David L Tabb

List of Publications by Year
in descending order

118 papers	22,046 citations	31902 53 h-index	17546 121 g-index
130 all docs	130 docs citations	130 times ranked	29701 citing authors

#	Article	IF	Citations
1	Skyline: an open source document editor for creating and analyzing targeted proteomics experiments. Bioinformatics, 2010, 26, 966-968.	1.8	3,968
2	A cross-platform toolkit for mass spectrometry and proteomics. Nature Biotechnology, 2012, 30, 918-920.	9.4	2,794
3	DTASelect and Contrast: Tools for Assembling and Comparing Protein Identifications from Shotgun Proteomics. Journal of Proteome Research, 2002, 1, 21-26.	1.8	1,327
4	Proteogenomic characterization of human colon and rectal cancer. Nature, 2014, 513, 382-387.	13.7	1,219
5	A proteomic view of the Plasmodium falciparum life cycle. Nature, 2002, 419, 520-526.	13.7	1,184
6	Multi-site assessment of the precision and reproducibility of multiple reaction monitoring–based measurements of proteins in plasma. Nature Biotechnology, 2009, 27, 633-641.	9.4	958
7	Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. Cell, 2016, 166, 755-765.	13.5	804
8	MyriMatch: Highly Accurate Tandem Mass Spectral Peptide Identification by Multivariate Hypergeometric Analysis. Journal of Proteome Research, 2007, 6, 654-661.	1.8	530
9	Repeatability and Reproducibility in Proteomic Identifications by Liquid Chromatography–Tandem Mass Spectrometry. Journal of Proteome Research, 2010, 9, 761-776.	1.8	505
10	Proteogenomic Analysis of Human Colon Cancer Reveals New Therapeutic Opportunities. Cell, 2019, 177, 1035-1049.e19.	13.5	498
11	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, 2162-2168.	0.7	350
12	IDPicker 2.0: Improved Protein Assembly with High Discrimination Peptide Identification Filtering. Journal of Proteome Research, 2009, 8, 3872-3881.	1.8	320
13	Proteomic Parsimony through Bipartite Graph Analysis Improves Accuracy and Transparency. Journal of Proteome Research, 2007, 6, 3549-3557.	1.8	318
14	Cleavage N-Terminal to Proline: Analysis of a Database of Peptide Tandem Mass Spectra. Analytical Chemistry, 2003, 75, 1963-1971.	3.2	297
15	GutenTag: High-Throughput Sequence Tagging via an Empirically Derived Fragmentation Model. Analytical Chemistry, 2003, 75, 6415-6421.	3.2	276
16	Proteogenomic Landscape of Breast Cancer Tumorigenesis and Targeted Therapy. Cell, 2020, 183, 1436-1456.e31.	13.5	273
17	Statistical Characterization of Ion Trap Tandem Mass Spectra from Doubly Charged Tryptic Peptides. Analytical Chemistry, 2003, 75, 1155-1163.	3.2	251
18	Four-Gene Pan-African Blood Signature Predicts Progression to Tuberculosis. American Journal of Respiratory and Critical Care Medicine, 2018, 197, 1198-1208.	2.5	217

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19	Employing ProteoWizard to Convert Raw Mass Spectrometry Data. Current Protocols in Bioinformatics, 2014, 46, 13.24.1-9.	25.8	215
20	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, 31458-31467.	1.6	202
21	The enterocyte microvillus is a vesicle-generating organelle. Journal of Cell Biology, 2009, 185, 1285-1298.	2.3	199
22	Validation of Tandem Mass Spectrometry Database Search Results Using DTASelect. Current Protocols in Bioinformatics, 2006, 16, Unit 13.4.	25.8	187
23	The Evolutionary Imprint of Domestication on Genome Variation and Function of the Filamentous Fungus Aspergillus oryzae. Current Biology, 2012, 22, 1403-1409.	1.8	177
24	Efficient and Specific Trypsin Digestion of Microgram to Nanogram Quantities of Proteins in Organicâˆ'Aqueous Solvent Systems. Analytical Chemistry, 2006, 78, 125-134.	3.2	168
25	Proteomic Analysis of Chinese Hamster Ovary Cells. Journal of Proteome Research, 2012, 11, 5265-5276.	1.8	168
26	Large-scale protein identification using mass spectrometry. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2003, 1646, 1-10.	1.1	167
27	Performance Metrics for Liquid Chromatography-Tandem Mass Spectrometry Systems in Proteomics Analyses. Molecular and Cellular Proteomics, 2010, 9, 225-241.	2.5	167
28	Similarity among Tandem Mass Spectra from Proteomic Experiments:â€‰ Detection, Significance, and Utility. Analytical Chemistry, 2003, 75, 2470-2477.	3.2	159
29	Protein Identification Using Customized Protein Sequence Databases Derived from RNA-Seq Data. Journal of Proteome Research, 2012, 11, 1009-1017.	1.8	156
30	Host blood RNA signatures predict the outcome of tuberculosis treatment. Tuberculosis, 2017, 107, 48-58.	0.8	156
31	Influence of Basic Residue Content on Fragment Ion Peak Intensities in Low-Energy Collision-Induced Dissociation Spectra of Peptides. Analytical Chemistry, 2004, 76, 1243-1248.	3.2	148
32	Interlaboratory Study Characterizing a Yeast Performance Standard for Benchmarking LC-MS Platform Performance. Molecular and Cellular Proteomics, 2010, 9, 242-254.	2.5	148
33	A Face in the Crowd: Recognizing Peptides Through Database Search. Molecular and Cellular Proteomics, 2011, 10, R111.009522.	2.5	147
34	Recognizing millions of consistently unidentified spectra across hundreds of shotgun proteomics datasets. Nature Methods, 2016, 13, 651-656.	9.0	147
35	DirecTag: Accurate Sequence Tags from Peptide MS/MS through Statistical Scoring. Journal of Proteome Research, 2008, 7, 3838-3846.	1.8	113
36	TagRecon: High-Throughput Mutation Identification through Sequence Tagging. Journal of Proteome Research, 2010, 9, 1716-1726.	1.8	104

