Retention time prediction using neural networks increa mass spectrometry

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Citation Report

#	Article	IF	Citations
1	Accurate Retention Time Prediction Based on Monolinked Peptide Information to Confidently Identify Cross-Linked Peptides. Journal of the American Society for Mass Spectrometry, 2021, 32, 2410-2416.	2.8	1
3	Label-free visual proteomics: Coupling MS- and EM-based approaches in structural biology. Molecular Cell, 2022, 82, 285-303.	9.7	21
4	Two-Dimensional Fractionation Method for Proteome-Wide Cross-Linking Mass Spectrometry Analysis. Analytical Chemistry, 2022, 94, 4236-4242.	6.5	13
5	Statistical analysis of isocratic chromatographic data using Bayesian modeling. Analytical and Bioanalytical Chemistry, 2022, 414, 3471-3481.	3.7	2
6	Ad hoc learning of peptide fragmentation from mass spectra enables an interpretable detection of phosphorylated and cross-linked peptides. Nature Machine Intelligence, 2022, 4, 378-388.	16.0	10
7	Improved Peptide Backbone Fragmentation Is the Primary Advantage of MS-Cleavable Crosslinkers. Analytical Chemistry, 2022, 94, 7779-7786.	6.5	15
8	Novel insight into the resilient drivers of bioaccumulation perchlorate on lipid nutrients alterations in goat milk by spatial multi-omics. LWT - Food Science and Technology, 2022, 165, 113717.	5.2	5
9	Prediction of peptide mass spectral libraries with machine learning. Nature Biotechnology, 2023, 41, 33-43.	17.5	31
11	inSPIRE: An Open-Source Tool for Increased Mass Spectrometry Identification Rates Using Prosit Spectral Prediction. Molecular and Cellular Proteomics, 2022, 21, 100432.	3.8	7
12	Volume-Corrected Free Energy as a New Criterion for Structural Elucidation in Chemical-Tagging-Based Metabolomics. Analytical Chemistry, 0, , .	6.5	1
14	Intriguing of pharmaceutical product development processes with the help of artificial intelligence and deep/machine learning or artificial neural network. Journal of Drug Delivery Science and Technology, 2023, 87, 104751.	3.0	2
15	Deep graph convolutional network for small-molecule retention time prediction. Journal of Chromatography A, 2023, 1711, 464439.	3.7	0
16	Deep Learning-Enabled Image Classification for the Determination of Aluminum Ions. Journal of Analytical Chemistry, 2023, 78, 1502-1510.	0.9	0
19	Acquisition and Analysis of DIA-Based Proteomic Data: A Comprehensive Survey inÂ2023. Molecular and Cellular Proteomics, 2024, 23, 100712.	3.8	0
20	Recent Developments in Machine Learning for Mass Spectrometry. ACS Measurement Science Au, 0, , .	4.4	0
21	Generic and accurate prediction of retention times in liquid chromatography by postâ€“projection calibration. Communications Chemistry, 2024, 7, .	4.5	0
22	AI-guided pipeline for proteinâ€“protein interaction drug discovery identifies a SARS-CoV-2 inhibitor. Molecular Systems Biology, 2024, 20, 428-457.	7.2	0