

Othman

List of Publications by Year in descending order

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Version: 2024-02-01

20
papers

5,496
citations

758635

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839053

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all docs

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docs citations

24
times ranked

11422
citing authors

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