Saiful M Chowdhury

List of Publications by Year
in descending order

32 papers	577 citations	687363 13 h-index	642732 23 g-index
34 all docs	34 docs citations	34 times ranked	863 citing authors

#	Article	IF	Citations
1	Identification of Cross-Linked Peptides after Click-Based Enrichment Using Sequential Collision-Induced Dissociation and Electron Transfer Dissociation Tandem Mass Spectrometry. Analytical Chemistry, 2009, 81, 5524-5532.	6.5	91
2	Xlink-Identifier: An Automated Data Analysis Platform for Confident Identifications of Chemically Cross-Linked Peptides Using Tandem Mass Spectrometry. Journal of Proteome Research, 2011, 10, 923-931.	3.7	55
3	Proteomic Investigation of the Time Course Responses of RAW 264.7 Macrophages to Infection with <i>Salmonella enterica</i>. Infection and Immunity, 2009, 77, 3227-3233.	2.2	54
4	Collisionally Activated Dissociation and Electron Capture Dissociation of Several Mass Spectrometry-Identifiable Chemical Cross-Linkers. Analytical Chemistry, 2006, 78, 8183-8193.	6.5	52
5	Stereodefined Synthesis of O3â€˜-Labeled Uracil Nucleosides. 3â€˜-[17O]-2â€˜-Azido-2â€˜-deoxyuridine 5â€˜-Diphosphate as a Probe for the Mechanism of Inactivation of Ribonucleotide Reductases. Journal of Organic Chemistry, 2002, 67, 1816-1819.	3.2	39
6	Evaluation of low energy CID and ECD fragmentation behavior of mono-oxidized thio-ether bonds in peptides. Journal of the American Society for Mass Spectrometry, 2007, 18, 493-501.	2.8	28
7	Inflammatory Proteomic Network Analysis of Statin-treated and Lipopolysaccharide-activated Macrophages. Scientific Reports, 2018, 8, 164.	3.3	23
8	A Method for Investigating Proteinâ€“Protein Interactions Related to <i>Salmonella</i> Typhimurium Pathogenesis. Journal of Proteome Research, 2009, 8, 1504-1514.	3.7	22
9	Differential Tandem Mass Spectrometry-Based Cross-Linker: A New Approach for High Confidence in Identifying Protein Cross-Linking. Analytical Chemistry, 2016, 88, 10215-10222.	6.5	22
10	Comparative and network-based proteomic analysis of low dose ethanol- and lipopolysaccharide-induced macrophages. PLoS ONE, 2018, 13, e0193104.	2.5	20
11	Proteomic Analysis of ABCA1-Null Macrophages Reveals a Role for Stomatin-Like Protein-2 in Raft Composition and Toll-Like Receptor Signaling. Molecular and Cellular Proteomics, 2015, 14, 1859-1870.	3.8	17
12	Cross-linking Proteomics Indicates Effects of Simvastatin on the TLR2 Interactome and Reveals ACTR1A as a Novel Regulator of the TLR2 Signal Cascade. Molecular and Cellular Proteomics, 2019, 18, 1732-1744.	3.8	15
13	A new maleimide-bound acid-cleavable solid-support reagent for profiling phosphorylation. Rapid Communications in Mass Spectrometry, 2005, 19, 899-909.	1.5	14
14	Arginine-Selective Chemical Labeling Approach for Identification and Enrichment of Reactive Arginine Residues in Proteins. ACS Omega, 2018, 3, 14229-14235.	3.5	14
15	Mass Spectrometry Cleavable Strategy for Identification and Differentiation of Prenylated Peptides. Analytical Chemistry, 2015, 87, 2178-2186.	6.5	13
16	Evaluation of chemical labeling methods for identifying functional arginine residues of proteins by mass spectrometry. Analytica Chimica Acta, 2016, 935, 197-206.	5.4	11
17	Improved inâ€‘solution trypsin digestion method for methanolâ€“chloroform precipitated cellular proteomics sample. Journal of Separation Science, 2020, 43, 2125-2132.	2.5	11
18	Multi-species comparisons of snakes identify coordinated signalling networks underlying post-feeding intestinal regeneration. Proceedings of the Royal Society B: Biological Sciences, 2019, 286, 20190910.	2.6	10

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19	Proteomic Investigation of a Diseased Gorgonian Coral Indicates Disruption of Essential Cell Function and Investment in Inflammatory and Other Immune Processes. Integrative and Comparative Biology, 2019, 59, 830-844.	2.0	10
20	Solid-phase N-terminal peptide enrichment study by optimizing trypsin proteolysis on homoarginine-modified proteins by mass spectrometry. Rapid Communications in Mass Spectrometry, 2014, 28, 635-644.	1.5	9
21	Evaluation of Different Stationary Phases in the Separation of Inter-Cross-Linked Peptides. Journal of Proteome Research, 2019, 18, 1916-1925.	3.7	9
22	High Confidence Identification of Cross-Linked Peptides by an Enrichment-Based Dual Cleavable Cross-Linking Technology and Data Analysis tool Cleave-XL. Journal of the American Society for Mass Spectrometry, 2020, 31, 173-182.	2.8	9
23	Gas-Phase Fragmentation Behavior of Oxidized Prenyl Peptides by CID and ETD Tandem Mass Spectrometry. Journal of the American Society for Mass Spectrometry, 2017, 28, 704-707.	2.8	7
24	Affinity and chemical enrichment strategies for mapping low‐abundance protein modifications and protein‐interaction networks. Journal of Separation Science, 2021, 44, 310-322.	2.5	6
25	Globular domain structure and function of restriction-like-endonuclease LINEs: similarities to eukaryotic splicing factor Prp8. Mobile DNA, 2017, 8, 16.	3.6	5
26	Evaluating the performance of an ETD-cleavable cross-linking strategy for elucidating protein structures. Journal of Proteomics, 2020, 225, 103846.	2.4	5
27	The cell-surface protein composition of a coral symbiont, Breviolum psygmophilum, reveals a mechanism for host specificity and displays dynamic regulation during temperature stress. Marine Biology, 2020, 167, 1.	1.5	3
28	Dual-Stage Neutral Loss Tandem Mass Spectrometric Strategy for Confident Identification of Protein Prenylation. Analytical Chemistry, 2021, 93, 13169-13176.	6.5	1
29	Proteomics Network Analysis of Polarized Macrophages. Methods in Molecular Biology, 2020, 2184, 61-75.	0.9	1
30	Identification of an integrated stress and growth response signaling switch that directs vertebrate intestinal regeneration. BMC Genomics, 2022, 23, 6.	2.8	1
31	Mass Spectrometry-Cleavable Protein N-Terminal Tagging Strategy for System-Level Protease Activity Profiling. Journal of the American Society for Mass Spectrometry, 2022, 33, 189-197.	2.8	0
32	Effect of Caffeic acid analogs on Transient receptor potential melastatin 2 Channel. FASEB Journal, 2022, 36, .	0.5	0