

Samuel H Payne

List of Publications by Year in descending order

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95
papers

8,103
citations

81900

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58581

82
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116
all docs

116
docs citations

116
times ranked

11319
citing authors

#	ARTICLE	IF	CITATIONS
1	A Preprocessing Tool for Enhanced Ion Mobilityâ€“Mass Spectrometry-Based Omics Workflows. <i>Journal of Proteome Research</i> , 2022, 21, 798-807.	3.7	44
2	Features of Peptide Fragmentation Spectra in Single-Cell Proteomics. <i>Journal of Proteome Research</i> , 2022, 21, 182-188.	3.7	25
3	Uncovering Hidden Members and Functions of the Soil Microbiome Using <i>De Novo</i> Metaproteomics. <i>Journal of Proteome Research</i> , 2022, 21, 2023-2035.	3.7	6
4	Fully Automated Sample Processing and Analysis Workflow for Low-Input Proteome Profiling. <i>Analytical Chemistry</i> , 2021, 93, 1658-1666.	6.5	72
5	Simplified and Unified Access to Cancer Proteogenomic Data. <i>Journal of Proteome Research</i> , 2021, 20, 1902-1910.	3.7	21
6	Proteogenomic insights into the biology and treatment of HPV-negative head and neck squamous cell carcinoma. <i>Cancer Cell</i> , 2021, 39, 361-379.e16.	16.8	189
7	Proteogenomic and metabolomic characterization of human glioblastoma. <i>Cancer Cell</i> , 2021, 39, 509-528.e20.	16.8	327
8	Spatially interacting phosphorylation sites and mutations in cancer. <i>Nature Communications</i> , 2021, 12, 2313.	12.8	12
9	AutoCCS: automated collision cross-section calculation software for ion mobility spectrometryâ€“mass spectrometry. <i>Bioinformatics</i> , 2021, 37, 4193-4201.	4.1	13
10	A proteogenomic portrait of lung squamous cell carcinoma. <i>Cell</i> , 2021, 184, 4348-4371.e40.	28.9	170
11	Proteogenomic characterization of pancreatic ductal adenocarcinoma. <i>Cell</i> , 2021, 184, 5031-5052.e26.	28.9	236
12	Online Tools for Teaching Cancer Bioinformatics. <i>Journal of Microbiology and Biology Education</i> , 2021, 22, .	1.0	2
13	Calculating Sample Size Requirements for Temporal Dynamics in Single-Cell Proteomics. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100085.	3.8	7
14	Detecting fabrication in large-scale molecular omics data. <i>PLoS ONE</i> , 2021, 16, e0260395.	2.5	6
15	A <i>Histoplasma capsulatum</i> Lipid Metabolic Map Identifies Antifungal Targets. <i>MBio</i> , 2021, 12, e0297221.	4.1	6
16	Proteogenomic Landscape of Breast Cancer Tumorigenesis and Targeted Therapy. <i>Cell</i> , 2020, 183, 1436-1456.e31.	28.9	273
17	Community Assessment of the Predictability of Cancer Protein and Phosphoprotein Levels from Genomics and Transcriptomics. <i>Cell Systems</i> , 2020, 11, 186-195.e9.	6.2	19
18	Simple and Efficient Data Analysis Dissemination for Individual Laboratories. <i>Journal of Proteome Research</i> , 2020, 19, 4191-4195.	3.7	1

