

# Huaxu Yu

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3715080/publications.pdf>

Version: 2024-02-01

12  
papers

167  
citations

1163065

8  
h-index

1199563

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g-index

13  
all docs

13  
docs citations

13  
times ranked

124  
citing authors

#	ARTICLE	IF	CITATIONS
1	Fold-Change Compression: An Unexplored But Correctable Quantitative Bias Caused by Nonlinear Electrospray Ionization Responses in Untargeted Metabolomics. <i>Analytical Chemistry</i> , 2020, 92, 7011-7019.	6.5	24
2	ISFrag: De Novo Recognition of In-Source Fragments for Liquid Chromatography–Mass Spectrometry Data. <i>Analytical Chemistry</i> , 2021, 93, 10243-10250.	6.5	23
3	EVA: Evaluation of Metabolic Feature Fidelity Using a Deep Learning Model Trained With Over 25000 Extracted Ion Chromatograms. <i>Analytical Chemistry</i> , 2021, 93, 12181-12186.	6.5	21
4	Parallel metabolomics and lipidomics enables the comprehensive study of mouse brain regional metabolite and lipid patterns. <i>Analytica Chimica Acta</i> , 2020, 1136, 168-177.	5.4	16
5	Global-Scale Metabolomic Profiling of Human Hair for Simultaneous Monitoring of Endogenous Metabolome, Short- and Long-Term Exposome. <i>Frontiers in Chemistry</i> , 2021, 9, 674265.	3.6	16
6	Patterned Signal Ratio Biases in Mass Spectrometry-Based Quantitative Metabolomics. <i>Analytical Chemistry</i> , 2021, 93, 2254-2262.	6.5	14
7	Computational Variation: An Underinvestigated Quantitative Variability Caused by Automated Data Processing in Untargeted Metabolomics. <i>Analytical Chemistry</i> , 2021, 93, 8719-8728.	6.5	14
8	Recognizing Contamination Fragment Ions in Liquid Chromatography–Tandem Mass Spectrometry Data. <i>Journal of the American Society for Mass Spectrometry</i> , 2021, 32, 2296-2305.	2.8	12
9	MAFFIN: metabolomics sample normalization using maximal density fold change with high-quality metabolic features and corrected signal intensities. <i>Bioinformatics</i> , 2022, 38, 3429-3437.	4.1	8
10	Comprehensive assessment of the diminished statistical power caused by nonlinear electrospray ionization responses in mass spectrometry-based metabolomics. <i>Analytica Chimica Acta</i> , 2022, 1200, 339614.	5.4	7
11	Adaptive Box–Cox Transformation: A Highly Flexible Feature-Specific Data Transformation to Improve Metabolomic Data Normality for Better Statistical Analysis. <i>Analytical Chemistry</i> , 2022, 94, 8267-8276.	6.5	7
12	JPA: Joint Metabolic Feature Extraction Increases the Depth of Chemical Coverage for LC-MS-Based Metabolomics and Exposomics. <i>Metabolites</i> , 2022, 12, 212.	2.9	5