David L Tabb

List of Publications by Year in Descending Order

115	16,522	50	128
papers	citations	h-index	g-index

130	19,918	9.3	6.1
ext. papers	ext. citations	avg, IF	L-index

#	Paper	IF	Citations
115	Open search algorithms discover patterns of chemical modifications via LC-MS/MS **2022**, 95-125		
114	Dysregulated healing responses in diabetic wounds occur in the early stages postinjury. *Journal of Molecular Endocrinology*, **2021**, 66, 141-155	4.5	2
113	Gaussian process modelling for improved resolution in Faraday depth reconstruction. *Monthly Notices of the Royal Astronomical Society*, **2021**, 502, 5839-5853	4.3	1
112	Interrogating Fractionation and Other Sources of Variability in Shotgun Proteomes Using Quality Metrics. *Proteomics*, **2020**, 20, e1900382	4.8	0
111	Targeted next-generation sequencing identifies novel variants in candidate genes for Parkinson's disease in Black South African and Nigerian patients. *BMC Medical Genetics*, **2020**, 21, 23	2.1	8
110	Open search unveils modification patterns in formalin-fixed, paraffin-embedded thermo HCD and SCIEX TripleTOF shotgun proteomes. *International Journal of Mass Spectrometry*, **2020**, 448, 116266	1.9	7
109	SWATH-MS based proteomic profiling of pancreatic ductal adenocarcinoma tumours reveals the interplay between the extracellular matrix and related intracellular pathways. *PLoS ONE*, **2020**, 15, e0240453	3.7	3
108	Proteogenomic Landscape of Breast Cancer Tumorigenesis and Targeted Therapy. *Cell*, **2020**, 183, 1436-1456.e31	56.2	71
107	Microbial function and genital inflammation in young South African women at high risk of HIV infection. *Microbiome*, **2020**, 8, 165	16.6	4
106	Integrated Proteomic and Glycoproteomic Characterization of Human High-Grade Serous Ovarian Carcinoma. *Cell Reports*, **2020**, 33, 108276	10.6	33
105	Proteogenomic Analysis of Human Colon Cancer Reveals New Therapeutic Opportunities. *Cell*, **2019**, 177, 1035-1049.e19	56.2	237
104	Immunometabolic Signatures Predict Risk of Progression to Active Tuberculosis and Disease Outcome. *Frontiers in Immunology*, **2019**, 10, 527	8.4	26
103	Four-Gene Pan-African Blood Signature Predicts Progression to Tuberculosis. *American Journal of Respiratory and Critical Care Medicine*, **2018**, 197, 1198-1208	10.2	125
102	Sipros Ensemble improves database searching and filtering for complex metaproteomics. *Bioinformatics*, **2018**, 34, 795-802	7.2	17
101	Characterization of Plant Glycoproteins: Analysis of Plant Glycopeptide Mass Spectrometry Data with plantGlycoMS, a Package in the R Statistical Computing Environment. *Methods in Molecular Biology*, **2018**, 1789, 205-220	1.4	1
100	A Serum Circulating miRNA Signature for Short-Term Risk of Progression to Active Tuberculosis Among Household Contacts. *Frontiers in Immunology*, **2018**, 9, 661	8.4	23
99	Quality control in mass spectrometry-based proteomics. *Mass Spectrometry Reviews*, **2018**, 37, 697-711	11	44