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19	Integrated Proteomic and Glycoproteomic Characterization of Human High-Grade Serous Ovarian Carcinoma. <i>Cell Reports</i> , 2020, 33, 108276.	6.4	83
20	Treatment of Fingertip Injuries. <i>JBJS Reviews</i> , 2020, 8, e0182-e0182.	2.0	7
21	Proteogenomic Characterization Reveals Therapeutic Vulnerabilities in Lung Adenocarcinoma. <i>Cell</i> , 2020, 182, 200-225.e35.	28.9	410
22	Proteogenomic Characterization of Endometrial Carcinoma. <i>Cell</i> , 2020, 180, 729-748.e26.	28.9	296
23	Proteogenomic Characterization of Ovarian HGSC Implicates Mitotic Kinases, Replication Stress in Observed Chromosomal Instability. <i>Cell Reports Medicine</i> , 2020, 1, 100004.	6.5	46
24	Reproducibility and Transparency by Design. <i>Molecular and Cellular Proteomics</i> , 2019, 18, S202-S204.	3.8	5
25	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. <i>Cell</i> , 2019, 179, 964-983.e31.	28.9	430
26	Regulated Phosphosignaling Associated with Breast Cancer Subtypes and Druggability*. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1630-1650.	3.8	14
27	Back Cover: Identification and Quantification of Proteoforms by Mass Spectrometry. <i>Proteomics</i> , 2019, 19, 1970085.	2.2	9
28	Extracting Pathway-level Signatures from Proteogenomic Data in Breast Cancer Using Independent Component Analysis. <i>Molecular and Cellular Proteomics</i> , 2019, 18, S169-S182.	3.8	15
29	Proteogenomic Analysis of Human Colon Cancer Reveals New Therapeutic Opportunities. <i>Cell</i> , 2019, 177, 1035-1049.e19.	28.9	498
30	Identification and Quantification of Proteoforms by Mass Spectrometry. <i>Proteomics</i> , 2019, 19, e1800361.	2.2	147
31	Bacterial Longevity Requires Protein Synthesis and a Stringent Response. <i>MBio</i> , 2019, 10, .	4.1	17
32	Rapidly Assessing the Quality of Targeted Proteomics Experiments through Monitoring Stable-Isotope Labeled Standards. <i>Journal of Proteome Research</i> , 2019, 18, 694-699.	3.7	11
33	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. <i>Cell Reports</i> , 2018, 23, 270-281.e3.	6.4	177
34	A Protein Standard That Emulates Homology for the Characterization of Protein Inference Algorithms. <i>Journal of Proteome Research</i> , 2018, 17, 1879-1886.	3.7	22
35	Inhibition of interleukin-1 receptor-associated kinase-1 is a therapeutic strategy for acute myeloid leukemia subtypes. <i>Leukemia</i> , 2018, 32, 2374-2387.	7.2	43
36	An algorithm to correct saturated mass spectrometry ion abundances for enhanced quantitation and mass accuracy in omic studies. <i>International Journal of Mass Spectrometry</i> , 2018, 427, 91-99.	1.5	25

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37	Individual Variability of Protein Expression in Human Tissues. <i>Journal of Proteome Research</i> , 2018, 17, 3914-3922.	3.7	15
38	Identification of Novel Protein Lysine Acetyltransferases in <i>Escherichia coli</i> . <i>MBio</i> , 2018, 9, .	4.1	86
39	ABRF Proteome Informatics Research Group (iPRG) 2016 Study: Inferring Proteoforms from Bottom-up Proteomics Data. <i>Journal of Biomolecular Techniques</i> , 2018, 29, 39-45.	1.5	6
40	Blazing Signature Filter: a library for fast pairwise similarity comparisons. <i>BMC Bioinformatics</i> , 2018, 19, 221.	2.6	6
41	Integrative omics analyses broaden treatment targets in human cancer. <i>Genome Medicine</i> , 2018, 10, 60.	8.2	17
42	Proteomics Goes to Court: A Statistical Foundation for Forensic Toxin/Organism Identification Using Bottom-Up Proteomics. <i>Journal of Proteome Research</i> , 2018, 17, 3075-3085.	3.7	16
43	Addressing the challenge of soil metaproteome complexity by improving metaproteome depth of coverage through two-dimensional liquid chromatography. <i>Soil Biology and Biochemistry</i> , 2018, 125, 290-299.	8.8	37
44	Methods, Tools and Current Perspectives in Proteogenomics. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 959-981.	3.8	130
45	PIXiE: an algorithm for automated ion mobility arrival time extraction and collision cross section calculation using global data association. <i>Bioinformatics</i> , 2017, 33, 2715-2722.	4.1	10
46	LIQUID: an open source software for identifying lipids in LC-MS/MS-based lipidomics data. <i>Bioinformatics</i> , 2017, 33, 1744-1746.	4.1	108
47	A structural examination and collision cross section database for over 500 metabolites and xenobiotics using drift tube ion mobility spectrometry. <i>Chemical Science</i> , 2017, 8, 7724-7736.	7.4	156
48	Genes essential for phototrophic growth by a purple alphaproteobacterium. <i>Environmental Microbiology</i> , 2017, 19, 3567-3578.	3.8	23
49	Informed-Proteomics: open-source software package for top-down proteomics. <i>Nature Methods</i> , 2017, 14, 909-914.	19.0	126
50	PECAN: library-free peptide detection for data-independent acquisition tandem mass spectrometry data. <i>Nature Methods</i> , 2017, 14, 903-908.	19.0	158
51	Ancient Regulatory Role of Lysine Acetylation in Central Metabolism. <i>MBio</i> , 2017, 8, .	4.1	105
52	Familiarity Vs Trust: A Comparative Study of Domain Scientists' Trust in Visual Analytics and Conventional Analysis Methods. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2017, 23, 271-280.	4.4	36
53	Multi-species Identification of Polymorphic Peptide Variants via Propagation in Spectral Networks. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 3501-3512.	3.8	6
54	A Skyline Plugin for Pathway-Centric Data Browsing. <i>Journal of the American Society for Mass Spectrometry</i> , 2016, 27, 1752-1757.	2.8	5

