

RÃ³nÃ¡n Daly

List of Publications by Year in descending order

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Version: 2024-02-01

17
papers

376
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1040056

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940533

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602
citing authors

#	ARTICLE	IF	CITATIONS
1	ViMMS 2.0: A framework to develop, test and optimise fragmentation strategies in LC-MS metabolomics. <i>Journal of Open Source Software</i> , 2022, 7, 3990.	4.6	5
2	Multi-omics & pathway analysis identify potential roles for tumor N-acetyl aspartate accumulation in murine models of castration-resistant prostate cancer. <i>IScience</i> , 2022, 25, 104056.	4.1	5
3	High sodium intake, glomerular hyperfiltration, and protein catabolism in patients with essential hypertension. <i>Cardiovascular Research</i> , 2021, 117, 1372-1381.	3.8	27
4	R package for statistical inference in dynamical systems using kernel based gradient matching: KCode. <i>Computational Statistics</i> , 2021, 36, 715-747.	1.5	0
5	Ranking Metabolite Sets by Their Activity Levels. <i>Metabolites</i> , 2021, 11, 103.	2.9	14
6	A monolithic single-chip point-of-care platform for metabolomic prostate cancer detection. <i>Microsystems and Nanoengineering</i> , 2021, 7, 21.	7.0	14
7	Rapid Development of Improved Data-Dependent Acquisition Strategies. <i>Analytical Chemistry</i> , 2021, 93, 5676-5683.	6.5	31
8	Ranking microbial metabolomic and genomic links in the NPLinker framework using complementary scoring functions. <i>PLoS Computational Biology</i> , 2021, 17, e1008920.	3.2	30
9	GraphOmics: an interactive platform to explore and integrate multi-omics data. <i>BMC Bioinformatics</i> , 2021, 22, 603.	2.6	8
10	Changes in Plasma Itaconate Elevation in Early Rheumatoid Arthritis Patients Elucidates Disease Activity Associated Macrophage Activation. <i>Metabolites</i> , 2020, 10, 241.	2.9	28
11	In Silico Optimization of Mass Spectrometry Fragmentation Strategies in Metabolomics. <i>Metabolites</i> , 2019, 9, 219.	2.9	18
12	Changing environments and genetic variation: natural variation in inbreeding does not compromise short-term physiological responses. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20192109.	2.6	6
13	ShinyKCode: an interactive application for ODE parameter inference using gradient matching. <i>Bioinformatics</i> , 2018, 34, 2314-2315.	4.1	3
14	MetaboCraft: building a Minecraft plugin for metabolomics. <i>Bioinformatics</i> , 2018, 34, 2693-2694.	4.1	3
15	PiMP my metabolome: an integrated, web-based tool for LC-MS metabolomics data. <i>Bioinformatics</i> , 2017, 33, 4007-4009.	4.1	41
16	Metabolomics Identifies Multiple Candidate Biomarkers to Diagnose and Stage Human African Trypanosomiasis. <i>PLoS Neglected Tropical Diseases</i> , 2016, 10, e0005140.	3.0	74
17	MetAssign: probabilistic annotation of metabolites from LC-MS data using a Bayesian clustering approach. <i>Bioinformatics</i> , 2014, 30, 2764-2771.	4.1	63