

# Paul M Thomas

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8563710/publications.pdf>

Version: 2024-02-01

121  
papers

8,344  
citations

38720

50  
h-index

49868

87  
g-index

126  
all docs

126  
docs citations

126  
times ranked

9879  
citing authors

| #  | ARTICLE   | IF  | CITATIONS |
|----|---|-----|-----------|
| 1  | The Blood Proteoform Atlas: A reference map of proteoforms in human hematopoietic cells. <i>Science</i> , 2022, 375, 411-418.   | 6.0 | 64        |
| 2  | Proteomics Standards Initiative's ProForma 2.0: Unifying the Encoding of Proteoforms and Peptidoforms. <i>Journal of Proteome Research</i> , 2022, 21, 1189-1195.   | 1.8 | 14        |
| 3  | A mixed-valent Fe(II)Fe(III) species converts cysteine to an oxazolone/thioamide pair in methanobactin biosynthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2123566119.   | 3.3 | 14        |
| 4  | ProSight Annotator: Complete control and customization of protein entries in UniProt XML files. <i>Proteomics</i> , 2022, 22, e2100209.   | 1.3 | 6         |
| 5  | The Human Proteoform Atlas: a FAIR community resource for experimentally derived proteoforms. <i>Nucleic Acids Research</i> , 2022, 50, D526-D533.  | 6.5 | 15        |
| 6  | Proteoform-Selective Imaging of Tissues Using Mass Spectrometry**. <i>Angewandte Chemie - International Edition</i> , 2022, 61, .   | 7.2 | 22        |
| 7  | InnenrÃ¼cktitelbild: Proteoform-Selective Imaging of Tissues Using Mass Spectrometry ( <i>Angew. Chem.</i> ) Tj ETQq1 1 0.784314 rgBT C   | 1.6 | 0         |
| 8  | <i>In vitro</i> -Constructed Ribosomes Enable Multi-site Incorporation of Noncanonical Amino Acids into Proteins. <i>Biochemistry</i> , 2021, 60, 161-169.  | 1.2 | 9         |
| 9  | Deeper Protein Identification Using Field Asymmetric Ion Mobility Spectrometry in Top-Down Proteomics. <i>Analytical Chemistry</i> , 2021, 93, 6323-6328.   | 3.2 | 40        |
| 10 | Characterization of a Copper-Chelating Natural Product from the Methanotroph <i>Methylosinus</i> sp. LW3. <i>Biochemistry</i> , 2021, 60, 2845-2850.  | 1.2 | 5         |
| 11 | Development of novel methods for non-canonical myeloma protein analysis with an innovative adaptation of immunofixation electrophoresis, native top-down mass spectrometry, and middle-down <i>de novo</i> sequencing. <i>Clinical Chemistry and Laboratory Medicine</i> , 2021, 59, 653-661. | 1.4 | 7         |
| 12 | Identification of <i>Plasmodium falciparum</i> proteoforms from liver stage models. <i>Malaria Journal</i> , 2020, 19, 10.  | 0.8 | 2         |
| 13 | Histone tail analysis reveals H3K36me2 and H4K16ac as epigenetic signatures of diffuse intrinsic pontine glioma. <i>Journal of Experimental and Clinical Cancer Research</i> , 2020, 39, 261.   | 3.5 | 16        |
| 14 | Chemical composition of material extractives influences microbial growth and dynamics on wetted wood materials. <i>Scientific Reports</i> , 2020, 10, 14500.  | 1.6 | 4         |
| 15 | Heterologous Expression of the Unusual Terreazepine Biosynthetic Gene Cluster Reveals a Promising Approach for Identifying New Chemical Scaffolds. <i>MBio</i> , 2020, 11, .  | 1.8 | 12        |
| 16 | The serine hydroxymethyltransferase-2 (SHMT2) initiates lymphoma development through epigenetic tumor suppressor silencing. <i>Nature Cancer</i> , 2020, 1, 653-664.  | 5.7 | 35        |
| 17 | NMT1 and NMT2 are lysine myristoyltransferases regulating the ARF6 GTPase cycle. <i>Nature Communications</i> , 2020, 11, 1067.   | 5.8 | 62        |
| 18 | Thorough Performance Evaluation of 213 nm Ultraviolet Photodissociation for Top-down Proteomics. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 405-420.  | 2.5 | 38        |