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37	An Analysis of the Sensitivity of Proteogenomic Mapping of Somatic Mutations and Novel Splicing Events in Cancer. Molecular and Cellular Proteomics, 2016, 15, 1060-1071.	2.5	104
38	ProRata: Â A Quantitative Proteomics Program for Accurate Protein Abundance Ratio Estimation with Confidence Interval Evaluation. Analytical Chemistry, 2006, 78, 7121-7131.	3.2	97
39	Proteomics Standards Initiative: Fifteen Years of Progress and Future Work. Journal of Proteome Research, 2017, 16, 4288-4298.	1.8	87
40	Evaluation of Strong Cation Exchange versus Isoelectric Focusing of Peptides for Multidimensional Liquid Chromatography-Tandem Mass Spectrometry. Journal of Proteome Research, 2008, 7, 5286-5294.	1.8	86
41	A Bioinformatics Workflow for Variant Peptide Detection in Shotgun Proteomics. Molecular and Cellular Proteomics, 2011, 10, M110.006536.	2.5	86
42	Proteomic analysis of the enterocyte brush border. American Journal of Physiology - Renal Physiology, 2011, 300, G914-G926.	1.6	84
43	Characterization of the 70S Ribosome from Rhodopseudomonas palustris Using an Integrated â€œTop-Downâ€ and â€œBottom-Upâ€ Mass Spectrometric Approach. Journal of Proteome Research, 2004, 3, 965-978.	1.8	83
44	Integrated Proteomic and Glycoproteomic Characterization of Human High-Grade Serous Ovarian Carcinoma. Cell Reports, 2020, 33, 108276.	2.9	83
45	Quality control in mass spectrometryâ€based proteomics. Mass Spectrometry Reviews, 2018, 37, 697-711.	2.8	82
46	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.	0.7	77
47	Determination and Comparison of the Baseline Proteomes of the Versatile MicrobeRhodopseudomonaspalustrisunder Its Major Metabolic States. Journal of Proteome Research, 2006, 5, 287-298.	1.8	69
48	Comprehensive Characterization of Glycosylation and Hydroxylation of Basement Membrane Collagen IV by High-Resolution Mass Spectrometry. Journal of Proteome Research, 2016, 15, 245-258.	1.8	64
49	Quality assessment for clinical proteomics. Clinical Biochemistry, 2013, 46, 411-420.	0.8	60
50	Networkâ€assisted protein identification and data interpretation in shotgun proteomics. Molecular Systems Biology, 2009, 5, 303.	3.2	59
51	MS2Grouper: Group assessment and synthetic replacement of duplicate proteomic tandem mass spectra. Journal of the American Society for Mass Spectrometry, 2005, 16, 1250-1261.	1.2	58
52	Pepitome: Evaluating Improved Spectral Library Search for Identification Complementarity and Quality Assessment. Journal of Proteome Research, 2012, 11, 1686-1695.	1.8	58
53	Neurovascular unit on a chip: implications for translational applications. Stem Cell Research and Therapy, 2013, 4, S18.	2.4	56
54	In-depth analysis of protein inference algorithms using multiple search engines and well-defined metrics. Journal of Proteomics, 2017, 150, 170-182.	1.2	56

