

Paul M Thomas

List of Publications by Year in descending order

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121
papers

8,344
citations

38738

50
h-index

49904

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.	12.6	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.	3.7	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.	7.1	14
4	ProSight Annotator: Complete control and customization of protein entries in UniProt XML files. <i>Proteomics</i> , 2022, 22, e2100209.	2.2	6
5	The Human Proteoform Atlas: a FAIR community resource for experimentally derived proteoforms. <i>Nucleic Acids Research</i> , 2022, 50, D526-D533.	14.5	15
6	Proteoform-Selective Imaging of Tissues Using Mass Spectrometry**. <i>Angewandte Chemie - International Edition</i> , 2022, 61, .	13.8	22
7	InnenrÃ¼cktitelbild: Proteoform-Selective Imaging of Tissues Using Mass Spectrometry (Angew. Chem.) Tj ETQq1,1 0.784314 rgBT C	2.0	14
8	<i>In vitro</i> -Constructed Ribosomes Enable Multi-site Incorporation of Noncanonical Amino Acids into Proteins. <i>Biochemistry</i> , 2021, 60, 161-169.	2.5	9
9	Deeper Protein Identification Using Field Asymmetric Ion Mobility Spectrometry in Top-Down Proteomics. <i>Analytical Chemistry</i> , 2021, 93, 6323-6328.	6.5	40
10	Characterization of a Copper-Chelating Natural Product from the Methanotroph <i>Methylosinus</i> sp. LW3. <i>Biochemistry</i> , 2021, 60, 2845-2850.	2.5	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.	2.3	7
12	Identification of Plasmodium falciparum proteoforms from liver stage models. <i>Malaria Journal</i> , 2020, 19, 10.	2.3	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.	8.6	16
14	Chemical composition of material extractives influences microbial growth and dynamics on wetted wood materials. <i>Scientific Reports</i> , 2020, 10, 14500.	3.3	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, .	4.1	12
16	The serine hydroxymethyltransferase-2 (SHMT2) initiates lymphoma development through epigenetic tumor suppressor silencing. <i>Nature Cancer</i> , 2020, 1, 653-664.	13.2	35
17	NMT1 and NMT2 are lysine myristoyltransferases regulating the ARF6 GTPase cycle. <i>Nature Communications</i> , 2020, 11, 1067.	12.8	62
18	Thorough Performance Evaluation of 213 nm Ultraviolet Photodissociation for Top-down Proteomics. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 405-420.	3.8	38