98	Challenges and Opportunities for Biological Mass Spectrometry Core Facilities in the Developing World. *Journal of Biomolecular Techniques*, **2018**, 29, 4-15	1.1	4
97	Proteomic analysis reveals that sulfamethoxazole induces oxidative stress in M. tuberculosis. *Tuberculosis*, **2018**, 111, 78-85	2.6	8
96	Chronic intermittent alcohol disrupts the GluN2B-associated proteome and specifically regulates group I mGlu receptor-dependent long-term depression. *Addiction Biology*, **2017**, 22, 275-290	4.6	22
95	The Human Proteome Organization-Proteomics Standards Initiative Quality Control Working Group: Making Quality Control More Accessible for Biological Mass Spectrometry. *Analytical Chemistry*, **2017**, 89, 4474-4479	7.8	12
94	Proteogenomic Investigation of Strain Variation in Clinical Mycobacterium tuberculosis Isolates. *Journal of Proteome Research*, **2017**, 16, 3841-3851	5.6	15
93	Proteomics Standards Initiative: Fifteen Years of Progress and Future Work. *Journal of Proteome Research*, **2017**, 16, 4288-4298	5.6	61
92	Host blood RNA signatures predict the outcome of tuberculosis treatment. *Tuberculosis*, **2017**, 107, 48-58	2.6	90
91	Quality Assessments of Long-Term Quantitative Proteomic Analysis of Breast Cancer Xenograft Tissues. *Journal of Proteome Research*, **2017**, 16, 4523-4530	5.6	14
90	In-depth analysis of protein inference algorithms using multiple search engines and well-defined metrics. *Journal of Proteomics*, **2017**, 150, 170-182	3.9	39
89	Recognizing millions of consistently unidentified spectra across hundreds of shotgun proteomics datasets. *Nature Methods*, **2016**, 13, 651-656	21.6	99
88	Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. *Cell*, **2016**, 166, 755-765	56.2	544
87	Comprehensive Characterization of Glycosylation and Hydroxylation of Basement Membrane Collagen IV by High-Resolution Mass Spectrometry. *Journal of Proteome Research*, **2016**, 15, 245-58	5.6	43
86	An Analysis of the Sensitivity of Proteogenomic Mapping of Somatic Mutations and Novel Splicing Events in Cancer. *Molecular and Cellular Proteomics*, **2016**, 15, 1060-71	7.6	80
85	proBAMsuite, a Bioinformatics Framework for Genome-Based Representation and Analysis of Proteomics Data. *Molecular and Cellular Proteomics*, **2016**, 15, 1164-75	7.6	20
84	Reproducibility of Differential Proteomic Technologies in CPTAC Fractionated Xenografts. *Journal of Proteome Research*, **2016**, 15, 691-706	5.6	35
83	Greazy: Open-Source Software for Automated Phospholipid Tandem Mass Spectrometry Identification. *Analytical Chemistry*, **2016**, 88, 5733-41	7.8	43
82	Site-Specific N-Glycosylation Characterization of Windmill Palm Tree Peroxidase Using Novel Tools for Analysis of Plant Glycopeptide Mass Spectrometry Data. *Journal of Proteome Research*, **2016**, 15, 2026-38	5.6	12
81	The SEQUEST family tree. *Journal of the American Society for Mass Spectrometry*, **2015**, 26, 1814-9	3.5	30

