

# Tyler B Hughes

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/584769/publications.pdf>

Version: 2024-02-01

16  
papers

926  
citations

623734

14  
h-index

940533

16  
g-index

16  
all docs

16  
docs citations

16  
times ranked

1544  
citing authors

#	ARTICLE	IF	CITATIONS
1	Modeling the Bioactivation and Subsequent Reactivity of Drugs. <i>Chemical Research in Toxicology</i> , 2021, 34, 584-600.	3.3	11
2	Metabolic Forest: Predicting the Diverse Structures of Drug Metabolites. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 4702-4716.	5.4	11
3	The Metabolic Rainbow: Deep Learning Phase I Metabolism in Five Colors. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 1146-1164.	5.4	26
4	Computationally Assessing the Bioactivation of Drugs by N-Dealkylation. <i>Chemical Research in Toxicology</i> , 2018, 31, 68-80.	3.3	30
5	Lamisil (terbinafine) toxicity: Determining pathways to bioactivation through computational and experimental approaches. <i>Biochemical Pharmacology</i> , 2018, 156, 10-21.	4.4	17
6	Modeling Small-Molecule Reactivity Identifies Promiscuous Bioactive Compounds. <i>Journal of Chemical Information and Modeling</i> , 2018, 58, 1483-1500.	5.4	28
7	Deep Learning to Predict the Formation of Quinone Species in Drug Metabolism. <i>Chemical Research in Toxicology</i> , 2017, 30, 642-656.	3.3	57
8	Computational Approach to Structural Alerts: Furans, Phenols, Nitroaromatics, and Thiophenes. <i>Chemical Research in Toxicology</i> , 2017, 30, 1046-1059.	3.3	32
9	Open Source Drug Discovery with the Malaria Box Compound Collection for Neglected Diseases and Beyond. <i>PLoS Pathogens</i> , 2016, 12, e1005763.	4.7	244
10	Modeling Reactivity to Biological Macromolecules with a Deep Multitask Network. <i>ACS Central Science</i> , 2016, 2, 529-537.	11.3	76
11	A simple model predicts UGT-mediated metabolism. <i>Bioinformatics</i> , 2016, 32, 3183-3189.	4.1	51
12	Enhancer Sequence Variants and Transcription-Factor Deregulation Synergize to Construct Pathogenic Regulatory Circuits in B-Cell Lymphoma. <i>Immunity</i> , 2015, 42, 186-198.	14.3	64
13	Modeling Epoxidation of Drug-like Molecules with a Deep Machine Learning Network. <i>ACS Central Science</i> , 2015, 1, 168-180.	11.3	130
14	Extending P450 site-of-metabolism models with region-resolution data. <i>Bioinformatics</i> , 2015, 31, 1966-1973.	4.1	15
15	Site of Reactivity Models Predict Molecular Reactivity of Diverse Chemicals with Glutathione. <i>Chemical Research in Toxicology</i> , 2015, 28, 797-809.	3.3	70
16	XenoSite server: a web-available site of metabolism prediction tool. <i>Bioinformatics</i> , 2015, 31, 1136-1137.	4.1	64