

Alan A Doucette

List of Publications by Year in descending order

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44
papers

1,485
citations

394421

19
h-index

330143

37
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46
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46
docs citations

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times ranked

1657
citing authors

#	ARTICLE	IF	CITATIONS
1	Gel-Eluted Liquid Fraction Entrapment Electrophoresis: An Electrophoretic Method for Broad Molecular Weight Range Proteome Separation. <i>Analytical Chemistry</i> , 2008, 80, 1568-1573.	6.5	174
2	Top-Down and Bottom-Up Proteomics of SDS-Containing Solutions Following Mass-Based Separation. <i>Journal of Proteome Research</i> , 2010, 9, 2863-2870.	3.7	146
3	Maximizing recovery of water-soluble proteins through acetone precipitation. <i>Analytica Chimica Acta</i> , 2013, 796, 48-54.	5.4	122
4	Multiplexed Size Separation of Intact Proteins in Solution Phase for Mass Spectrometry. <i>Analytical Chemistry</i> , 2009, 81, 6201-6209.	6.5	117
5	Protein Concentration and Enzyme Digestion on Microbeads for MALDI-TOF Peptide Mass Mapping of Proteins from Dilute Solutions. <i>Analytical Chemistry</i> , 2000, 72, 3355-3362.	6.5	82
6	Comparison of sodium dodecyl sulfate depletion techniques for proteome analysis by mass spectrometry. <i>Journal of Chromatography A</i> , 2015, 1418, 158-166.	3.7	68
7	Two-Layer Sample Preparation Method for MALDI Mass Spectrometric Analysis of Protein and Peptide Samples Containing Sodium Dodecyl Sulfate. <i>Analytical Chemistry</i> , 2001, 73, 2968-2975.	6.5	58
8	Rapid and Quantitative Protein Precipitation for Proteome Analysis by Mass Spectrometry. <i>Journal of Proteome Research</i> , 2020, 19, 2035-2042.	3.7	58
9	Resolubilization of Precipitated Intact Membrane Proteins with Cold Formic Acid for Analysis by Mass Spectrometry. <i>Journal of Proteome Research</i> , 2014, 13, 6001-6012.	3.7	47
10	Preventing N- and O-formylation of proteins when incubated in concentrated formic acid. <i>Proteomics</i> , 2016, 16, 1059-1068.	2.2	47
11	Differential Proteome Analysis of Extracellular Vesicles from Breast Cancer Cell Lines by Chaperone Affinity Enrichment. <i>Proteomes</i> , 2017, 5, 25.	3.5	47
12	Microcolumn Capture and Digestion of Proteins Combined with Mass Spectrometry for Protein Identification. <i>Journal of Proteome Research</i> , 2002, 1, 537-547.	3.7	43
13	Intact proteome fractionation strategies compatible with mass spectrometry. <i>Expert Review of Proteomics</i> , 2011, 8, 787-800.	3.0	40
14	Rapid and Effective Focusing in a Carrier Ampholyte Solution Isoelectric Focusing System: A Proteome Prefractionation Tool. <i>Journal of Proteome Research</i> , 2008, 7, 1761-1766.	3.7	38
15	Implications of partial tryptic digestion in organic-aqueous solvent systems for bottom-up proteome analysis. <i>Analytica Chimica Acta</i> , 2011, 703, 194-203.	5.4	27
16	A two-stage spin cartridge for integrated protein precipitation, digestion and SDS removal in a comparative bottom-up proteomics workflow. <i>Journal of Proteomics</i> , 2015, 118, 140-150.	2.4	26
17	The benefits (and misfortunes) of SDS in top-down proteomics. <i>Journal of Proteomics</i> , 2018, 175, 75-86.	2.4	25
18	Recent advances in top-down proteome sample processing ahead of MS analysis. <i>Mass Spectrometry Reviews</i> , 2023, 42, 457-495.	5.4	24