80	Advanced Proteogenomic Analysis Reveals Multiple Peptide Mutations and Complex Immunoglobulin Peptides in Colon Cancer. *Journal of Proteome Research*, **2015**, 14, 3555-67	5.6	22
79	Proteomic analysis of colon and rectal carcinoma using standard and customized databases. *Scientific Data*, **2015**, 2, 150022	8.2	20
78	Correcting systematic bias and instrument measurement drift with mzRefinery. *Bioinformatics*, **2015**, 31, 3838-40	7.2	15
77	The 2012/2013 ABRF Proteomic Research Group Study: Assessing Longitudinal Intralaboratory Variability in Routine Peptide Liquid Chromatography Tandem Mass Spectrometry Analyses. *Molecular and Cellular Proteomics*, **2015**, 14, 3299-309	7.6	8
76	Wavelet-based peak detection and a new charge inference procedure for MS/MS implemented in ProteoWizard's msConvert. *Journal of Proteome Research*, **2015**, 14, 1299-307	5.6	27
75	QC metrics from CPTAC raw LC-MS/MS data interpreted through multivariate statistics. *Analytical Chemistry*, **2014**, 86, 2497-509	7.8	31
74	Proteogenomic characterization of human colon and rectal cancer. *Nature*, **2014**, 513, 382-7	50.4	900
73	Employing ProteoWizard to Convert Raw Mass Spectrometry Data. *Current Protocols in Bioinformatics*, **2014**, 46, 13.24.1-9	24.2	131
72	A standardized framing for reporting protein identifications in mzIdentML 1.2. *Proteomics*, **2014**, 14, 2389-99	4.8	16
71	Basophile: accurate fragment charge state prediction improves peptide identification rates. *Genomics, Proteomics and Bioinformatics*, **2013**, 11, 86-95	6.5	1
70	Identification of proteins at active, stalled, and collapsed replication forks using isolation of proteins on nascent DNA (iPOND) coupled with mass spectrometry. *Journal of Biological Chemistry*, **2013**, 288, 31458-67	5.4	140
69	Neurovascular unit on a chip: implications for translational applications. *Stem Cell Research and Therapy*, **2013**, 4 Suppl 1, S18	8.3	48
68	IDPQuantify: combining precursor intensity with spectral counts for protein and peptide quantification. *Journal of Proteome Research*, **2013**, 12, 4111-21	5.6	16
67	Informatics of protein and posttranslational modification detection via shotgun proteomics. *Methods in Molecular Biology*, **2013**, 1002, 167-79	1.4	18
66	Quality assessment for clinical proteomics. *Clinical Biochemistry*, **2013**, 46, 411-20	3.5	53
65	HI-bone: a scoring system for identifying phenylisothiocyanate-derivatized peptides based on precursor mass and high intensity fragment ions. *Analytical Chemistry*, **2013**, 85, 3515-20	7.8	6
64	Proteomic analysis of Chinese hamster ovary cells. *Journal of Proteome Research*, **2012**, 11, 5265-76	5.6	128
63	The evolutionary imprint of domestication on genome variation and function of the filamentous fungus Aspergillus oryzae. *Current Biology*, **2012**, 22, 1403-9	6.3	122

62	QuaMeter: multivendor performance metrics for LC-MS/MS proteomics instrumentation. *Analytical Chemistry*, **2012**, 84, 5845-50	7.8	44
61	A cross-platform toolkit for mass spectrometry and proteomics. *Nature Biotechnology*, **2012**, 30, 918-20	44.5	1583
60	Pepitome: evaluating improved spectral library search for identification complementarity and quality assessment. *Journal of Proteome Research*, **2012**, 11, 1686-95	5.6	52
59	Mapping serum albumin adducts of the food-borne carcinogen 2-amino-1-methyl-6-phenylimidazo[4,5-b]pyridine by data-dependent tandem mass spectrometry. *Chemical Research in Toxicology*, **2012**, 25, 2179-93	4	18
58	Protein identification using customized protein sequence databases derived from RNA-Seq data. *Journal of Proteome Research*, **2012**, 11, 1009-17	5.6	128
57	Identifying proteomic LC-MS/MS data sets with Bumbershoot and IDPicker. *Current Protocols in Bioinformatics*, **2012**, Chapter 13, Unit13.17	24.2	31
56	Refining comparative proteomics by spectral counting to account for shared peptides and multiple search engines. *Analytical and Bioanalytical Chemistry*, **2012**, 404, 1115-25	4.4	6
55	Obesity and altered glucose metabolism impact HDL composition in CETP transgenic mice: a role for ovarian hormones. *Journal of Lipid Research*, **2012**, 53, 379-389	6.3	31
54	Bioinformatics and Database Searching **2011**, 231-252		
53	ScanRanker: Quality assessment of tandem mass spectra via sequence tagging. *Journal of Proteome Research*, **2011**, 10, 2896-904	5.6	23
52	Sequence tagging reveals unexpected modifications in toxicoproteomics. *Chemical Research in Toxicology*, **2011**, 24, 204-16	4	24
51	A face in the crowd: recognizing peptides through database search. *Molecular and Cellular Proteomics*, **2011**, 10, R111.009522	7.6	106
50	A bioinformatics workflow for variant peptide detection in shotgun proteomics. *Molecular and Cellular Proteomics*, **2011**, 10, M110.006536	7.6	73
49	Proteomic analysis of the enterocyte brush border. *American Journal of Physiology - Renal Physiology*, **2011**, 300, G914-26	5.1	60
48	Supporting tool suite for production proteomics. *Bioinformatics*, **2011**, 27, 3214-5	7.2	28
47	Differential localization and dynamics of class I myosins in the enterocyte microvillus. *Molecular Biology of the Cell*, **2010**, 21, 970-8	3.5	35
46	Interlaboratory study characterizing a yeast performance standard for benchmarking LC-MS platform performance. *Molecular and Cellular Proteomics*, **2010**, 9, 242-54	7.6	130
45	Identification and validation of novel spinophilin-associated proteins in rodent striatum using an enhanced ex vivo shotgun proteomics approach. *Molecular and Cellular Proteomics*, **2010**, 9, 1243-59	7.6	26

