

# Mass Spec Studio for Integrative Structural Biology

Structure

22, 1538-1548

DOI: [10.1016/j.str.2014.08.013](https://doi.org/10.1016/j.str.2014.08.013)

Citation Report

#	ARTICLE	IF	CITATIONS
1	Toward Standardizing Deuterium Content Reporting in Hydrogen Exchange-MS. <i>Analytical Chemistry</i> , 2014, 86, 11962-11965.	3.2	8
2	<scp>HXâ€MS</scp>2 for high performance conformational analysis of complex protein states. <i>Protein Science</i> , 2015, 24, 1313-1324.	3.1	8
3	Exposing the subunit diversity and modularity of protein complexes by structural mass spectrometry approaches. <i>Proteomics</i> , 2015, 15, 2777-2791.	1.3	9
4	Applications of hydrogen deuterium exchange (HDX) for the characterization of conformational dynamics in light-activated photoreceptors. <i>Frontiers in Molecular Biosciences</i> , 2015, 2, 33.	1.6	10
5	Towards integrative structural mass spectrometry: Benefits from hybrid approaches. <i>Methods</i> , 2015, 89, 4-12.	1.9	24
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9	MEMHDX: an interactive tool to expedite the statistical validation and visualization of large HDX-MS datasets. <i>Bioinformatics</i> , 2016, 32, 3413-3419.	1.8	52
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13	Mapping Proteinâ€™Ligand Interactions with Proteolytic Fragmentation, Hydrogen/Deuterium Exchange-Mass Spectrometry. <i>Methods in Enzymology</i> , 2016, 566, 357-404.	0.4	57
14	A Guided Tour of Selected Image Processing and Analysis Methods for Fluorescence and Electron Microscopy. <i>IEEE Journal on Selected Topics in Signal Processing</i> , 2016, 10, 6-30.	7.3	52
15	Isotope Labeling of Biomolecules. <i>Methods in Enzymology</i> , 2016, 566, 405-426.	0.4	25
16	Novel Allosteric Pathway of Eg5 Regulation Identified through Multivariate Statistical Analysis of Hydrogen-Exchange Mass Spectrometry (HX-MS) Ligand Screening Data. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 428-437.	2.5	12
17	Nanospray HX-MS configuration for structural interrogation of large protein systems. <i>Analyst</i> , The, 2017, 142, 904-910.	1.7	19
18	Structural and functional characterization of the PNKPâ€™XRCC4â€™LigIV DNA repair complex. <i>Nucleic Acids Research</i> , 2017, 45, 6238-6251.	6.5	39
19	Simulated Isotope Exchange Patterns Enable Protein Structure Determination. <i>Angewandte Chemie - International Edition</i> , 2017, 56, 9396-9399.	7.2	19

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20	Amino Acid Insertion Frequencies Arising from Photoproducts Generated Using Aliphatic Diazirines. <i>Journal of the American Society for Mass Spectrometry</i> , 2017, 28, 2011-2021.	1.2	42
21	An overview of hydrogen deuterium exchange mass spectrometry (HDX-MS) in drug discovery. <i>Expert Opinion on Drug Discovery</i> , 2017, 12, 981-994.	2.5	110
22	Combining H/D Exchange Mass Spectrometry and Computational Docking To Derive the Structure of Protein-Protein Complexes. <i>Biochemistry</i> , 2017, 56, 6329-6342.	1.2	20
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39	Reliable Identification of Significant Differences in Differential Hydrogen Exchange-Mass Spectrometry Measurements Using a Hybrid Significance Testing Approach. <i>Analytical Chemistry</i> , 2019, 91, 8008-8016.	3.2	71
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