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|----|--|-----|-----------|
| 19 | Targeted detection and quantitation of histone modifications from 1,000 cells. PLoS ONE, 2020, 15, e0240829.   | 1.1 | 3         |
| 20 | Targeted detection and quantitation of histone modifications from 1,000 cells. , 2020, 15, e0240829.   |     | 0         |
| 21 | Targeted detection and quantitation of histone modifications from 1,000 cells. , 2020, 15, e0240829.   |     | 0         |
| 22 | Targeted detection and quantitation of histone modifications from 1,000 cells. , 2020, 15, e0240829.   |     | 0         |
| 23 | Targeted detection and quantitation of histone modifications from 1,000 cells. , 2020, 15, e0240829.   |     | 0         |
| 24 | Targeted detection and quantitation of histone modifications from 1,000 cells. , 2020, 15, e0240829.   |     | 0         |
| 25 | Targeted detection and quantitation of histone modifications from 1,000 cells. , 2020, 15, e0240829.   |     | 0         |
| 26 | Targeted detection and quantitation of histone modifications from 1,000 cells. , 2020, 15, e0240829.   |     | 0         |
| 27 | Targeted detection and quantitation of histone modifications from 1,000 cells. , 2020, 15, e0240829.   |     | 0         |
| 28 | Coupling Fluorescence-Activated Cell Sorting and Targeted Analysis of Histone Modification Profiles in Primary Human Leukocytes. Journal of the American Society for Mass Spectrometry, 2019, 30, 2526-2534. | 1.2 | 9         |
| 29 | A Highly Productive, One-Pot Cell-Free Protein Synthesis Platform Based on Genomically Recoded Escherichia coli. Cell Chemical Biology, 2019, 26, 1743-1754.e9.  | 2.5 | 59        |
| 30 | A five-level classification system for proteoform identifications. Nature Methods, 2019, 16, 939-940.  | 9.0 | 55        |
| 31 | Multidimensional Top-Down Proteomics of Brain-Region-Specific Mouse Brain Proteoforms Responsive to Cocaine and Estradiol. Journal of Proteome Research, 2019, 18, 3999-4012.                                | 1.8 | 12        |
| 32 | Native top-down mass spectrometry provides insights into the copper centers of membrane-bound methane monooxygenase. Nature Communications, 2019, 10, 2675.  | 5.8 | 74        |
| 33 | Biotin Identification Proteomics in Three-Dimensional Organotypic Human Skin Cultures. Methods in Molecular Biology, 2019, 2109, 185-197.  | 0.4 | 3         |
| 34 | Identification and Quantification of Proteoforms by Mass Spectrometry. Proteomics, 2019, 19, e1800361.   | 1.3 | 147       |
| 35 | Microbial and metabolic succession on common building materials under high humidity conditions. Nature Communications, 2019, 10, 1767.   | 5.8 | 46        |
| 36 | A clinically relevant murine model unmasks a "two-hit" mechanism for reactivation and dissemination of cytomegalovirus after kidney transplant. American Journal of Transplantation, 2019, 19, 2421-2433.    | 2.6 | 28        |

