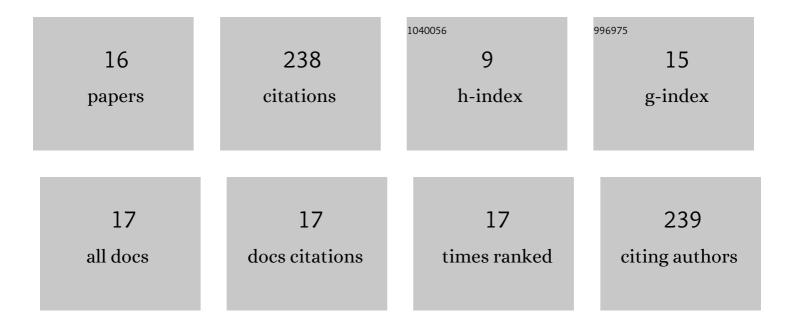
## Hannes Planatscher

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/11702010/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Pesticide mixture effects on liver protein abundance in HepaRG cells. Toxicology, 2021, 458, 152839.	4.2	8
2	A targeted transcriptomics approach for the determination of mixture effects of pesticides. Toxicology, 2021, 460, 152892.	4.2	5
3	Matrix and Sampling Effects on Quantification of Protein Biomarkers of Drug-Induced Liver Injury. Journal of Proteome Research, 2021, 20, 4985-4994.	3.7	2
4	RNA-protein correlation of liver toxicity markers in HepaRG cells. EXCLI Journal, 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. EXCLI Journal, 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. Analytical Chemistry, 2019, 91, 3902-3911.	6.5	10
7	Mass Spectrometry-Based Immunoassay for the Quantification of Banned Ruminant Processed Animal Proteins in Vegetal Feeds. Analytical Chemistry, 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. Drug Metabolism and Disposition, 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. Journal of Agricultural and Food Chemistry, 2018, 66, 10327-10335.	5.2	14
10	Indirect protein quantification of drug-transforming enzymes using peptide group-specific immunoaffinity enrichment and mass spectrometry. Scientific Reports, 2015, 5, 8759.	3.3	25
11	Identification of short terminal motifs enriched by antibodies using peptide mass fingerprinting. Bioinformatics, 2014, 30, 1205-1213.	4.1	4
12	Catch and measure–mass spectrometryâ€based immunoassays in biomarker research. Biochimica Et Biophysica Acta - Proteins and Proteomics, 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. Journal of Proteomics, 2013, 90, 85-95.	2.4	7
14	From spots to beads— <scp>PTM</scp> â€peptide bead arrays for the characterization of antiâ€histone antibodies. Proteomics, 2013, 13, 1010-1015.	2.2	19
15	Targeting Peptide Termini, a Novel Immunoaffinity Approach to Reduce Complexity in Mass Spectrometric Protein Identification. Molecular and Cellular Proteomics, 2011, 10, S1-S11.	3.8	37
16	Optimal selection of epitopes for TXP-immunoaffinity mass spectrometry. Algorithms for Molecular Biology, 2010, 5, 28.	1.2	15