

Saiful M Chowdhury

List of Publications by Year in descending order

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papers

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34
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docs citations

34
times ranked

863
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification of an integrated stress and growth response signaling switch that directs vertebrate intestinal regeneration. <i>BMC Genomics</i> , 2022, 23, 6.	2.8	1
2	Mass Spectrometry-Cleavable Protein N-Terminal Tagging Strategy for System-Level Protease Activity Profiling. <i>Journal of the American Society for Mass Spectrometry</i> , 2022, 33, 189-197.	2.8	0
3	Effect of Caffeic acid analogs on Transient receptor potential melastatin 2 Channel. <i>FASEB Journal</i> , 2022, 36, .	0.5	0
4	Affinity and chemical enrichment strategies for mapping low-abundance protein modifications and protein-protein interaction networks. <i>Journal of Separation Science</i> , 2021, 44, 310-322.	2.5	6
5	Dual-Stage Neutral Loss Tandem Mass Spectrometric Strategy for Confident Identification of Protein Prenylation. <i>Analytical Chemistry</i> , 2021, 93, 13169-13176.	6.5	1
6	High Confidence Identification of Cross-Linked Peptides by an Enrichment-Based Dual Cleavable Cross-Linking Technology and Data Analysis tool Cleave-XL. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 173-182.	2.8	9
7	Evaluating the performance of an ETD-cleavable cross-linking strategy for elucidating protein structures. <i>Journal of Proteomics</i> , 2020, 225, 103846.	2.4	5
8	Improved in-solution trypsin digestion method for methanol-chloroform precipitated cellular proteomics sample. <i>Journal of Separation Science</i> , 2020, 43, 2125-2132.	2.5	11
9	The cell-surface protein composition of a coral symbiont, <i>Breviolum psygmophilum</i> , reveals a mechanism for host specificity and displays dynamic regulation during temperature stress. <i>Marine Biology</i> , 2020, 167, 1.	1.5	3
10	Proteomics Network Analysis of Polarized Macrophages. <i>Methods in Molecular Biology</i> , 2020, 2184, 61-75.	0.9	1
11	Multi-species comparisons of snakes identify coordinated signalling networks underlying post-feeding intestinal regeneration. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2019, 286, 20190910.	2.6	10
12	Cross-linking Proteomics Indicates Effects of Simvastatin on the TLR2 Interactome and Reveals ACTR1A as a Novel Regulator of the TLR2 Signal Cascade. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1732-1744.	3.8	15
13	Proteomic Investigation of a Diseased Gorgonian Coral Indicates Disruption of Essential Cell Function and Investment in Inflammatory and Other Immune Processes. <i>Integrative and Comparative Biology</i> , 2019, 59, 830-844.	2.0	10
14	Evaluation of Different Stationary Phases in the Separation of Inter-Cross-Linked Peptides. <i>Journal of Proteome Research</i> , 2019, 18, 1916-1925.	3.7	9
15	Inflammatory Proteomic Network Analysis of Statin-treated and Lipopolysaccharide-activated Macrophages. <i>Scientific Reports</i> , 2018, 8, 164.	3.3	23
16	Arginine-Selective Chemical Labeling Approach for Identification and Enrichment of Reactive Arginine Residues in Proteins. <i>ACS Omega</i> , 2018, 3, 14229-14235.	3.5	14
17	Comparative and network-based proteomic analysis of low dose ethanol- and lipopolysaccharide-induced macrophages. <i>PLoS ONE</i> , 2018, 13, e0193104.	2.5	20
18	Gas-Phase Fragmentation Behavior of Oxidized Prenyl Peptides by CID and ETD Tandem Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2017, 28, 704-707.	2.8	7

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19	Globular domain structure and function of restriction-like-endonuclease LINEs: similarities to eukaryotic splicing factor Prp8. <i>Mobile DNA</i> , 2017, 8, 16.	3.6	5
20	Evaluation of chemical labeling methods for identifying functional arginine residues of proteins by mass spectrometry. <i>Analytica Chimica Acta</i> , 2016, 935, 197-206.	5.4	11
21	Differential Tandem Mass Spectrometry-Based Cross-Linker: A New Approach for High Confidence in Identifying Protein Cross-Linking. <i>Analytical Chemistry</i> , 2016, 88, 10215-10222.	6.5	22
22	Mass Spectrometry Cleavable Strategy for Identification and Differentiation of Prenylated Peptides. <i>Analytical Chemistry</i> , 2015, 87, 2178-2186.	6.5	13
23	Proteomic Analysis of ABCA1-Null Macrophages Reveals a Role for Stomatin-Like Protein-2 in Raft Composition and Toll-Like Receptor Signaling. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 1859-1870.	3.8	17
24	Solid-phase N-terminal peptide enrichment study by optimizing trypsin proteolysis on homoarginine-modified proteins by mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2014, 28, 635-644.	1.5	9
25	Xlink-Identifier: An Automated Data Analysis Platform for Confident Identifications of Chemically Cross-Linked Peptides Using Tandem Mass Spectrometry. <i>Journal of Proteome Research</i> , 2011, 10, 923-931.	3.7	55
26	Proteomic Investigation of the Time Course Responses of RAW 264.7 Macrophages to Infection with <i>Salmonella enterica</i> . <i>Infection and Immunity</i> , 2009, 77, 3227-3233.	2.2	54
27	A Method for Investigating Protein-Protein Interactions Related to <i>Salmonella</i> Typhimurium Pathogenesis. <i>Journal of Proteome Research</i> , 2009, 8, 1504-1514.	3.7	22
28	Identification of Cross-Linked Peptides after Click-Based Enrichment Using Sequential Collision-Induced Dissociation and Electron Transfer Dissociation Tandem Mass Spectrometry. <i>Analytical Chemistry</i> , 2009, 81, 5524-5532.	6.5	91
29	Evaluation of low energy CID and ECD fragmentation behavior of mono-oxidized thio-ether bonds in peptides. <i>Journal of the American Society for Mass Spectrometry</i> , 2007, 18, 493-501.	2.8	28
30	Collisionally Activated Dissociation and Electron Capture Dissociation of Several Mass Spectrometry-Identifiable Chemical Cross-Linkers. <i>Analytical Chemistry</i> , 2006, 78, 8183-8193.	6.5	52
31	A new maleimide-bound acid-cleavable solid-support reagent for profiling phosphorylation. <i>Rapid Communications in Mass Spectrometry</i> , 2005, 19, 899-909.	1.5	14
32	Stereodefined Synthesis of O ³ -Labeled Uracil Nucleosides. ³ -[17O]- ² -Azido- ² -deoxyuridine 5'-Diphosphate as a Probe for the Mechanism of Inactivation of Ribonucleotide Reductases. <i>Journal of Organic Chemistry</i> , 2002, 67, 1816-1819.	3.2	39