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|----|--|-----|-----------|
| 37 | USP7 Cooperates with NOTCH1 to Drive the Oncogenic Transcriptional Program in T-Cell Leukemia. <i>Clinical Cancer Research</i> , 2019, 25, 222-239.  | 3.2 | 66        |
| 38 | Identification and targeting of novel CDK9 complexes in acute myeloid leukemia. <i>Blood</i> , 2019, 133, 1171-1185.   | 0.6 | 26        |
| 39 | Accurate Estimation of Context-Dependent False Discovery Rates in Top-Down Proteomics. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 796-805.   | 2.5 | 27        |
| 40 | Top-Down Proteomics Enables Comparative Analysis of Brain Proteoforms Between Mouse Strains. <i>Analytical Chemistry</i> , 2018, 90, 3802-3810.  | 3.2 | 27        |
| 41 | Identification of the First Diketomorpholine Biosynthetic Pathway Using FAC-MS Technology. <i>ACS Chemical Biology</i> , 2018, 13, 1142-1147.  | 1.6 | 30        |
| 42 | How many human proteoforms are there?. <i>Nature Chemical Biology</i> , 2018, 14, 206-214.   | 3.9 | 580       |
| 43 | The biosynthesis of methanobactin. <i>Science</i> , 2018, 359, 1411-1416.  | 6.0 | 101       |
| 44 | Cell-free protein synthesis from genomically recoded bacteria enables multisite incorporation of noncanonical amino acids. <i>Nature Communications</i> , 2018, 9, 1203.                                     | 5.8 | 165       |
| 45 | Interrogation of Benzomalvin Biosynthesis Using Fungal Artificial Chromosomes with Metabolomic Scoring (FAC-MS): Discovery of a Benzodiazepine Synthase Activity. <i>Biochemistry</i> , 2018, 57, 3237-3243. | 1.2 | 19        |
| 46 | Characterization of a long overlooked copper protein from methane- and ammonia-oxidizing bacteria. <i>Nature Communications</i> , 2018, 9, 4276.   | 5.8 | 46        |
| 47 | The vermiform appendix impacts the risk of developing Parkinson's disease. <i>Science Translational Medicine</i> , 2018, 10, .   | 5.8 | 205       |
| 48 | Stability of histone post-translational modifications in samples derived from liver tissue and primary hepatic cells. <i>PLoS ONE</i> , 2018, 13, e0203351.  | 1.1 | 4         |
| 49 | The unique biomineralization transcriptome and proteome of <i>Lytechinus variegatus</i> teeth. <i>Connective Tissue Research</i> , 2018, 59, 20-29.  | 1.1 | 2         |
| 50 | The Value of Activated Ion Electron Transfer Dissociation for High-Throughput Top-Down Characterization of Intact Proteins. <i>Analytical Chemistry</i> , 2018, 90, 8553-8560.                               | 3.2 | 35        |
| 51 | EphA2 proteomics in human keratinocytes reveals a novel association with afadin and epidermal tight junctions. <i>Journal of Cell Science</i> , 2017, 130, 111-118.  | 1.2 | 21        |
| 52 | Expansion for the <i>Brachylophosaurus canadensis</i> Collagen I Sequence and Additional Evidence of the Preservation of Cretaceous Protein. <i>Journal of Proteome Research</i> , 2017, 16, 920-932.        | 1.8 | 80        |
| 53 | Programmed Ribosomal Frameshifting Generates a Copper Transporter and a Copper Chaperone from the Same Gene. <i>Molecular Cell</i> , 2017, 65, 207-219.  | 4.5 | 81        |
| 54 | High-Throughput Analysis of Intact Human Proteins Using UVPD and HCD on an Orbitrap Mass Spectrometer. <i>Journal of Proteome Research</i> , 2017, 16, 2072-2079.  | 1.8 | 69        |

