

Hannes Planatscher

List of Publications by Year in descending order

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17
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239
citing authors

#	ARTICLE	IF	CITATIONS
1	Pesticide mixture effects on liver protein abundance in HepaRG cells. <i>Toxicology</i> , 2021, 458, 152839.	4.2	8
2	A targeted transcriptomics approach for the determination of mixture effects of pesticides. <i>Toxicology</i> , 2021, 460, 152892.	4.2	5
3	Matrix and Sampling Effects on Quantification of Protein Biomarkers of Drug-Induced Liver Injury. <i>Journal of Proteome Research</i> , 2021, 20, 4985-4994.	3.7	2
4	RNA-protein correlation of liver toxicity markers in HepaRG cells. <i>EXCLI Journal</i> , 2020, 19, 135-153.	0.7	6
5	Induction and repression effects on CYP and transporter protein abundance by azole mixture uptake in rat liver. <i>EXCLI Journal</i> , 2020, 19, 904-916.	0.7	1
6	Application of Mass Spectrometry-Based Immunoassays for the Species- and Tissue-Specific Quantification of Banned Processed Animal Proteins in Feeds. <i>Analytical Chemistry</i> , 2019, 91, 3902-3911.	6.5	10
7	Mass Spectrometry-Based Immunoassay for the Quantification of Banned Ruminant Processed Animal Proteins in Vegetal Feeds. <i>Analytical Chemistry</i> , 2018, 90, 4135-4143.	6.5	15
8	Direct Quantification of Cytochromes P450 and Drug Transporters—A Rapid, Targeted Mass Spectrometry-Based Immunoassay Panel for Tissues and Cell Culture Lysates. <i>Drug Metabolism and Disposition</i> , 2018, 46, 387-396.	3.3	32
9	Species Differentiation and Quantification of Processed Animal Proteins and Blood Products in Fish Feed Using an 8-Plex Mass Spectrometry-Based Immunoassay. <i>Journal of Agricultural and Food Chemistry</i> , 2018, 66, 10327-10335.	5.2	14
10	Indirect protein quantification of drug-transforming enzymes using peptide group-specific immunoaffinity enrichment and mass spectrometry. <i>Scientific Reports</i> , 2015, 5, 8759.	3.3	25
11	Identification of short terminal motifs enriched by antibodies using peptide mass fingerprinting. <i>Bioinformatics</i> , 2014, 30, 1205-1213.	4.1	4
12	Catch and measure—mass spectrometry-based immunoassays in biomarker research. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 927-932.	2.3	37
13	G protein-coupled receptor quantification using peptide group-specific enrichment combined with internal peptide standard reporter calibration. <i>Journal of Proteomics</i> , 2013, 90, 85-95.	2.4	7
14	From spots to beads—PTM-peptide bead arrays for the characterization of anti-histone antibodies. <i>Proteomics</i> , 2013, 13, 1010-1015.	2.2	19
15	Targeting Peptide Termini, a Novel Immunoaffinity Approach to Reduce Complexity in Mass Spectrometric Protein Identification. <i>Molecular and Cellular Proteomics</i> , 2011, 10, S1-S11.	3.8	37
16	Optimal selection of epitopes for TXP-immunoaffinity mass spectrometry. <i>Algorithms for Molecular Biology</i> , 2010, 5, 28.	1.2	15