Othman

List of Publications by Year
in descending order

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20 papers	5,496 citations	759055 12 h-index	839398 18 g-index
24 all docs	24 docs citations	24 times ranked	11422 citing authors

#	Article	IF	Citations
1	EcoToxXplorer: Leveraging Design Thinking to Develop a Standardized Webâ€Based Transcriptomics Analytics Platform for Diverse Users. Environmental Toxicology and Chemistry, 2022, 41, 21-29.	2.2	6
2	Characterizing toxicity pathways of fluoxetine to predict adverse outcomes in adult fathead minnows (Pimephales promelas). Science of the Total Environment, 2022, 817, 152747.	3.9	5
3	A novel graph mining approach to predict and evaluate food-drug interactions. Scientific Reports, 2022, 12, 1061.	1.6	13
4	FastBMD: an online tool for rapid benchmark doseâ€“response analysis of transcriptomics data. Bioinformatics, 2021, 37, 1035-1036.	1.8	19
5	Development of a Comprehensive Toxicity Pathway Model for 17Î±-Ethinylestradiol in Early Life Stage Fathead Minnows (Pimephales promelas). Environmental Science & Technology, 2021, 55, 5024-5036.	4.6	13
6	Discovering Missing Edges in Drug-Protein Networks: Repurposing Drugs for SARS-CoV-2. , 2021, , .		0
7	miRNet 2.0: network-based visual analytics for miRNA functional analysis and systems biology. Nucleic Acids Research, 2020, 48, W244-W251.	6.5	461
8	EcoToxModules: Custom Gene Sets to Organize and Analyze Toxicogenomics Data from Ecological Species. Environmental Science & Technology, 2020, 54, 4376-4387.	4.6	16
9	Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. Nature Communications, 2019, 10, 2674.	5.8	240
10	NetworkAnalyst 3.0: a visual analytics platform for comprehensive gene expression profiling and meta-analysis. Nucleic Acids Research, 2019, 47, W234-W241.	6.5	1,191
11	Systematic selection of chemical fingerprint features improves the Gibbs energy prediction of biochemical reactions. Bioinformatics, 2019, 35, 2634-2643.	1.8	11
12	Transcriptome and physiological analysis reveal alterations in muscle metabolisms and immune responses of grass carp (Ctenopharyngodon idellus) cultured at different stocking densities. Aquaculture, 2019, 503, 186-197.	1.7	36
13	T1000: a reduced gene set prioritized for toxicogenomic studies. PeerJ, 2019, 7, e7975.	0.9	15
14	MetaboAnalyst 4.0: towards more transparent and integrative metabolomics analysis. Nucleic Acids Research, 2018, 46, W486-W494.	6.5	3,199
15	DPubChem: a web tool for QSAR modeling and high-throughput virtual screening. Scientific Reports, 2018, 8, 9110.	1.6	40
16	DRABAL: novel method to mine large high-throughput screening assays using Bayesian active learning. Journal of Cheminformatics, 2016, 8, 64.	2.8	20
17	DASPfind: new efficient method to predict drugâ€“target interactions. Journal of Cheminformatics, 2016, 8, 15.	2.8	88
18	DWFS: A Wrapper Feature Selection Tool Based on a Parallel Genetic Algorithm. PLoS ONE, 2015, 10, e0117988.	1.1	94

#	Article	IF	Citations
19	Mining Chemical Activity Status from High-Throughput Screening Assays. PLoS ONE, 2015, 10, e0144426.	1.1	15
20	DANNP: an efficient artificial neural network pruning tool. PeerJ Computer Science, 0, 3, e137.	2.7	13