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55	The abundant marine bacterium <i>Pelagibacter</i> simultaneously catabolizes dimethylsulfoniopropionate to the gases dimethyl sulfide and methanethiol. <i>Nature Microbiology</i> , 2016, 1, 16065.	13.3	110
56	Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. <i>Cell</i> , 2016, 166, 755-765.	28.9	804
57	An Analysis of the Sensitivity of Proteogenomic Mapping of Somatic Mutations and Novel Splicing Events in Cancer. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1060-1071.	3.8	104
58	Reproducibility of Differential Proteomic Technologies in CPTAC Fractionated Xenografts. <i>Journal of Proteome Research</i> , 2016, 15, 691-706.	3.7	44
59	Abstract 774: Proteogenomic characterization of high-grade serous ovarian cancer. , 2016, , .		0
60	The Pacific Northwest National Laboratory library of bacterial and archaeal proteomic biodiversity. <i>Scientific Data</i> , 2015, 2, 150041.	5.3	14
61	Toward a standard in structural genome annotation for prokaryotes. <i>Standards in Genomic Sciences</i> , 2015, 10, 45.	1.5	14
62	An Optimized Informatics Pipeline for Mass Spectrometry-Based Peptidomics. <i>Journal of the American Society for Mass Spectrometry</i> , 2015, 26, 2002-2008.	2.8	10
63	Correcting systematic bias and instrument measurement drift with mzRefinery. <i>Bioinformatics</i> , 2015, 31, 3838-3840.	4.1	32
64	Peptide-Centric Proteome Analysis: An Alternative Strategy for the Analysis of Tandem Mass Spectrometry Data. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2301-2307.	3.8	146
65	The utility of protein and mRNA correlation. <i>Trends in Biochemical Sciences</i> , 2015, 40, 1-3.	7.5	168
66	Comprehensive Quantitative Analysis of Ovarian and Breast Cancer Tumor Peptidomes. <i>Journal of Proteome Research</i> , 2015, 14, 422-433.	3.7	26
67	Bayesian Proteoform Modeling Improves Protein Quantification of Global Proteomic Measurements. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3639-3646.	3.8	38
68	Proteogenomic strategies for identification of aberrant cancer peptides using large-scale next-generation sequencing data. <i>Proteomics</i> , 2014, 14, 2719-2730.	2.2	62
69	PGP: parallel prokaryotic proteogenomics pipeline for MPI clusters, high-throughput batch clusters and multicore workstations. <i>Bioinformatics</i> , 2014, 30, 1469-1470.	4.1	19
70	Accounting for Population Variation in Targeted Proteomics. <i>Journal of Proteome Research</i> , 2014, 13, 321-323.	3.7	4
71	Automated Data Extraction from <i>In Situ</i> Protein-Stable Isotope Probing Studies. <i>Journal of Proteome Research</i> , 2014, 13, 1200-1210.	3.7	20
72	Detecting and Removing Data Artifacts in Hadamard Transform Ion Mobility-Mass Spectrometry Measurements. <i>Journal of the American Society for Mass Spectrometry</i> , 2014, 25, 2020-2027.	2.8	42