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19	Targeted detection and quantitation of histone modifications from 1,000 cells. PLoS ONE, 2020, 15, e0240829.	2.5	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.	2.8	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.	5.2	59
30	A five-level classification system for proteoform identifications. Nature Methods, 2019, 16, 939-940.	19.0	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.	3.7	12
32	Native top-down mass spectrometry provides insights into the copper centers of membrane-bound methane monooxygenase. Nature Communications, 2019, 10, 2675.	12.8	74
33	Biotin Identification Proteomics in Three-Dimensional Organotypic Human Skin Cultures. Methods in Molecular Biology, 2019, 2109, 185-197.	0.9	3
34	Identification and Quantification of Proteoforms by Mass Spectrometry. Proteomics, 2019, 19, e1800361.	2.2	147
35	Microbial and metabolic succession on common building materials under high humidity conditions. Nature Communications, 2019, 10, 1767.	12.8	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.	4.7	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.	7.0	66
38	Identification and targeting of novel CDK9 complexes in acute myeloid leukemia. <i>Blood</i> , 2019, 133, 1171-1185.	1.4	26
39	Accurate Estimation of Context-Dependent False Discovery Rates in Top-Down Proteomics. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 796-805.	3.8	27
40	Top-Down Proteomics Enables Comparative Analysis of Brain Proteoforms Between Mouse Strains. <i>Analytical Chemistry</i> , 2018, 90, 3802-3810.	6.5	27
41	Identification of the First Diketomorpholine Biosynthetic Pathway Using FAC-MS Technology. <i>ACS Chemical Biology</i> , 2018, 13, 1142-1147.	3.4	30
42	How many human proteoforms are there?. <i>Nature Chemical Biology</i> , 2018, 14, 206-214.	8.0	580
43	The biosynthesis of methanobactin. <i>Science</i> , 2018, 359, 1411-1416.	12.6	101
44	Cell-free protein synthesis from genomically recoded bacteria enables multisite incorporation of noncanonical amino acids. <i>Nature Communications</i> , 2018, 9, 1203.	12.8	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.	2.5	19
46	Characterization of a long overlooked copper protein from methane- and ammonia-oxidizing bacteria. <i>Nature Communications</i> , 2018, 9, 4276.	12.8	46
47	The vermiform appendix impacts the risk of developing Parkinson's disease. <i>Science Translational Medicine</i> , 2018, 10, .	12.4	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.	2.5	4
49	The unique biomineralization transcriptome and proteome of <i>Lytechinus variegatus</i> teeth. <i>Connective Tissue Research</i> , 2018, 59, 20-29.	2.3	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.	6.5	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.	2.0	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.	3.7	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.	9.7	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.	3.7	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.	4.7	37
56	A scalable platform to identify fungal secondary metabolites and their gene clusters. <i>Nature Chemical Biology</i> , 2017, 13, 895-901.	8.0	154
57	PAI-1 is a critical regulator of FGF23 homeostasis. <i>Science Advances</i> , 2017, 3, e1603259.	10.3	24
58	Diversity of Amyloid-beta Proteoforms in the Alzheimer's Disease Brain. <i>Scientific Reports</i> , 2017, 7, 9520.	3.3	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.	3.7	81
60	Bioinformatics Analysis of Top-Down Mass Spectrometry Data with ProSight Lite. <i>Methods in Molecular Biology</i> , 2017, 1558, 381-394.	0.9	27
61	A synthetic biology approach to probing nucleosome symmetry. <i>ELife</i> , 2017, 6, .	6.0	16
62	High-Throughput Natural Products Discovery in Fungi Using FAC-MS Technology. <i>FASEB Journal</i> , 2017, 31, 766.6.	0.5	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.	2.2	22
64	Characterization of Methanobactin from <i>Methylosinus</i> sp. LW4. <i>Journal of the American Chemical Society</i> , 2016, 138, 11124-11127.	13.7	34
65	Reply to "Uveal melanoma cells are resistant to EZH2 inhibition regardless of BAP1 status". <i>Nature Medicine</i> , 2016, 22, 578-579.	30.7	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.	3.8	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.	3.8	56
68	Bone protein extractomics: 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.	2.0	38
69	Therapeutic Targeting of the Histone Ubiquitination-Methylation Axis in T Cell Leukemia. <i>Blood</i> , 2016, 128, 1532-1532.	1.4	0
70	Cover Picture: Proteomics 7'15. <i>Proteomics</i> , 2015, 15, NA-NA.	2.2	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.	3.7	24