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55	Verification of automated peptide identifications from proteomic tandem mass spectra. Nature Protocols, 2006, 1, 2213-2222.	5.5	55
56	What's Driving False Discovery Rates?. Journal of Proteome Research, 2008, 7, 45-46.	1.8	53
57	The SEQUEST Family Tree. Journal of the American Society for Mass Spectrometry, 2015, 26, 1814-1819.	1.2	51
58	QuaMeter: Multivendor Performance Metrics for LC–MS/MS Proteomics Instrumentation. Analytical Chemistry, 2012, 84, 5845-5850.	3.2	50
59	Greazy: Open-Source Software for Automated Phospholipid Tandem Mass Spectrometry Identification. Analytical Chemistry, 2016, 88, 5733-5741.	3.2	50
60	Differential Localization and Dynamics of Class I Myosins in the Enterocyte Microvillus. Molecular Biology of the Cell, 2010, 21, 970-978.	0.9	48
61	DBDigger: Reorganized Proteomic Database Identification That Improves Flexibility and Speed. Analytical Chemistry, 2005, 77, 2464-2474.	3.2	47
62	MASPIC: Intensity-Based Tandem Mass Spectrometry Scoring Scheme That Improves Peptide Identification at High Confidence. Analytical Chemistry, 2005, 77, 7581-7593.	3.2	46
63	Reproducibility of Differential Proteomic Technologies in CPTAC Fractionated Xenografts. Journal of Proteome Research, 2016, 15, 691-706.	1.8	44
64	QC Metrics from CPTAC Raw LC-MS/MS Data Interpreted through Multivariate Statistics. Analytical Chemistry, 2014, 86, 2497-2509.	3.2	42
65	A Serum Circulating miRNA Signature for Short-Term Risk of Progression to Active Tuberculosis Among Household Contacts. Frontiers in Immunology, 2018, 9, 661.	2.2	42
66	MS for Identification of Single Nucleotide Polymorphisms and MS/MS for Discrimination of Isomeric PCR Products. Analytical Chemistry, 2000, 72, 4033-4040.	3.2	40
67	Robust Estimation of Peptide Abundance Ratios and Rigorous Scoring of Their Variability and Bias in Quantitative Shotgun Proteomics. Analytical Chemistry, 2006, 78, 7110-7120.	3.2	40
68	Immunometabolic Signatures Predict Risk of Progression to Active Tuberculosis and Disease Outcome. Frontiers in Immunology, 2019, 10, 527.	2.2	40
69	Prostate cancer serum biomarker discovery through proteomic analysis of alpha-2 macroglobulin protein complexes. Proteomics - Clinical Applications, 2008, 2, 1223-1233.	0.8	39
70	Supporting tool suite for production proteomics. Bioinformatics, 2011, 27, 3214-3215.	1.8	38
71	Wavelet-Based Peak Detection and a New Charge Inference Procedure for MS/MS Implemented in ProteoWizard's msConvert. Journal of Proteome Research, 2015, 14, 1299-1307.	1.8	38
72	Protein Identification by SEQUEST. Principles and Practice, 2001, , 125-142.	0.3	38

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73	Use of Fluorescence-activated Vesicle Sorting for Isolation of Naked2-associated, Basolaterally Targeted Exocytic Vesicles for Proteomics Analysis. Molecular and Cellular Proteomics, 2008, 7, 1651-1667.	2.5	36
74	Advanced Proteogenomic Analysis Reveals Multiple Peptide Mutations and Complex Immunoglobulin Peptides in Colon Cancer. Journal of Proteome Research, 2015, 14, 3555-3567.	1.8	36
75	Sipros Ensemble improves database searching and filtering for complex metaproteomics. Bioinformatics, 2018, 34, 795-802.	1.8	35
76	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.	2.0	34
77	Identifying Proteomic LC–MS/MS Data Sets with Bumbershoot and IDPicker. Current Protocols in Bioinformatics, 2012, 37, Unit13.17.	25.8	33
78	Correcting systematic bias and instrument measurement drift with mzRefinery. Bioinformatics, 2015, 31, 3838-3840.	1.8	32
79	Informatics of Protein and Posttranslational Modification Detection via Shotgun Proteomics. Methods in Molecular Biology, 2013, 1002, 167-179.	0.4	31
80	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.	1.2	30
81	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, 1243-1259.	2.5	30
82	ScanRanker: Quality Assessment of Tandem Mass Spectra via Sequence Tagging. Journal of Proteome Research, 2011, 10, 2896-2904.	1.8	30
83	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, 1069-1076.	1.7	27
84	Proteogenomic Investigation of Strain Variation in Clinical <i>Mycobacterium tuberculosis</i> Isolates. Journal of Proteome Research, 2017, 16, 3841-3851.	1.8	27
85	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.	1.4	26
86	Sequence Tagging Reveals Unexpected Modifications in Toxicoproteomics. Chemical Research in Toxicology, 2011, 24, 204-216.	1.7	25
87	proBAMsuite, a Bioinformatics Framework for Genome-Based Representation and Analysis of Proteomics Data. Molecular and Cellular Proteomics, 2016, 15, 1164-1175.	2.5	25
88	A standardized framing for reporting protein identifications in mzIdentML 1.2. Proteomics, 2014, 14, 2389-2399.	1.3	23
89	Microbial function and genital inflammation in young South African women at high risk of HIV infection. Microbiome, 2020, 8, 165.	4.9	23
90	Tandem mass spectrometry for the detection of plant pathogenic fungi and the effects of database composition on protein inferences. Proteomics, 2007, 7, 3932-3942.	1.3	22