44	TagRecon: high-throughput mutation identification through sequence tagging. *Journal of Proteome Research*, **2010**, 9, 1716-26	5.6	100
43	Repeatability and reproducibility in proteomic identifications by liquid chromatography-tandem mass spectrometry. *Journal of Proteome Research*, **2010**, 9, 761-76	5.6	377
42	Skyline: an open source document editor for creating and analyzing targeted proteomics experiments. *Bioinformatics*, **2010**, 26, 966-8	7.2	2910
41	Performance metrics for liquid chromatography-tandem mass spectrometry systems in proteomics analyses. *Molecular and Cellular Proteomics*, **2010**, 9, 225-41	7.6	147
40	The enterocyte microvillus is a vesicle-generating organelle. *Journal of Cell Biology*, **2009**, 185, 1285-98	7.3	165
39	Multi-site assessment of the precision and reproducibility of multiple reaction monitoring-based measurements of proteins in plasma. *Nature Biotechnology*, **2009**, 27, 633-41	44.5	859
38	IDPicker 2.0: Improved protein assembly with high discrimination peptide identification filtering. *Journal of Proteome Research*, **2009**, 8, 3872-81	5.6	274
37	Network-assisted protein identification and data interpretation in shotgun proteomics. *Molecular Systems Biology*, **2009**, 5, 303	12.2	45
36	The bis-electrophile diepoxybutane cross-links DNA to human histones but does not result in enhanced mutagenesis in recombinant systems. *Chemical Research in Toxicology*, **2009**, 22, 1069-76	4	23
35	DirecTag: accurate sequence tags from peptide MS/MS through statistical scoring. *Journal of Proteome Research*, **2008**, 7, 3838-46	5.6	100
34	What's driving false discovery rates?. *Journal of Proteome Research*, **2008**, 7, 45-6	5.6	50
33	Evaluation of strong cation exchange versus isoelectric focusing of peptides for multidimensional liquid chromatography-tandem mass spectrometry. *Journal of Proteome Research*, **2008**, 7, 5286-94	5.6	82
32	A proteomics analysis of yeast Mot1p protein-protein associations: insights into mechanism. *Molecular and Cellular Proteomics*, **2008**, 7, 2090-106	7.6	15
31	Use of fluorescence-activated vesicle sorting for isolation of Naked2-associated, basolaterally targeted exocytic vesicles for proteomics analysis. *Molecular and Cellular Proteomics*, **2008**, 7, 1651-67	7.6	32
30	Prostate cancer serum biomarker discovery through proteomic analysis of alpha-2 macroglobulin protein complexes. *Proteomics - Clinical Applications*, **2008**, 2, 1223	3.1	26
29	MyriMatch: highly accurate tandem mass spectral peptide identification by multivariate hypergeometric analysis. *Journal of Proteome Research*, **2007**, 6, 654-61	5.6	458
28	Proteomic parsimony through bipartite graph analysis improves accuracy and transparency. *Journal of Proteome Research*, **2007**, 6, 3549-57	5.6	266
27	Tandem mass spectrometry for the detection of plant pathogenic fungi and the effects of database composition on protein inferences. *Proteomics*, **2007**, 7, 3932-42	4.8	18

