

Stefani N Thomas

List of Publications by Year in descending order

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62
papers

4,645
citations

201674

27
h-index

138484

58
g-index

66
all docs

66
docs citations

66
times ranked

7966
citing authors

#	ARTICLE	IF	CITATIONS
1	Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. <i>Cell</i> , 2016, 166, 755-765.	28.9	804
2	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. <i>Cell</i> , 2019, 179, 964-983.e31.	28.9	430
3	Multi-laboratory assessment of reproducibility, qualitative and quantitative performance of SWATH-mass spectrometry. <i>Nature Communications</i> , 2017, 8, 291.	12.8	423
4	Reproducible workflow for multiplexed deep-scale proteome and phosphoproteome analysis of tumor tissues by liquid chromatography–mass spectrometry. <i>Nature Protocols</i> , 2018, 13, 1632-1661.	12.0	377
5	Proteogenomic Landscape of Breast Cancer Tumorigenesis and Targeted Therapy. <i>Cell</i> , 2020, 183, 1436-1456.e31.	28.9	273
6	Alzheimer Disease-specific Conformation of Hyperphosphorylated Paired Helical Filament-Tau Is Polyubiquitinated through Lys-48, Lys-11, and Lys-6 Ubiquitin Conjugation. <i>Journal of Biological Chemistry</i> , 2006, 281, 10825-10838.	3.4	242
7	Advances in mass spectrometry-based clinical biomarker discovery. <i>Clinical Proteomics</i> , 2016, 13, 1.	2.1	218
8	Recommendations for the Generation, Quantification, Storage, and Handling of Peptides Used for Mass Spectrometry–Based Assays. <i>Clinical Chemistry</i> , 2016, 62, 48-69.	3.2	187
9	CPTAC Assay Portal: a repository of targeted proteomic assays. <i>Nature Methods</i> , 2014, 11, 703-704.	19.0	150
10	Proteomic Analysis of Exfoliation Deposits. , 2007, 48, 1447.		119
11	Lysine methylation is an endogenous post-translational modification of tau protein in human brain and a modulator of aggregation propensity. <i>Biochemical Journal</i> , 2014, 462, 77-88.	3.7	102
12	High-Throughput Proteomic-Based Identification of Oxidatively Induced Protein Carbonylation in Mouse Brain. <i>Pharmaceutical Research</i> , 2003, 20, 1713-1720.	3.5	98
13	Doxorubicin Down-regulates KrÄ¼ppel-associated Box Domain-associated Protein 1 Sumoylation That Relieves Its Transcription Repression on p21WAF1/CIP1 in Breast Cancer MCF-7 Cells. <i>Journal of Biological Chemistry</i> , 2007, 282, 1595-1606.	3.4	94
14	Dual modification of Alzheimer’s disease PHF-tau protein by lysine methylation and ubiquitylation: a mass spectrometry approach. <i>Acta Neuropathologica</i> , 2012, 123, 105-117.	7.7	90
15	Integrated Proteomic and Glycoproteomic Characterization of Human High-Grade Serous Ovarian Carcinoma. <i>Cell Reports</i> , 2020, 33, 108276.	6.4	83
16	Site-Specific Fucosylation Analysis Identifying Glycoproteins Associated with Aggressive Prostate Cancer Cell Lines Using Tandem Affinity Enrichments of Intact Glycopeptides Followed by Mass Spectrometry. <i>Analytical Chemistry</i> , 2017, 89, 7623-7630.	6.5	65
17	Aberrant sphingomyelin/ceramide metabolic-induced neuronal endosomal/lysosomal dysfunction: potential pathological consequences in age-related neurodegeneration. <i>Advanced Drug Delivery Reviews</i> , 2003, 55, 1515-1524.	13.7	56
18	N-GlycositeAtlas: a database resource for mass spectrometry-based human N-linked glycoprotein and glycosylation site mapping. <i>Clinical Proteomics</i> , 2019, 16, 35.	2.1	56

