

Gordon W Slysz

List of Publications by Year in descending order

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21
papers

1,005
citations

567281

15
h-index

713466

21
g-index

21
all docs

21
docs citations

21
times ranked

1354
citing authors

#	ARTICLE	IF	CITATIONS
1	Blending Protein Separation and Peptide Analysis through Real-Time Proteolytic Digestion. <i>Analytical Chemistry</i> , 2005, 77, 1572-1579.	6.5	188
2	GlycReSoft: A Software Package for Automated Recognition of Glycans from LC/MS Data. <i>PLoS ONE</i> , 2012, 7, e45474.	2.5	126
3	A Unique Mode of Microtubule Stabilization Induced by Peloruside A. <i>Journal of Molecular Biology</i> , 2008, 378, 1016-1030.	4.2	110
4	On-column digestion of proteins in aqueous-organic solvents. <i>Rapid Communications in Mass Spectrometry</i> , 2003, 17, 1044-1050.	1.5	103
5	Detection and Identification of Sub-nanogram Levels of Protein in a NanoLC-Trypsin-MS System. <i>Journal of Proteome Research</i> , 2006, 5, 1959-1966.	3.7	73
6	Hydra: software for tailored processing of H/D exchange data from MS or tandem MS analyses. <i>BMC Bioinformatics</i> , 2009, 10, 162.	2.6	70
7	A Statistical Method for Assessing Peptide Identification Confidence in Accurate Mass and Time Tag Proteomics. <i>Analytical Chemistry</i> , 2011, 83, 6135-6140.	6.5	46
8	Restraining Expansion of the Peak Envelope in H/D Exchange-MS and Its Application in Detecting Perturbations of Protein Structure/Dynamics. <i>Analytical Chemistry</i> , 2008, 80, 7004-7011.	6.5	43
9	Structural Mass Spectrometry of the $\alpha\beta$ -Tubulin Dimer Supports a Revised Model of Microtubule Assembly. <i>Biochemistry</i> , 2009, 48, 4858-4870.	2.5	43
10	LC-IMS-MS Feature Finder: detecting multidimensional liquid chromatography, ion mobility and mass spectrometry features in complex datasets. <i>Bioinformatics</i> , 2013, 29, 2804-2805.	4.1	32
11	Increasing confidence of LC-MS identifications by utilizing ion mobility spectrometry. <i>International Journal of Mass Spectrometry</i> , 2013, 354-355, 312-317.	1.5	27
12	Comprehensive Quantitative Analysis of Ovarian and Breast Cancer Tumor Peptidomes. <i>Journal of Proteome Research</i> , 2015, 14, 422-433.	3.7	26
13	An algorithm to correct saturated mass spectrometry ion abundances for enhanced quantitation and mass accuracy in omic studies. <i>International Journal of Mass Spectrometry</i> , 2018, 427, 91-99.	1.5	25
14	Automated Data Extraction from <i>In Situ</i> Protein-Stable Isotope Probing Studies. <i>Journal of Proteome Research</i> , 2014, 13, 1200-1210.	3.7	20
15	Surrogate H/D Detection Strategy for Protein Conformational Analysis Using MS/MS Data. <i>Analytical Chemistry</i> , 2009, 81, 7900-7907.	6.5	17
16	Improving <i>N</i> -Glycan Coverage using HPLC-MS with Electrospray Ionization at Subambient Pressure. <i>Analytical Chemistry</i> , 2012, 84, 9208-9213.	6.5	13
17	GlyQ-IQ: Glycomics Quintivariate-Informed Quantification with High-Performance Computing and GlycoGrid 4D Visualization. <i>Analytical Chemistry</i> , 2014, 86, 6268-6276.	6.5	11
18	Identification of <i>Salmonella</i> Typhimurium Deubiquitinase SseL Substrates by Immunoaffinity Enrichment and Quantitative Proteomic Analysis. <i>Journal of Proteome Research</i> , 2015, 14, 4029-4038.	3.7	11

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19	An Optimized Informatics Pipeline for Mass Spectrometry-Based Peptidomics. Journal of the American Society for Mass Spectrometry, 2015, 26, 2002-2008.	2.8	10
20	Short-Term Stable Isotope Probing of Proteins Reveals Taxa Incorporating Inorganic Carbon in a Hot Spring Microbial Mat. Applied and Environmental Microbiology, 2020, 86, .	3.1	7
21	Integrating Accelerated Tryptic Digestion into Proteomics Workflows. Methods in Molecular Biology, 2009, 492, 241-254.	0.9	4