

John C Tran

List of Publications by Year in descending order

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Version: 2024-02-01

31
papers

2,211
citations

304743

22
h-index

454955

30
g-index

31
all docs

31
docs citations

31
times ranked

2207
citing authors

#	ARTICLE	IF	CITATIONS
1	Mapping intact protein isoforms in discovery mode using top-down proteomics. <i>Nature</i> , 2011, 480, 254-258.	27.8	587
2	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
3	Large-scale Top-down Proteomics of the Human Proteome: Membrane Proteins, Mitochondria, and Senescence. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3465-3473.	3.8	132
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	A protease for 'middle-down' proteomics. <i>Nature Methods</i> , 2012, 9, 822-824.	19.0	103
6	The emerging process of Top Down mass spectrometry for protein analysis: biomarkers, protein-therapeutics, and achieving high throughput. <i>Molecular BioSystems</i> , 2010, 6, 1532.	2.9	92
7	A robust two-dimensional separation for top-down tandem mass spectrometry of the low-mass proteome. <i>Journal of the American Society for Mass Spectrometry</i> , 2009, 20, 2183-2191.	2.8	91
8	Size-Sorting Combined with Improved Nanocapillary Liquid Chromatography-Mass Spectrometry for Identification of Intact Proteins up to 80 kDa. <i>Analytical Chemistry</i> , 2010, 82, 1234-1244.	6.5	91
9	Analysis of Intact Protein Isoforms by Mass Spectrometry. <i>Journal of Biological Chemistry</i> , 2011, 286, 25451-25458.	3.4	88
10	Evaluation of the Compact High-Field Orbitrap for Top-Down Proteomics of Human Cells. <i>Journal of Proteome Research</i> , 2012, 11, 4308-4314.	3.7	84
11	Optimizing capillary electrophoresis for top-down proteomics of 30-80 kDa proteins. <i>Proteomics</i> , 2014, 14, 1158-1164.	2.2	76
12	Top Down Proteomics of Human Membrane Proteins from Enriched Mitochondrial Fractions. <i>Analytical Chemistry</i> , 2013, 85, 1880-1888.	6.5	72
13	Robust Analysis of the Yeast Proteome under 50 kDa by Molecular-Mass-Based Fractionation and Top-Down Mass Spectrometry. <i>Analytical Chemistry</i> , 2012, 84, 209-215.	6.5	62
14	Mass Spectrometry and Antibody-Based Characterization of Blood Vessels from <i>Brachyophosaurus canadensis</i> . <i>Journal of Proteome Research</i> , 2015, 14, 5252-5262.	3.7	59
15	Intact mass detection, interpretation, and visualization to automate Top-Down proteomics on a large scale. <i>Proteomics</i> , 2010, 10, 3589-3597.	2.2	48
16	Intact proteome fractionation strategies compatible with mass spectrometry. <i>Expert Review of Proteomics</i> , 2011, 8, 787-800.	3.0	40
17	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
18	Nano-LC FTICR Tandem Mass Spectrometry for Top-Down Proteomics: Routine Baseline Unit Mass Resolution of Whole Cell Lysate Proteins up to 72 kDa. <i>Analytical Chemistry</i> , 2012, 84, 2111-2117.	6.5	38

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19	High-throughput antibody screening from complex matrices using intact protein electrospray mass spectrometry. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 9851-9856.	7.1	38
20	Automated Affinity Capture and On-Tip Digestion to Accurately Quantitate <i>in Vivo</i> Deamidation of Therapeutic Antibodies. Analytical Chemistry, 2016, 88, 11521-11526.	6.5	29
21	Novel Interface for High-Throughput Analysis of Biotherapeutics by Electrospray Mass Spectrometry. Analytical Chemistry, 2020, 92, 2186-2193.	6.5	28
22	Cyclic polyamide oligomers extracted from nylon 66 membrane filter disks as a source of contamination in liquid chromatography/mass spectrometry. Journal of the American Society for Mass Spectrometry, 2006, 17, 652-656.	2.8	27
23	Intact Protein Mass Spectrometry for Therapeutic Protein Quantitation, Pharmacokinetics, and Biotransformation in Preclinical and Clinical Studies: An Industry Perspective. Journal of the American Society for Mass Spectrometry, 2021, 32, 1886-1900.	2.8	19
24	Online Matrix Removal Platform for Coupling Gel-Based Separations to Whole Protein Electrospray Ionization Mass Spectrometry. Journal of Proteome Research, 2015, 14, 2199-2206.	3.7	18
25	Identification of Small-Molecule Noncovalent Binders Utilizing SAMDI Technology. SLAS Discovery, 2017, 22, 1211-1217.	2.7	16
26	Automated On-tip Affinity Capture Coupled with Mass Spectrometry to Characterize Intact Antibody-Drug Conjugates from Blood. Journal of the American Society for Mass Spectrometry, 2018, 29, 1532-1537.	2.8	10
27	Evaluation of a solution isoelectric focusing protocol as an alternative to ion exchange chromatography for charge-based proteome prefractionation. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2009, 877, 807-813.	2.3	9
28	Improved translation of stability for conjugated antibodies using an in vitro whole blood assay. MAbs, 2020, 12, 1715705.	5.2	9
29	Characterizing and Quantitating Therapeutic Tethered Multimeric Antibody Degradation Using Affinity Capture Mass Spectrometry. Analytical Chemistry, 2020, 92, 6839-6843.	6.5	8
30	A Cross Company Perspective on the Assessment of Therapeutic Protein Biotransformation. Drug Metabolism and Disposition, 2022, 50, 846-857.	3.3	8
31	Using a peptide-based mass spectrometry approach to quantitate proteolysis of an intact heterogeneous procollagen substrate by BMP1 for antagonistic antibody screening. Analytical and Bioanalytical Chemistry, 0, , .	3.7	0