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91	Proteomic analysis of colon and rectal carcinoma using standard and customized databases. Scientific Data, 2015, 2, 150022.	2.4	22
92	The Human Proteome Organizationâ€"Proteomics Standards Initiative Quality Control Working Group: Making Quality Control More Accessible for Biological Mass Spectrometry. Analytical Chemistry, 2017, 89, 4474-4479.	3.2	22
93	IDPQuantify: Combining Precursor Intensity with Spectral Counts for Protein and Peptide Quantification. Journal of Proteome Research, 2013, 12, 4111-4121.	1.8	21
94	Mapping Serum Albumin Adducts of the Food-Borne Carcinogen 2-Amino-1-methyl-6-phenylimidazo[4,5-<i>b</i>]pyridine by Data-Dependent Tandem Mass Spectrometry. Chemical Research in Toxicology, 2012, 25, 2179-2193.	1.7	19
95	Evaluating protein interactions through cross-linking mass spectrometry. Nature Methods, 2012, 9, 879-881.	9.0	18
96	Quality Assessments of Long-Term Quantitative Proteomic Analysis of Breast Cancer Xenograft Tissues. Journal of Proteome Research, 2017, 16, 4523-4530.	1.8	17
97	A Proteomics Analysis of Yeast Mot1p Protein-Protein Associations. Molecular and Cellular Proteomics, 2008, 7, 2090-2106.	2.5	16
98	Site-Specific <i>N</i>-Glycosylation Characterization of Windmill Palm Tree Peroxidase Using Novel Tools for Analysis of Plant Glycopeptide Mass Spectrometry Data. Journal of Proteome Research, 2016, 15, 2026-2038.	1.8	16
99	Proteomic analysis reveals that sulfamethoxazole induces oxidative stress in M. tuberculosis. Tuberculosis, 2018, 111, 78-85.	0.8	14
100	Targeted next-generation sequencing identifies novel variants in candidate genes for Parkinsonâ€™s disease in Black South African and Nigerian patients. BMC Medical Genetics, 2020, 21, 23.	2.1	14
101	Dysregulated healing responses in diabetic wounds occur in the early stages postinjury. Journal of Molecular Endocrinology, 2021, 66, 141-155.	1.1	12
102	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, 3299-3309.	2.5	11
103	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.	1.1	9
104	Challenges and Opportunities for Biological Mass Spectrometry Core Facilities in the Developing World. Journal of Biomolecular Techniques, 2018, 29, 4-15.	0.8	8
105	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.	0.7	8
106	Refining comparative proteomics by spectral counting to account for shared peptides and multiple search engines. Analytical and Bioanalytical Chemistry, 2012, 404, 1115-1125.	1.9	7
107	HI-Bone: A Scoring System for Identifying Phenylisothiocyanate-Derivatized Peptides Based on Precursor Mass and High Intensity Fragment Ions. Analytical Chemistry, 2013, 85, 3515-3520.	3.2	7
108	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, 2755-2762.	0.7	4

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109	Gaussian process modelling for improved resolution in Faraday depth reconstruction. Monthly Notices of the Royal Astronomical Society, 2021, 502, 5839-5853.	1.6	4
110	A Label-Free Proteomic and Complementary Metabolomic Analysis of Leaves of the Resurrection Plant Xerophyta schlechteri during Dehydration. Life, 2021, 11, 1242.	1.1	3
111	Proteomic Identification and Meta-Analysis in Salvia hispanica RNA-Seq de novo Assemblies. Plants, 2021, 10, 765.	1.6	2
112	Basophile: Accurate Fragment Charge State Prediction Improves Peptide Identification Rates. Genomics, Proteomics and Bioinformatics, 2013, 11, 86-95.	3.0	1
113	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.	0.4	1
114	Interrogating Fractionation and Other Sources of Variability in Shotgun Proteomes Using Quality Metrics. Proteomics, 2020, 20, 1900382.	1.3	1
115	Technologies for Large-Scale Proteomic Tandem Mass Spectrometry. , 2006, , 91-109.		0
116	Network Approaches for Shotgun Proteomics Data Analysis. , 2009, , .		0
117	A Laboratory-Targeted, Data Management and Processing System for the Early Detection Research Network. , 2014, , .		0
118	Open search algorithms discover patterns of chemical modifications via LC-MS/MS. , 2022, , 95-125.		0