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73	Fungal artificial chromosomes for mining of the fungal secondary metabolome. BMC Genomics, 2015, 16, 343.	2.8	76
74	Top Down Proteomics Reveals Mature Proteoforms Expressed in Subcellular Fractions of the <i>Echinococcus granulosus</i> Preadult Stage. Journal of Proteome Research, 2015, 14, 4805-4814.	3.7	19
75	Loss of BAP1 function leads to EZH2-dependent transformation. Nature Medicine, 2015, 21, 1344-1349.	30.7	297
76	Mass Spectrometry and Antibody-Based Characterization of Blood Vessels from <i>Brachyophosaurus canadensis</i> . Journal of Proteome Research, 2015, 14, 5252-5262.	3.7	59
77	ProSight Lite: Graphical software to analyze top-down mass spectrometry data. Proteomics, 2015, 15, 1235-1238.	2.2	196
78	BAP1 Loss Results in EZH2-Dependent Transformation in Myelodysplastic Syndromes. Blood, 2015, 126, 713-713.	1.4	0
79	Top-Down Proteomics with Mass Spectrometry Imaging: A Pilot Study towards Discovery of Biomarkers for Neurodevelopmental Disorders. PLoS ONE, 2014, 9, e92831.	2.5	37
80	Site-specific human histone H3 methylation stability: fast K4me3 turnover. Proteomics, 2014, 14, 2190-2199.	2.2	30
81	The first pilot project of the consortium for top-down proteomics: <i>scp</i> status report. Proteomics, 2014, 14, 1130-1140.	2.2	90
82	Applying Label-Free Quantitation to Top Down Proteomics. Analytical Chemistry, 2014, 86, 4961-4968.	6.5	88
83	Deep and quantitative top-down proteomics in clinical and translational research. Expert Review of Proteomics, 2014, 11, 649-651.	3.0	35
84	The C-Score: A Bayesian Framework to Sharply Improve Proteoform Scoring in High-Throughput Top Down Proteomics. Journal of Proteome Research, 2014, 13, 3231-3240.	3.7	76
85	Ultraviolet Photodissociation for Characterization of Whole Proteins on a Chromatographic Time Scale. Analytical Chemistry, 2014, 86, 2185-2192.	6.5	81
86	Fragmentation of Integral Membrane Proteins in the Gas Phase. Analytical Chemistry, 2014, 86, 4627-4634.	6.5	25
87	Measurement of acetylation turnover at distinct lysines in human histones identifies long-lived acetylation sites. Nature Communications, 2013, 4, 2203.	12.8	100
88	Large-scale Top-down Proteomics of the Human Proteome: Membrane Proteins, Mitochondria, and Senescence. Molecular and Cellular Proteomics, 2013, 12, 3465-3473.	3.8	132
89	The emergence of top-down proteomics in clinical research. Genome Medicine, 2013, 5, 53.	8.2	89
90	Developing top down proteomics to maximize proteome and sequence coverage from cells and tissues. Current Opinion in Chemical Biology, 2013, 17, 787-794.	6.1	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.	13.7	297
92	Top Down Proteomics of Human Membrane Proteins from Enriched Mitochondrial Fractions. <i>Analytical Chemistry</i> , 2013, 85, 1880-1888.	6.5	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.	7.1	129
94	High-definition De Novo Sequencing of Crustacean Hyperglycemic Hormone (CHH)-family Neuropeptides. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1951-1964.	3.8	31
95	Analysis of Intact Monoclonal Antibody IgG1 by Electron Transfer Dissociation Orbitrap FTMS. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1758-1767.	3.8	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.	6.5	62
97	Mechanism-Based Small Molecule Cross-Linkers of HECT E3 Ubiquitin Ligase-Substrate Pairs. <i>Biochemistry</i> , 2012, 51, 8327-8329.	2.5	7
98	A protease for 'middle-down' proteomics. <i>Nature Methods</i> , 2012, 9, 822-824.	19.0	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.	3.7	84
100	On the Scalability and Requirements of Whole Protein Mass Spectrometry. <i>Analytical Chemistry</i> , 2011, 83, 6868-6874.	6.5	177
101	Mapping intact protein isoforms in discovery mode using top-down proteomics. <i>Nature</i> , 2011, 480, 254-258.	27.8	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.	1.4	300
103	Deciphering the Late Biosynthetic Steps of Antimalarial Compound FR-900098. <i>Chemistry and Biology</i> , 2010, 17, 57-64.	6.0	35
104	Kinetics of Re-establishing H3K79 Methylation Marks in Global Human Chromatin*. <i>Journal of Biological Chemistry</i> , 2010, 285, 32778-32786.	3.4	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.	6.5	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.	17.5	125
108	In Vitro Biosynthesis of Unnatural Enterocin and Wailupemycin Polyketides. <i>Journal of Natural Products</i> , 2009, 72, 469-472.	3.0	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.	6.0	88
110	Deconstruction of Iterative Multidomain Polyketide Synthase Function. <i>Science</i> , 2008, 320, 243-246.	12.6	202
111	Gatekeeping versus Promiscuity in the Early Stages of the Andrimid Biosynthetic Assembly Line. <i>ACS Chemical Biology</i> , 2008, 3, 542-554.	3.4	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.	6.5	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.	13.8	38
114	Unusual transformations in the biosynthesis of the antibiotic phosphinothricin tripeptide. <i>Nature Chemical Biology</i> , 2007, 3, 480-485.	8.0	126
115	Heterologous Production of Fosfomycin and Identification of the Minimal Biosynthetic Gene Cluster. <i>Chemistry and Biology</i> , 2006, 13, 1171-1182.	6.0	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.	7.1	215
117	TRACKING ACIDIC PHARMACEUTICALS, CAFFEINE, AND TRICLOSAN THROUGH THE WASTEWATER TREATMENT PROCESS. <i>Environmental Toxicology and Chemistry</i> , 2005, 24, 25.	4.3	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.	1.7	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.	3.9	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.	5.2	35
121	Proteome-Selective Imaging of Tissues Using Mass Spectrometry. <i>Angewandte Chemie</i> , 0, , .	2.0	0