

# 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  | A Cross Company Perspective on the Assessment of Therapeutic Protein Biotransformation. <i>Drug Metabolism and Disposition</i> , 2022, 50, 846-857.  | 3.3  | 8         |
| 2  | Intact Protein Mass Spectrometry for Therapeutic Protein Quantitation, Pharmacokinetics, and Biotransformation in Preclinical and Clinical Studies: An Industry Perspective. <i>Journal of the American Society for Mass Spectrometry</i> , 2021, 32, 1886-1900. | 2.8  | 19        |
| 3  | Novel Interface for High-Throughput Analysis of Biotherapeutics by Electrospray Mass Spectrometry. <i>Analytical Chemistry</i> , 2020, 92, 2186-2193.  | 6.5  | 28        |
| 4  | Characterizing and Quantitating Therapeutic Tethered Multimeric Antibody Degradation Using Affinity Capture Mass Spectrometry. <i>Analytical Chemistry</i> , 2020, 92, 6839-6843.  | 6.5  | 8         |
| 5  | High-throughput antibody screening from complex matrices using intact protein electrospray mass spectrometry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 9851-9856.                                     | 7.1  | 38        |
| 6  | Improved translation of stability for conjugated antibodies using an in vitro whole blood assay. <i>MAbs</i> , 2020, 12, 1715705.  | 5.2  | 9         |
| 7  | Automated On-tip Affinity Capture Coupled with Mass Spectrometry to Characterize Intact Antibody-Drug Conjugates from Blood. <i>Journal of the American Society for Mass Spectrometry</i> , 2018, 29, 1532-1537.   | 2.8  | 10        |
| 8  | Identification of Small-Molecule Noncovalent Binders Utilizing SAMDI Technology. <i>SLAS Discovery</i> , 2017, 22, 1211-1217.  | 2.7  | 16        |
| 9  | Automated Affinity Capture and On-Tip Digestion to Accurately Quantitate <i>in Vivo</i> Deamidation of Therapeutic Antibodies. <i>Analytical Chemistry</i> , 2016, 88, 11521-11526.  | 6.5  | 29        |
| 10 | Online Matrix Removal Platform for Coupling Gel-Based Separations to Whole Protein Electrospray Ionization Mass Spectrometry. <i>Journal of Proteome Research</i> , 2015, 14, 2199-2206.   | 3.7  | 18        |
| 11 | 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        |
| 12 | Optimizing capillary electrophoresis for top-down proteomics of 30-80 kDa proteins. <i>Proteomics</i> , 2014, 14, 1158-1164.   | 2.2  | 76        |
| 13 | 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       |
| 14 | Top Down Proteomics of Human Membrane Proteins from Enriched Mitochondrial Fractions. <i>Analytical Chemistry</i> , 2013, 85, 1880-1888.   | 6.5  | 72        |
| 15 | 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        |
| 16 | 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        |
| 17 | A protease for 'middle-down' proteomics. <i>Nature Methods</i> , 2012, 9, 822-824.   | 19.0 | 103       |
| 18 | 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        |

| #  | ARTICLE   | IF   | CITATIONS |
|----|---|------|-----------|
| 19 | Mapping intact protein isoforms in discovery mode using top-down proteomics. <i>Nature</i> , 2011, 480, 254-258.  | 27.8 | 587       |
| 20 | Intact proteome fractionation strategies compatible with mass spectrometry. <i>Expert Review of Proteomics</i> , 2011, 8, 787-800.  | 3.0  | 40        |
| 21 | Analysis of Intact Protein Isoforms by Mass Spectrometry. <i>Journal of Biological Chemistry</i> , 2011, 286, 25451-25458.  | 3.4  | 88        |
| 22 | 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        |
| 23 | 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        |
| 24 | 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        |
| 25 | 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        |
| 26 | 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         |
| 27 | Multiplexed Size Separation of Intact Proteins in Solution Phase for Mass Spectrometry. <i>Analytical Chemistry</i> , 2009, 81, 6201-6209.  | 6.5  | 117       |
| 28 | 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        |
| 29 | 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       |
| 30 | Cyclic polyamide oligomers extracted from nylon 66 membrane filter disks as a source of contamination in liquid chromatography/mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2006, 17, 652-656.                                       | 2.8  | 27        |
| 31 | Using a peptide-based mass spectrometry approach to quantitate proteolysis of an intact heterogeneous procollagen substrate by BMP1 for antagonistic antibody screening. <i>Analytical and Bioanalytical Chemistry</i> , 0, , .   | 3.7  | 0         |