26	Validation of tandem mass spectrometry database search results using DTASelect. *Current Protocols in Bioinformatics*, **2007**, Chapter 13, Unit 13.4	24.2	153
25	Verification of automated peptide identifications from proteomic tandem mass spectra. *Nature Protocols*, **2006**, 1, 2213-22	18.8	50
24	ProRata: A quantitative proteomics program for accurate protein abundance ratio estimation with confidence interval evaluation. *Analytical Chemistry*, **2006**, 78, 7121-31	7.8	86
23	Efficient and specific trypsin digestion of microgram to nanogram quantities of proteins in organic-aqueous solvent systems. *Analytical Chemistry*, **2006**, 78, 125-34	7.8	157
22	Robust estimation of peptide abundance ratios and rigorous scoring of their variability and bias in quantitative shotgun proteomics. *Analytical Chemistry*, **2006**, 78, 7110-20	7.8	36
21	Determination and comparison of the baseline proteomes of the versatile microbe Rhodopseudomonas palustris under its major metabolic states. *Journal of Proteome Research*, **2006**, 5, 287-98	5.6	64
20	Technologies for Large-Scale Proteomic Tandem Mass Spectrometry **2006**, 91-109		
19	Determination of peptide and protein ion charge states by Fourier transformation of isotope-resolved mass spectra. *Journal of the American Society for Mass Spectrometry*, **2006**, 17, 903-915	3.5	27
18	MASPIC: intensity-based tandem mass spectrometry scoring scheme that improves peptide identification at high confidence. *Analytical Chemistry*, **2005**, 77, 7581-93	7.8	44
17	DBDigger: reorganized proteomic database identification that improves flexibility and speed. *Analytical Chemistry*, **2005**, 77, 2464-74	7.8	45
16	MS2Grouper: group assessment and synthetic replacement of duplicate proteomic tandem mass spectra. *Journal of the American Society for Mass Spectrometry*, **2005**, 16, 1250-61	3.5	51
15	MS1, MS2, and SQT-three unified, compact, and easily parsed file formats for the storage of shotgun proteomic spectra and identifications. *Rapid Communications in Mass Spectrometry*, **2004**, 18, 2162-8	2.2	295
14	Influence of basic residue content on fragment ion peak intensities in low-energy collision-induced dissociation spectra of peptides. *Analytical Chemistry*, **2004**, 76, 1243-8	7.8	136
13	Characterization of the 70S Ribosome from Rhodopseudomonas palustris using an integrated "top-down" and "bottom-up" mass spectrometric approach. *Journal of Proteome Research*, **2004**, 3, 965-78	5.6	78
12	Automated discrimination of polymerase chain reaction products with closely related sequences by software-based detection of characteristic peaks in product ion spectra. *Rapid Communications in Mass Spectrometry*, **2003**, 17, 2755-62	2.2	3
11	Large-scale protein identification using mass spectrometry. *Biochimica Et Biophysica Acta - Proteins and Proteomics*, **2003**, 1646, 1-10	4	137
10	GutenTag: high-throughput sequence tagging via an empirically derived fragmentation model. *Analytical Chemistry*, **2003**, 75, 6415-21	7.8	240
9	Cleavage N-terminal to proline: analysis of a database of peptide tandem mass spectra. *Analytical Chemistry*, **2003**, 75, 1963-71	7.8	274

8	Statistical characterization of ion trap tandem mass spectra from doubly charged tryptic peptides. *Analytical Chemistry*, **2003**, 75, 1155-63	7.8	232
7	Similarity among tandem mass spectra from proteomic experiments: detection, significance, and utility. *Analytical Chemistry*, **2003**, 75, 2470-7	7.8	143
6	The influence of histidine on cleavage C-terminal to acidic residues in doubly protonated tryptic peptides. *International Journal of Mass Spectrometry*, **2002**, 219, 233-244	1.9	72
5	A proteomic view of the Plasmodium falciparum life cycle. *Nature*, **2002**, 419, 520-6	50.4	1066
4	DTASelect and Contrast: tools for assembling and comparing protein identifications from shotgun proteomics. *Journal of Proteome Research*, **2002**, 1, 21-6	5.6	1156
3	Protein Identification by SEQUEST. *Principles and Practice*, **2001**, 125-142		29
2	MS for identification of single nucleotide polymorphisms and MS/MS for discrimination of isomeric PCR products. *Analytical Chemistry*, **2000**, 72, 4033-40	7.8	38
1	MetaNovo: a probabilistic approach to peptide and polymorphism discovery in complex metaproteomic datasets		4