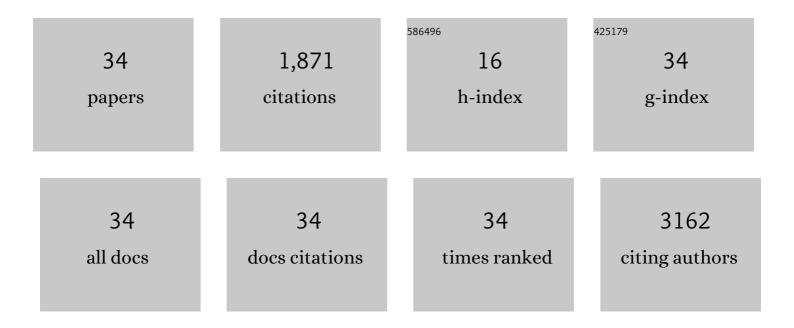
Patrick D Mcmullen

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7006255/publications.pdf Version: 2024-02-01



PATRICK D MCMILLEN

#	Article	IF	CITATIONS
1	Biological system considerations for application of toxicogenomics in next-generation risk assessment and predictive toxicology. Toxicology in Vitro, 2022, 80, 105311.	1.1	6
2	Considerations for Improving Metabolism Predictions for In Vitro to In Vivo Extrapolation. Frontiers in Toxicology, 2022, 4, 894569.	1.6	10
3	A systematic approach to evaluate plausible modes of actions for mouse lung tumors in mice exposed to 4-methylimidozole. Regulatory Toxicology and Pharmacology, 2021, 124, 104977.	1.3	2
4	RNA-Sequencing (transcriptomic) Data Collected in Liver and Lung of Male and Female B6C3F1 Mice Exposed to Various Dose Levels of 4-Methylimidazole for 2, 5, or 28 days. Data in Brief, 2021, 38, 107420.	0.5	1
5	ldentifying qualitative differences in PPARα signaling networks in human and rat hepatocytes and their significance for next generation chemical risk assessment methods. Toxicology in Vitro, 2020, 64, 104463.	1.1	12
6	A toxicogenomic approach for the risk assessment of the food contaminant acetamide. Toxicology and Applied Pharmacology, 2020, 388, 114872.	1.3	18
7	Population Life-course exposure to health effects model (PLETHEM): An R package for PBPK modeling. Computational Toxicology, 2020, 13, 100115.	1.8	15
8	The role of fit-for-purpose assays within tiered testing approaches: A case study evaluating prioritized estrogen-active compounds in an in vitro human uterotrophic assay. Toxicology and Applied Pharmacology, 2020, 387, 114774.	1.3	10
9	The TTC Data Mart: An interactive browser for threshold of toxicological concern calculations. Computational Toxicology, 2020, 15, 100128.	1.8	3
10	Application of a combined aggregate exposure pathway and adverse outcome pathway (AEP-AOP) approach to inform a cumulative risk assessment: A case study with phthalates. Toxicology in Vitro, 2020, 66, 104855.	1.1	21
11	Addressing systematic inconsistencies between in vitro and in vivo transcriptomic mode of action signatures. Toxicology in Vitro, 2019, 58, 1-12.	1.1	15
12	Developing context appropriate toxicity testing approaches using new alternative methods (NAMs). ALTEX: Alternatives To Animal Experimentation, 2019, 36, 532-534.	0.9	30
13	Evaluating opportunities for advancing the use of alternative methods in risk assessment through the development of fit-for-purpose in vitro assays. Toxicology in Vitro, 2018, 48, 310-317.	1.1	25
14	A Qualitative Modeling Approach for Whole Genome Prediction Using High-Throughput Toxicogenomics Data and Pathway-Based Validation. Frontiers in Pharmacology, 2018, 9, 1072.	1.6	6
15	Strain-related differences in mouse lung gene expression over a two-year period of inhalation exposure to styrene: Relevance to human risk assessment. Regulatory Toxicology and Pharmacology, 2018, 96, 153-166.	1.3	14
16	Application of transcriptomic data, visualization tools and bioinformatics resources for informing mode of action. Current Opinion in Toxicology, 2018, 9, 21-27.	2.6	12
17	Combining transcriptomics and PBPK modeling indicates a primary role of hypoxia and altered circadian signaling in dichloromethane carcinogenicity in mouse lung and liver. Toxicology and Applied Pharmacology, 2017, 332, 149-158.	1.3	22
18	Assessing molecular initiating events (MIEs), key events (KEs) and modulating factors (MFs) for styrene responses in mouse lungs using whole genome gene expression profiling following 1-day and multi-week exposures. Toxicology and Applied Pharmacology, 2017, 335, 28-40.	1.3	38

PATRICK D MCMULLEN

#	Article	IF	CITATIONS
19	Multiple receptors shape the estrogen response pathway and are critical considerations for the future of <i>in vitro</i> -based risk assessment efforts. Critical Reviews in Toxicology, 2017, 47, 570-586.	1.9	26
20	Information-dependent enrichment analysis reveals time-dependent transcriptional regulation of the estrogen pathway of toxicity. Archives of Toxicology, 2017, 91, 1749-1762.	1.9	24
21	The Human Toxome Collaboratorium: A Shared Environment for Multi-Omic Computational Collaboration within a Consortium. Frontiers in Pharmacology, 2016, 6, 322.	1.6	8
22	Pathway Based Toxicology and Fit-for-Purpose Assays. Advances in Experimental Medicine and Biology, 2016, 856, 205-230.	0.8	11
23	Developing tools for defining and establishing pathways of toxicity. Archives of Toxicology, 2015, 89, 809-812.	1.9	11
24	Using gene expression profiling to evaluate cellular responses in mouse lungs exposed to V2O5 and a group of other mouse lung tumorigens and non-tumorigens. Regulatory Toxicology and Pharmacology, 2015, 73, 339-347.	1.3	14
25	The Human Toxome Project. ALTEX: Alternatives To Animal Experimentation, 2015, 32, 112-124.	0.9	52
26	Profiling Dose-Dependent Activation of p53-Mediated Signaling Pathways by Chemicals with Distinct Mechanisms of DNA Damage. Toxicological Sciences, 2014, 142, 56-73.	1.4	43
27	A map of the PPARα transcription regulatory network for primary human hepatocytes. Chemico-Biological Interactions, 2014, 209, 14-24.	1.7	89
28	MYC Is an Early Response Regulator of Human Adipogenesis in Adipose Stem Cells. PLoS ONE, 2014, 9, e114133.	1.1	28
29	Recent advances in 2D and 3D in vitro systems using primary hepatocytes, alternative hepatocyte sources and non-parenchymal liver cells and their use in investigating mechanisms of hepatotoxicity, cell signaling and ADME. Archives of Toxicology, 2013, 87, 1315-1530.	1.9	1,089
30	Toxicogenomics for transcription factor-governed molecular pathways: moving on to roles beyond classification and prediction. Archives of Toxicology, 2013, 87, 7-11.	1.9	20
31	Identification of a Tissue-Selective Heat Shock Response Regulatory Network. PLoS Genetics, 2013, 9, e1003466.	1.5	100
32	Modeling Drug- and Chemical-Induced Hepatotoxicity with Systems Biology Approaches. Frontiers in Physiology, 2012, 3, 462.	1.3	53
33	Macro-level Modeling of the Response of C. elegans Reproduction to Chronic Heat Stress. PLoS Computational Biology, 2012, 8, e1002338.	1.5	33
34	Physically grounded approach for estimating gene expression from microarray data. Proceedings of the United States of America, 2010, 107, 13690-13695.	3.3	10