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19	Automated SDS Depletion for Mass Spectrometry of Intact Membrane Proteins through Transmembrane Electrophoresis. <i>Journal of Proteome Research</i> , 2016, 15, 2634-2642.	3.7	23
20	Mass Spectrometry of Intact Proteins Reveals +98 u Chemical Artifacts Following Precipitation in Acetone. <i>Journal of Proteome Research</i> , 2017, 16, 889-897.	3.7	23
21	Chromatographic behaviour of peptides following dimethylation with H ₂ /D ₂ -formaldehyde: Implications for comparative proteomics. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2012, 908, 59-66.	2.3	21
22	Dual LC-MS Platform for High-Throughput Proteome Analysis. <i>Journal of Proteome Research</i> , 2013, 12, 5963-5970.	3.7	20
23	Proteomic Workflows for Biomarker Identification Using Mass Spectrometry – Technical and Statistical Considerations during Initial Discovery. <i>Proteomes</i> , 2013, 1, 109-127.	3.5	20
24	Review of Membrane Separation Models and Technologies: Processing Complex Food-Based Biomolecular Fractions. <i>Food and Bioprocess Technology</i> , 2021, 14, 415-428.	4.7	19
25	Mass spectrometric study of the effects of hydrophobic surface chemistry and morphology on the digestion of surface-bound proteins. <i>Journal of the American Society for Mass Spectrometry</i> , 2003, 14, 203-214.	2.8	18
26	Alterations in urinary metabolites due to unilateral ureteral obstruction in a rodent model. <i>Molecular BioSystems</i> , 2011, 7, 2181.	2.9	17
27	Mass spectrometry profiling of low molecular weight proteins and peptides isolated by acetone precipitation. <i>Analytica Chimica Acta</i> , 2020, 1138, 38-48.	5.4	17
28	A qualitative proteome investigation of the sediment portion of human urine: Implications in the biomarker discovery process. <i>Proteomics - Clinical Applications</i> , 2009, 3, 95-105.	1.6	15
29	A robust strategy for proteomic identification of biomarkers of invasive phenotype complexed with extracellular heat shock proteins. <i>Cell Stress and Chaperones</i> , 2019, 24, 1197-1209.	2.9	14
30	Investigation of the applicability of a sequential digestion protocol using trypsin and leucine aminopeptidase M for protein identification by matrix-assisted laser desorption/ionization - time of flight mass spectrometry. <i>Proteomics</i> , 2001, 1, 987-1000.	2.2	12
31	Perfluorooctanoic acid and ammonium perfluorooctanoate: volatile surfactants for proteome analysis?. <i>Rapid Communications in Mass Spectrometry</i> , 2012, 26, 523-531.	1.5	12
32	Critical assessment of the spectroscopic activity assay for monitoring trypsin activity in organic-aqueous solvent. <i>Analytical Biochemistry</i> , 2013, 435, 131-136.	2.4	12
33	Evaluation of a solution isoelectric focusing protocol as an alternative to ion exchange chromatography for charge-based proteome prefractionation. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2009, 877, 807-813.	2.3	9
34	A universal, high recovery assay for protein quantitation through temperature programmed liquid chromatography (TPLC). <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2013, 921-922, 75-80.	2.3	8
35	Proteomic analysis of rat proximal tubule cells following stretch-induced apoptosis in an in vitro model of kidney obstruction. <i>Journal of Proteomics</i> , 2014, 100, 125-135.	2.4	8
36	Molecular-Formula Determination through Accurate-Mass Analysis: A Forensic Investigation. <i>Journal of Chemical Education</i> , 2019, 96, 1458-1464.	2.3	8

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37	Membrane-Based SDS Depletion Ahead of Peptide and Protein Analysis by Mass Spectrometry. <i>Proteomics</i> , 2018, 18, e1700025.	2.2	6
38	Salt-Mediated Organic Solvent Precipitation for Enhanced Recovery of Peptides Generated by Pepsin Digestion. <i>Proteomes</i> , 2021, 9, 44.	3.5	6
39	Organic Solvent-Based Protein Precipitation for Robust Proteome Purification Ahead of Mass Spectrometry. <i>Journal of Visualized Experiments</i> , 2022, , .	0.3	4
40	Precipitation of Detergent-Containing Samples for Top-Down and Bottom-Up Proteomics. , 0, , .		2
41	Developing front-end devices for improved sample preparation in MS-based proteome analysis. <i>Journal of Mass Spectrometry</i> , 2020, 55, e4494.	1.6	1
42	Automated Electrokinetic Platform for High-Throughput Sodium Dodecyl Sulfate Depletion Ahead of Proteome Analysis by Mass Spectrometry. <i>Analytical Chemistry</i> , 2021, 93, 14042-14047.	6.5	1
43	Reprint of "cGELFrEE fractionation combined with mass spectrometry for proteome analysis of secreted toxins from Enteropathogenic Escherichia coli (EPEC)" Molecular and Cellular Probes, 2014, 28, 83-90.	2.1	0
44	Exosomal proteomic analysis reveals changes in the urinary proteome of rats with unilateral ureteral obstruction. <i>Canadian Journal of Chemistry</i> , 2018, 96, 771-778.	1.1	0