210, 23-30.	8.5	78
35	Usf1, a suppressor of the circadian Clock mutant, reveals the nature of the DNA-binding of the CLOCK:BMAL1 complex in mice. ELife, 2013, 2, e00426.	6.0	63
36	Evaluating genetic markers and neurobiochemical analytes for fluoxetine response using a panel of mouse inbred strains. Psychopharmacology, 2012, 221, 297-315.	3.1	51

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37	Extensive recombination rate variation in the house mouse species complex inferred from genetic linkage maps. Genome Research, 2011, 21, 114-125.	5.5	73
38	Genetic Dissection of a Key Reproductive Barrier Between Nascent Species of House Mice. Genetics, 2011, 189, 289-304.	2.9	79
39	Genetic architecture of voluntary exercise in an advanced intercross line of mice. Physiological Genomics, 2010, 42, 190-200.	2.3	55
40	Quantitative trait locus and haplotype mapping in closely related inbred strains identifies a locus for open field behavior. Mammalian Genome, 2010, 21, 231-246.	2.2	24
41	Genome Wide Analysis of Inbred Mouse Lines Identifies a Locus Containing Ppar-Î ³ as Contributing to Enhanced Malaria Survival. PLoS ONE, 2010, 5, e10903.	2.5	22
42	Integrative Analysis of Low- and High-Resolution eQTL. PLoS ONE, 2010, 5, e13920.	2.5	12
43	A Novel Allele of Myosin VIIa Reveals a Critical Function for the C-Terminal FERM Domain for Melanosome Transport in Retinal Pigment Epithelial Cells. Journal of Neuroscience, 2009, 29, 15810-15818.	3.6	40
44	Mutations in LOXHD1, an Evolutionarily Conserved Stereociliary Protein, Disrupt Hair Cell Function in Mice and Cause Progressive Hearing Loss in Humans. American Journal of Human Genetics, 2009, 85, 328-337.	6.2	129
45	A mouse model for nonsyndromic deafness (DFNB12) links hearing loss to defects in tip links of mechanosensory hair cells. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 5252-5257.	7.1	81
46	A Common and Unstable Copy Number Variant Is Associated with Differences in Glo1 Expression and Anxiety-Like Behavior. PLoS ONE, 2009, 4, e4649.	2.5	108
47	Expression analysis of G Protein-Coupled Receptors in mouse macrophages. Immunome Research, 2008, 4, 5.	0.1	400
48	Genetical Genomics: Spotlight on QTL Hotspots. PLoS Genetics, 2008, 4, e1000232.	3.5	172
49	Gene Set Enrichment in eQTL Data Identifies Novel Annotations and Pathway Regulators. PLoS Genetics, 2008, 4, e1000070.	3.5	90
50	The Modifier of hemostasis (Mh) locus on chromosome 4 controls in vivo hemostasis of Gp6â^'/â^' mice. Blood, 2008, 111, 1266-1273.	1.4	32
51	A Forward Genetics Screen in Mice Identifies Recessive Deafness Traits and Reveals That Pejvakin Is Essential for Outer Hair Cell Function. Journal of Neuroscience, 2007, 27, 2163-2175.	3.6	159
52	Genomewide Association Analysis in Diverse Inbred Mice: Power and Population Structure. Genetics, 2007, 176, 675-683.	2.9	68
53	Marked Interindividual Variability in the Response to Selective Inhibitors of Cyclooxygenase-2. Gastroenterology, 2006, 130, 55-64.	1.3	131
54	Databases of free expression. Mammalian Genome, 2006, 17, 1141-1146.	2.2	1

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55	Comparative analysis of haplotype association mapping algorithms. BMC Bioinformatics, 2006, 7, 61.	2.6	52
56	A mutant mouse with a highly specific contextual fear-conditioning deficit found in an N-ethyl-N-nitrosourea (ENU) mutagenesis screen. Learning and Memory, 2006, 13, 143-149.	1.3	33
57	Utilization of a whole genome SNP panel for efficient genetic mapping in the mouse. Genome Research, 2006, 16, 436-440.	5.5	89
58	Quantitative Trait Loci That Determine BMD in C57BL/6J and 129S1/SvImJ Inbred Mice. Journal of Bone and Mineral Research, 2005, 21, 105-112.	2.8	39
59	Uncovering regulatory pathways that affect hematopoietic stem cell function using 'genetical genomics'. Nature Genetics, 2005, 37, 225-232.	21.4	366
60	Genome-wide linkage identifies novel modifier loci of aganglionosis in the Sox10Dom model of Hirschsprung disease. Human Molecular Genetics, 2005, 14, 1549-1558.	2.9	37
61	c-Myb and p300 Regulate Hematopoietic Stem Cell Proliferation and Differentiation. Developmental Cell, 2005, 8, 153-166.	7.0	251
62	Inositol (1,4,5) trisphosphate 3 kinase B controls positive selection of T cells and modulates Erk activity. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 5604-5609.	7.1	74
63	Use of a Dense Single Nucleotide Polymorphism Map for In Silico Mapping in the Mouse. PLoS Biology, 2004, 2, e393.	5.6	210
64	The Collaborative Cross, a community resource for the genetic analysis of complex traits. Nature Genetics, 2004, 36, 1133-1137.	21.4	1,034
65	A gene atlas of the mouse and human protein-encoding transcriptomes. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 6062-6067.	7.1	3,290
66	Genome-wide single-nucleotide polymorphism analysis defines haplotype patterns in mouse. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 3380-3385.	7.1	222
67	Large-scale analysis of the human and mouse transcriptomes. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 4465-4470.	7.1	1,366
68	Use of Comparative Physical and Sequence Mapping to Annotate Mouse Chromosome 16 and Human Chromosome 21. Genomics, 2001, 74, 45-54.	2.9	40
69	High-Resolution BAC-Based Map of the Central Portion of Mouse Chromosome 5. Genome Research, 2001, 11, 1746-1757.	5.5	1
70	A High-Resolution Radiation Hybrid Map of the Proximal Portion of Mouse Chromosome 5. Genomics, 2000, 66, 55-64.	2.9	7
71	Mutations in the homeodomain of the human SIX3 gene cause holoprosencephaly. Nature Genetics, 1999, 22, 196-198.	21.4	398
72	High-resolution comparative physical mapping of mouse Chromosome 10 in the region of homology with human Chromosome 21. Mammalian Genome, 1999, 10, 229-234.	2.2	9

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73	A Sequence-Ready BAC Contig of the GABA _A Receptor Gene Cluster <i>Gabrg1–Gabra2–Gabrb1</i> on Mouse Chromosome 5. Genome Research, 1999, 9, 732-738.	5.5	6
74	Physical Mapping of the Evolutionary Boundary between Human Chromosomes 21 and 22 on Mouse Chromosome 10. Genomics, 1998, 50, 109-111.	2.9	10
75	Physical and Comparative Mapping of Distal Mouse Chromosome 16. Genome Research, 1998, 8, 940-950.	5.5	15
76	A genetic strategy for differential screening of meiotic germ-cell cDNA libraries. Molecular Reproduction and Development, 1996, 43, 403-413.	2.0	6
77	Induced Premature G2/M-Phase Transition in Pachytene Spermatocytes Includes Events Unique to Meiosis. Developmental Biology, 1995, 169, 557-567.	2.0	127