David Tonoli

List of Publications by Year in descending order

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623734 794594 19 900 14 19 citations h-index g-index papers 20 20 20 1481 citing authors docs citations times ranked all docs

#	Article	IF	CITATIONS
1	The use of mass spectrometry to analyze dried blood spots. Mass Spectrometry Reviews, 2016, 35, 361-438.	5.4	193
2	High-resolution mass spectrometry for integrated qualitative and quantitative analysis of pharmaceuticals in biological matrices. Analytical and Bioanalytical Chemistry, 2012, 402, 2587-2596.	3.7	137
3	Metabolomic analysis of urine samples by UHPLC-QTOF-MS: Impact of normalization strategies. Analytica Chimica Acta, 2017, 955, 27-35.	5.4	129
4	Evaluation of steroidomics by liquid chromatography hyphenated to mass spectrometry as a powerful analytical strategy for measuring human steroid perturbations. Journal of Chromatography A, 2016, 1430, 97-112.	3.7	80
5	Prediction of retention time in reversed-phase liquid chromatography as a tool for steroid identification. Analytica Chimica Acta, 2016, 916, 8-16.	5.4	58
6	Human urinary biomarkers of dioxin exposure: Analysis by metabolomics and biologically driven data dimensionality reduction. Toxicology Letters, 2014, 230, 234-243.	0.8	51
7	Quantification of acetaminophen and two of its metabolites in human plasma by ultra-high performance liquid chromatography–low and high resolution tandem mass spectrometry. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2012, 904, 42-50.	2.3	43
8	Steroid profiling in H295R cells to identify chemicals potentially disrupting the production of adrenal steroids. Toxicology, 2017, 381, 51-63.	4.2	42
9	Evaluation and identification of dioxin exposure biomarkers in human urine by high-resolution metabolomics, multivariate analysis and in vitro synthesis. Toxicology Letters, 2016, 240, 22-31.	0.8	27
10	Enhanced metabolite annotation via dynamic retention time prediction: Steroidogenesis alterations as a case study. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2017, 1071, 11-18.	2.3	25
11	Steroidomic Footprinting Based on Ultra-High Performance Liquid Chromatography Coupled with Qualitative and Quantitative High-Resolution Mass Spectrometry for the Evaluation of Endocrine Disrupting Chemicals in H295R Cells. Chemical Research in Toxicology, 2015, 28, 955-966.	3.3	24
12	An Integrative Multi-Omics Workflow to Address Multifactorial Toxicology Experiments. Metabolites, 2019, 9, 79.	2.9	24
13	Internal calibration as an emerging approach for endogenous analyte quantification: Application to steroids. Talanta, 2022, 240, 123149.	5 . 5	18
14	Steroid profiles in both blood serum and seminal plasma are not correlated and do not reflect sperm quality: Study on the male reproductive health of fifty young Swiss men. Clinical Biochemistry, 2018, 62, 39-46.	1.9	16
15	Mass Spectrometric QUAL/QUAN Approaches for Drug Metabolism and Metabolomics. Chimia, 2012, 66, 218-222.	0.6	10
16	Removal of batch effects using stratified subsampling of metabolomic data for in vitro endocrine disruptors screening. Talanta, 2019, 195, 77-86.	5 . 5	10
17	Protein pathway analysis to study development-dependent effects of acute and repeated trimethyltin (TMT) treatments in 3D rat brain cell cultures. Toxicology in Vitro, 2019, 60, 281-292.	2.4	5
18	Performance enhancement and sample throughput increase of a multiresidue pesticides method in fruits and vegetables using Data-Dependent MS acquisition. Food Additives and Contaminants - Part A Chemistry, Analysis, Control, Exposure and Risk Assessment, 2020, 37, 110-120.	2.3	5

#	ARTICLE	IF	CITATIONS
19	Therapeutic drug monitoring and clinical outcomes in severely ill patients receiving amoxicillin: a single-centre prospective cohort study. International Journal of Antimicrobial Agents, 2022, 59, 106601.	2.5	3