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|----|--|------|-----------|
| 55 | Proteoforms in Peripheral Blood Mononuclear Cells as Novel Rejection Biomarkers in Liver Transplant Recipients. <i>American Journal of Transplantation</i> , 2017, 17, 2458-2467.                                    | 2.6  | 37        |
| 56 | A scalable platform to identify fungal secondary metabolites and their gene clusters. <i>Nature Chemical Biology</i> , 2017, 13, 895-901.  | 3.9  | 154       |
| 57 | PAI-1 is a critical regulator of FGF23 homeostasis. <i>Science Advances</i> , 2017, 3, e1603259.   | 4.7  | 24        |
| 58 | Diversity of Amyloid-beta Proteoforms in the Alzheimer's Disease Brain. <i>Scientific Reports</i> , 2017, 7, 9520.   | 1.6  | 125       |
| 59 | Identification and Characterization of Human Proteoforms by Top-Down LC-21 Tesla FT-ICR Mass Spectrometry. <i>Journal of Proteome Research</i> , 2017, 16, 1087-1096.  | 1.8  | 81        |
| 60 | Bioinformatics Analysis of Top-Down Mass Spectrometry Data with ProSight Lite. <i>Methods in Molecular Biology</i> , 2017, 1558, 381-394.  | 0.4  | 27        |
| 61 | A synthetic biology approach to probing nucleosome symmetry. <i>ELife</i> , 2017, 6, .   | 2.8  | 16        |
| 62 | High-Throughput Natural Products Discovery in Fungi Using FACMS Technology. <i>FASEB Journal</i> , 2017, 31, 766.6.  | 0.2  | 0         |
| 63 | Comparative top down proteomics of peripheral blood mononuclear cells from kidney transplant recipients with normal kidney biopsies or acute rejection. <i>Proteomics</i> , 2016, 16, 2048-2058.                     | 1.3  | 22        |
| 64 | Characterization of Methanobactin from <i>Methylosinus</i> sp. LW4. <i>Journal of the American Chemical Society</i> , 2016, 138, 11124-11127.  | 6.6  | 34        |
| 65 | Reply to "Uveal melanoma cells are resistant to EZH2 inhibition regardless of BAP1 status". <i>Nature Medicine</i> , 2016, 22, 578-579.  | 15.2 | 7         |
| 66 | Integrated Bottom-Up and Top-Down Proteomics of Patient-Derived Breast Tumor Xenografts. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 45-56.   | 2.5  | 68        |
| 67 | Unabridged Analysis of Human Histone H3 by Differential Top-Down Mass Spectrometry Reveals Hypermethylated Proteoforms from MMSET/NSD2 Overexpression. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 776-790. | 2.5  | 56        |
| 68 | Bone protein extracts: comparing the efficiency of bone protein extractions of <i>Gallus gallus</i> in tandem mass spectrometry, with an eye towards paleoproteomics. <i>PeerJ</i> , 2016, 4, e2603.                 | 0.9  | 38        |
| 69 | Therapeutic Targeting of the Histone Ubiquitination-Methylation Axis in T Cell Leukemia. <i>Blood</i> , 2016, 128, 1532-1532.  | 0.6  | 0         |
| 70 | Cover Picture: Proteomics 7'15. <i>Proteomics</i> , 2015, 15, NA-NA.   | 1.3  | 119       |
| 71 | Reducing protein oxidation in low-flow electrospray enables deeper investigation of proteoforms by top down proteomics. <i>EuPA Open Proteomics</i> , 2015, 8, 40-47.  | 2.5  | 8         |
| 72 | Defining the Neuropeptidome of the Spiny Lobster <i>Panulirus interruptus</i> Brain Using a Multidimensional Mass Spectrometry-Based Platform. <i>Journal of Proteome Research</i> , 2015, 14, 4776-4791.            | 1.8  | 24        |