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19	Exosomal Proteome Profiling: A Potential Multi-Marker Cellular Phenotyping Tool to Characterize Hypoxia-Induced Radiation Resistance in Breast Cancer. <i>Proteomes</i> , 2013, 1, 87-108.	3.5	44
20	Molecular Features of Phosphatase and Tensin Homolog (PTEN) Regulation by C-terminal Phosphorylation. <i>Journal of Biological Chemistry</i> , 2016, 291, 14160-14169.	3.4	41
21	Modification of Sialic Acids on Solid Phase: Accurate Characterization of Protein Sialylation. <i>Analytical Chemistry</i> , 2017, 89, 6330-6335.	6.5	39
22	Quantification of Tau Protein Lysine Methylation in Aging and Alzheimer's Disease. <i>Journal of Alzheimer's Disease</i> , 2019, 71, 979-991.	2.6	39
23	PhosphoScan: A Probability-Based Method for Phosphorylation Site Prediction Using MS2/MS3 Pair Information. <i>Journal of Proteome Research</i> , 2008, 7, 2803-2811.	3.7	34
24	Enzymatic Analysis of PTEN Ubiquitylation by WWP2 and NEDD4-1 E3 Ligases. <i>Biochemistry</i> , 2016, 55, 3658-3666.	2.5	34
25	Using the CPTAC Assay Portal to Identify and Implement Highly Characterized Targeted Proteomics Assays. <i>Methods in Molecular Biology</i> , 2016, 1410, 223-236.	0.9	33
26	Multiplexed Targeted Mass Spectrometry-Based Assays for the Quantification of N-Linked Glycosite-Containing Peptides in Serum. <i>Analytical Chemistry</i> , 2015, 87, 10830-10838.	6.5	32
27	Neuronal endosomal/lysosomal membrane destabilization activates caspases and induces abnormal accumulation of the lipid secondary messenger ceramide. <i>Brain Research Bulletin</i> , 2003, 59, 523-531.	3.0	31
28	Reduced neuronal expression of synaptic transmission modulator HNK-1/neural cell adhesion molecule as a potential consequence of amyloid beta-mediated oxidative stress: a proteomic approach. <i>Journal of Neurochemistry</i> , 2005, 92, 705-717.	3.9	27
29	Using proteomics and network analysis to elucidate the consequences of synaptic protein oxidation in a PS1+AI ² PP mouse model of Alzheimer's disease. <i>Journal of Alzheimer's Disease</i> , 2005, 8, 227-241.	2.6	24
30	Comparative analysis of the catalytic regulation of NEDD4-1 and WWP2 ubiquitin ligases. <i>Journal of Biological Chemistry</i> , 2019, 294, 17421-17436.	3.4	23
31	Orthogonal Proteomic Platforms and Their Implications for the Stable Classification of High-Grade Serous Ovarian Cancer Subtypes. <i>iScience</i> , 2020, 23, 101079.	4.1	23
32	Proteomic Analysis of Protein Phosphorylation and Ubiquitination in Alzheimer's Disease. <i>Methods in Molecular Biology</i> , 2009, 566, 109-121.	0.9	21
33	IsoQuant: A Software Tool for Stable Isotope Labeling by Amino Acids in Cell Culture-Based Mass Spectrometry Quantitation. <i>Analytical Chemistry</i> , 2012, 84, 4535-4543.	6.5	21
34	Initial determination of COVID-19 seroprevalence among outpatients and healthcare workers in Minnesota using a novel SARS-CoV-2 total antibody ELISA. <i>Clinical Biochemistry</i> , 2021, 90, 15-22.	1.9	19
35	Rapid Characterization of Amyloid- β Side-Chain Oxidation by Tandem Mass Spectrometry and the Scoring Algorithm for Spectral Analysis. <i>Pharmaceutical Research</i> , 2004, 21, 1094-1102.	3.5	17
36	Quality Assessments of Long-Term Quantitative Proteomic Analysis of Breast Cancer Xenograft Tissues. <i>Journal of Proteome Research</i> , 2017, 16, 4523-4530.	3.7	17