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73	GlyQ-IQ: Glycomics Quintivariate-Informed Quantification with High-Performance Computing and GlycoGrid 4D Visualization. <i>Analytical Chemistry</i> , 2014, 86, 6268-6276.	6.5	11
74	Signatures for Mass Spectrometry Data Quality. <i>Journal of Proteome Research</i> , 2014, 13, 2215-2222.	3.7	18
75	LC-IMS-MS Feature Finder: detecting multidimensional liquid chromatography, ion mobility and mass spectrometry features in complex datasets. <i>Bioinformatics</i> , 2013, 29, 2804-2805.	4.1	32
76	Identification of Widespread Adenosine Nucleotide Binding in <i>Mycobacterium tuberculosis</i> . <i>Chemistry and Biology</i> , 2013, 20, 123-133.	6.0	45
77	<i>H</i> archaeosortase is required for motility, mating, and C-terminal processing of the S-layer glycoprotein. <i>Molecular Microbiology</i> , 2013, 88, 1164-1175.	2.5	61
78	Increasing confidence of LC-MS identifications by utilizing ion mobility spectrometry. <i>International Journal of Mass Spectrometry</i> , 2013, 354-355, 312-317.	1.5	27
79	Top-Down Characterization of the Post-Translationally Modified Intact Periplasmic Proteome from the Bacterium <i>Novosphingobium aromaticivorans</i> . <i>International Journal of Proteomics</i> , 2013, 1-10.	2.0	19
80	How many signal peptides are there in bacteria?. <i>Environmental Microbiology</i> , 2013, 15, 983-990.	3.8	29
81	Unexpected Diversity of Signal Peptides in Prokaryotes. <i>MBio</i> , 2012, 3, .	4.1	30
82	Archaeosortases and Exosortases Are Widely Distributed Systems Linking Membrane Transit with Posttranslational Modification. <i>Journal of Bacteriology</i> , 2012, 194, 36-48.	2.2	64
83	VESPA: software to facilitate genomic annotation of prokaryotic organisms through integration of proteomic and transcriptomic data. <i>BMC Genomics</i> , 2012, 13, 131.	2.8	31
84	Comparative Omics-Driven Genome Annotation Refinement: Application across <i>Yersinia</i> . <i>PLoS ONE</i> , 2012, 7, e33903.	2.5	30
85	Characterizing the <i>Escherichia coli</i> O157:H7 Proteome Including Protein Associations with Higher Order Assemblies. <i>PLoS ONE</i> , 2011, 6, e26554.	2.5	20
86	Experimental annotation of post-translational features and translated coding regions in the pathogen <i>Salmonella Typhimurium</i> . <i>BMC Genomics</i> , 2011, 12, 433.	2.8	29
87	Proteogenomic Analysis of Bacteria and Archaea: A 46 Organism Case Study. <i>PLoS ONE</i> , 2011, 6, e27587.	2.5	62
88	A proteogenomic update to <i>Yersinia</i> : enhancing genome annotation. <i>BMC Genomics</i> , 2010, 11, 460.	2.8	50
89	Accurate Annotation of Peptide Modifications through Unrestrictive Database Search. <i>Journal of Proteome Research</i> , 2008, 7, 170-181.	3.7	50
90	Phosphorylation-Specific MS/MS Scoring for Rapid and Accurate Phosphoproteome Analysis. <i>Journal of Proteome Research</i> , 2008, 7, 3373-3381.	3.7	51

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91	A Multidimensional Chromatography Technology for In-depth Phosphoproteome Analysis. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 1389-1396.	3.8	472
92	Discovery and revision of <i>Arabidopsis</i> genes by proteogenomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 21034-21038.	7.1	268
93	Population-Based Sample Reveals Gene-Gender Interactions in Blood Pressure in White Americans. <i>Hypertension</i> , 2007, 49, 96-106.	2.7	107
94	Retention and Loss of Amino Acid Biosynthetic Pathways Based on Analysis of Whole-Genome Sequences. <i>Eukaryotic Cell</i> , 2006, 5, 272-276.	3.4	117
95	cis -Acting Site Controlling Bidirectional Transcription at the Growth-Differentiation Transition in <i>Dictyostelium discoideum</i> . <i>Eukaryotic Cell</i> , 2006, 5, 1104-1110.	3.4	2