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|----|--|------|-----------|
| 73 | Fungal artificial chromosomes for mining of the fungal secondary metabolome. <i>BMC Genomics</i> , 2015, 16, 343.  | 1.2  | 76        |
| 74 | Top Down Proteomics Reveals Mature Proteoforms Expressed in Subcellular Fractions of the <i>Echinococcus granulosus</i> Preadult Stage. <i>Journal of Proteome Research</i> , 2015, 14, 4805-4814. | 1.8  | 19        |
| 75 | Loss of BAP1 function leads to EZH2-dependent transformation. <i>Nature Medicine</i> , 2015, 21, 1344-1349.  | 15.2 | 297       |
| 76 | Mass Spectrometry and Antibody-Based Characterization of Blood Vessels from <i>Brachyophosaurus canadensis</i> . <i>Journal of Proteome Research</i> , 2015, 14, 5252-5262.                        | 1.8  | 59        |
| 77 | ProSight Lite: Graphical software to analyze top-down mass spectrometry data. <i>Proteomics</i> , 2015, 15, 1235-1238.   | 1.3  | 196       |
| 78 | BAP1 Loss Results in EZH2-Dependent Transformation in Myelodysplastic Syndromes. <i>Blood</i> , 2015, 126, 713-713.  | 0.6  | 0         |
| 79 | Top-Down Proteomics with Mass Spectrometry Imaging: A Pilot Study towards Discovery of Biomarkers for Neurodevelopmental Disorders. <i>PLoS ONE</i> , 2014, 9, e92831.                             | 1.1  | 37        |
| 80 | Site-specific human histone H3 methylation stability: fast K4me3 turnover. <i>Proteomics</i> , 2014, 14, 2190-2199.  | 1.3  | 30        |
| 81 | The first pilot project of the consortium for top-down proteomics: status report. <i>Proteomics</i> , 2014, 14, 1130-1140.   | 1.3  | 90        |
| 82 | Applying Label-Free Quantitation to Top Down Proteomics. <i>Analytical Chemistry</i> , 2014, 86, 4961-4968.  | 3.2  | 88        |
| 83 | Deep and quantitative top-down proteomics in clinical and translational research. <i>Expert Review of Proteomics</i> , 2014, 11, 649-651.  | 1.3  | 35        |
| 84 | The C-Score: A Bayesian Framework to Sharply Improve Proteoform Scoring in High-Throughput Top Down Proteomics. <i>Journal of Proteome Research</i> , 2014, 13, 3231-3240.                         | 1.8  | 76        |
| 85 | Ultraviolet Photodissociation for Characterization of Whole Proteins on a Chromatographic Time Scale. <i>Analytical Chemistry</i> , 2014, 86, 2185-2192.   | 3.2  | 81        |
| 86 | Fragmentation of Integral Membrane Proteins in the Gas Phase. <i>Analytical Chemistry</i> , 2014, 86, 4627-4634.   | 3.2  | 25        |
| 87 | Measurement of acetylation turnover at distinct lysines in human histones identifies long-lived acetylation sites. <i>Nature Communications</i> , 2013, 4, 2203.                                   | 5.8  | 100       |
| 88 | Large-scale Top-down Proteomics of the Human Proteome: Membrane Proteins, Mitochondria, and Senescence. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3465-3473.                            | 2.5  | 132       |
| 89 | The emergence of top-down proteomics in clinical research. <i>Genome Medicine</i> , 2013, 5, 53.   | 3.6  | 89        |
| 90 | Developing top down proteomics to maximize proteome and sequence coverage from cells and tissues. <i>Current Opinion in Chemical Biology</i> , 2013, 17, 787-794.                                  | 2.8  | 45        |

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| 91  | Complete Protein Characterization Using Top-Down Mass Spectrometry and Ultraviolet Photodissociation. <i>Journal of the American Chemical Society</i> , 2013, 135, 12646-12651.  | 6.6  | 297       |
| 92  | Top Down Proteomics of Human Membrane Proteins from Enriched Mitochondrial Fractions. <i>Analytical Chemistry</i> , 2013, 85, 1880-1888.   | 3.2  | 72        |
| 93  | Total kinetic analysis reveals how combinatorial methylation patterns are established on lysines 27 and 36 of histone H3. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 13549-13554. | 3.3  | 129       |
| 94  | High-definition De Novo Sequencing of Crustacean Hyperglycemic Hormone (CHH)-family Neuropeptides. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1951-1964.   | 2.5  | 31        |
| 95  | Analysis of Intact Monoclonal Antibody IgG1 by Electron Transfer Dissociation Orbitrap FTMS. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1758-1767.   | 2.5  | 137       |
| 96  | 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.  | 3.2  | 62        |
| 97  | Mechanism-Based Small Molecule Cross-Linkers of HECT E3 Ubiquitin Ligase-Substrate Pairs. <i>Biochemistry</i> , 2012, 51, 8327-8329.   | 1.2  | 7         |
| 98  | A protease for 'middle-down' proteomics. <i>Nature Methods</i> , 2012, 9, 822-824.   | 9.0  | 103       |
| 99  | Evaluation of the Compact High-Field Orbitrap for Top-Down Proteomics of Human Cells. <i>Journal of Proteome Research</i> , 2012, 11, 4308-4314.   | 1.8  | 84        |
| 100 | On the Scalability and Requirements of Whole Protein Mass Spectrometry. <i>Analytical Chemistry</i> , 2011, 83, 6868-6874.   | 3.2  | 177       |
| 101 | Mapping intact protein isoforms in discovery mode using top-down proteomics. <i>Nature</i> , 2011, 480, 254-258.   | 13.7 | 587       |
| 102 | The MMSET histone methyl transferase switches global histone methylation and alters gene expression in t(4;14) multiple myeloma cells. <i>Blood</i> , 2011, 117, 211-220.  | 0.6  | 300       |
| 103 | Deciphering the Late Biosynthetic Steps of Antimalarial Compound FR-900098. <i>Chemistry and Biology</i> , 2010, 17, 57-64.  | 6.2  | 35        |
| 104 | Kinetics of Re-establishing H3K79 Methylation Marks in Global Human Chromatin*. <i>Journal of Biological Chemistry</i> , 2010, 285, 32778-32786.   | 1.6  | 56        |
| 105 | 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.   | 3.2  | 91        |
| 106 | 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        |
| 107 | A proteomics approach to discovering natural products and their biosynthetic pathways. <i>Nature Biotechnology</i> , 2009, 27, 951-956.  | 9.4  | 125       |
| 108 | In Vitro Biosynthesis of Unnatural Enterocin and Wailupemycin Polyketides. <i>Journal of Natural Products</i> , 2009, 72, 469-472.   | 1.5  | 43        |