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37	Targeting lipid metabolism in the treatment of ovarian cancer. <i>Oncotarget</i> , 2022, 13, 768-783.	1.8	16
38	The Serological Sciences Network (SeroNet) for COVID-19: Depth and Breadth of Serology Assays and Plans for Assay Harmonization. <i>MSphere</i> , 2022, 7, .	2.9	16
39	Quantitative Mass Spectrometry-Based Proteomics for Biomarker Development in Ovarian Cancer. <i>Molecules</i> , 2021, 26, 2674.	3.8	15
40	Quantitative proteomic analysis of mitochondrial proteins reveals prosurvival mechanisms in the perpetuation of radiation-induced genomic instability. <i>Free Radical Biology and Medicine</i> , 2012, 53, 618-628.	2.9	13
41	Mass Spectrometry Analysis of Lysine Posttranslational Modifications of Tau Protein from Alzheimer's Disease Brain. <i>Methods in Molecular Biology</i> , 2017, 1523, 161-177.	0.9	13
42	Phosphorylation of Serine 51 Regulates the Interaction of Human DNA Ligase I with Replication Factor C and Its Participation in DNA Replication and Repair*. <i>Journal of Biological Chemistry</i> , 2012, 287, 36711-36719.	3.4	12
43	An Internal Standard-Assisted Synthesis and Degradation Proteomic Approach Reveals the Potential Linkage between VPS4B Depletion and Activation of Fatty Acid β -Oxidation in Breast Cancer Cells. <i>International Journal of Proteomics</i> , 2013, 2013, 1-13.	2.0	12
44	Ultrasensitive detection of salivary SARS-CoV-2 IgG antibodies in individuals with natural and COVID-19 vaccine-induced immunity. <i>Scientific Reports</i> , 2022, 12, .	3.3	12
45	MRMPlus: an open source quality control and assessment tool for SRM/MRM assay development. <i>BMC Bioinformatics</i> , 2015, 16, 411.	2.6	11
46	Targeted proteomic assays for the verification of global proteomics insights. <i>Expert Review of Proteomics</i> , 2016, 13, 897-899.	3.0	11
47	Stable Isotope Labeling with Amino Acids in Cell Culture Based Mass Spectrometry Approach to Detect Transient Protein Interactions Using Substrate Trapping. <i>Analytical Chemistry</i> , 2011, 83, 5511-5518.	6.5	9
48	Advancing signaling networks through proteomics. <i>Expert Review of Proteomics</i> , 2007, 4, 573-583.	3.0	8
49	Targeted Proteomic Analyses of Histone H4 Acetylation Changes Associated with Homologous-Recombination-Deficient High-Grade Serous Ovarian Carcinomas. <i>Journal of Proteome Research</i> , 2017, 16, 3704-3710.	3.7	8
50	Application of quantitative proteomics to the integrated analysis of the ubiquitylated and global proteomes of xenograft tumor tissues. <i>Clinical Proteomics</i> , 2015, 12, 14.	2.1	7
51	Type IV Pilus Secretins Have Extracellular C Termini. <i>MBio</i> , 2015, 6, .	4.1	6
52	Proteomic characterization of primary and metastatic prostate cancer reveals reduced proteinase activity in aggressive tumors. <i>Scientific Reports</i> , 2021, 11, 18936.	3.3	6
53	Proteomic Analysis Reveals Low-Dose PARP Inhibitor-Induced Differential Protein Expression in BRCA1-Mutated High-Grade Serous Ovarian Cancer Cells. <i>Journal of the American Society for Mass Spectrometry</i> , 2022, 33, 242-250.	2.8	5
54	Mission, Organization, and Future Direction of the Serological Sciences Network for COVID-19 (SeroNet) Epidemiologic Cohort Studies. <i>Open Forum Infectious Diseases</i> , 2022, 9, .	0.9	5

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55	Initial Determination of COVID-19 Seroprevalence Among Outpatients and Healthcare Workers in Minnesota Using a Novel SARS-CoV-2 Total Antibody ELISA. SSRN Electronic Journal, 0, , .	0.4	4
56	Alzheimer amyloid precursor aspartyl proteinase activity in CHAPSO homogenates of Spodoptera frugiperda cells. Alzheimer Disease and Associated Disorders, 2004, 18, 261-3.	1.3	4
57	Method comparison of SARS-CoV-2 serology assays involving three commercially available platforms and a novel in-house developed enzyme-linked immunosorbent assay. Clinical Biochemistry, 2020, 86, 34-35.	1.9	3
58	Use of Cotton Balls in Diapers for Collection of Urine Samples Impacts the Analysis of Routine Chemistry Tests: An Evaluation of Cotton Balls, Diapers, and Chemistry Analyzers. Journal of Pediatrics, 2022, , .	1.8	3
59	MudPIT (Multidimensional Protein Identification Technology) for Identification of Post-Translational Protein Modifications in Complex Biological Mixtures. , 2006, , 233-252.		2
60	Transient hyperphosphatasemia following pediatric liver transplantation in a patient with hepatic and skeletal abnormalities. Clinica Chimica Acta, 2021, 519, 48-50.	1.1	1
61	How Sweet It Is: The Coming of Age of Continuous Glucose Monitoring. Clinical Chemistry, 2019, 65, 1184-1185.	3.2	0
62	A 9-Month-Old with Skeletal Abnormalities and a Consanguineous Sibling with Mucopolysaccharidosis IVA: The Role of Urinary Glycosaminoglycan Testing in Disease Diagnosis and Treatment Monitoring. Clinical Medicine Insights: Case Reports, 2021, 14, 117954762199940.	0.7	0