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|-----|---|-----|-----------|
| 109 | Cloning, Expression, and Biochemical Characterization of <i>Streptomyces rubellomurinus</i> Genes Required for Biosynthesis of Antimalarial Compound FR900098. <i>Chemistry and Biology</i> , 2008, 15, 765-770.  | 6.2 | 88        |
| 110 | Deconstruction of Iterative Multidomain Polyketide Synthase Function. <i>Science</i> , 2008, 320, 243-246.  | 6.0 | 202       |
| 111 | Gatekeeping versus Promiscuity in the Early Stages of the Andrimid Biosynthetic Assembly Line. <i>ACS Chemical Biology</i> , 2008, 3, 542-554.  | 1.6 | 36        |
| 112 | Top-Down Proteomics on a Chromatographic Time Scale Using Linear Ion Trap Fourier Transform Hybrid Mass Spectrometers. <i>Analytical Chemistry</i> , 2007, 79, 7984-7991.   | 3.2 | 116       |
| 113 | Reassignment of the Structure of the Antibiotic A53868 Reveals an Unusual Amino Dehydrophosphonic Acid. <i>Angewandte Chemie - International Edition</i> , 2007, 46, 9089-9092.   | 7.2 | 38        |
| 114 | Unusual transformations in the biosynthesis of the antibiotic phosphinothricin tripeptide. <i>Nature Chemical Biology</i> , 2007, 3, 480-485.   | 3.9 | 126       |
| 115 | Heterologous Production of Fosfomycin and Identification of the Minimal Biosynthetic Gene Cluster. <i>Chemistry and Biology</i> , 2006, 13, 1171-1182.  | 6.2 | 116       |
| 116 | Discovery and in vitro biosynthesis of haloduracin, a two-component lantibiotic. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 17243-17248.   | 3.3 | 215       |
| 117 | TRACKING ACIDIC PHARMACEUTICALS, CAFFEINE, AND TRICLOSAN THROUGH THE WASTEWATER TREATMENT PROCESS. <i>Environmental Toxicology and Chemistry</i> , 2005, 24, 25.  | 2.2 | 169       |
| 118 | Determination of Nonsteroidal Anti-inflammatory Drugs, Caffeine, and Triclosan in Wastewater by Gas Chromatography-Mass Spectrometry. <i>Journal of Environmental Science and Health - Part A Toxic/Hazardous Substances and Environmental Engineering</i> , 2004, 39, 1969-1978. | 0.9 | 54        |
| 119 | Mass spectral determinations of the folic acid content of fortified breads from Chile. <i>Journal of Food Composition and Analysis</i> , 2003, 16, 281-286.   | 1.9 | 20        |
| 120 | Determination of 5-Methyltetrahydrofolic Acid and Folic Acid in Citrus Juices Using Stable Isotope Dilution-Mass Spectrometry. <i>Journal of Agricultural and Food Chemistry</i> , 2003, 51, 1293-1296.   | 2.4 | 35        |
| 121 | Proteome-Selective Imaging of Tissues Using Mass Spectrometry. <i>Angewandte Chemie</i> , 0, , .  | 1.6 | 0         |