

David L Tabb

List of Publications by Citations

Source: <https://exaly.com/author-pdf/1064114/david-l-tabb-publications-by-citations.pdf>

Version: 2024-04-25

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

115
papers

16,522
citations

50
h-index

128
g-index

130
ext. papers

19,918
ext. citations

9.3
avg, IF

6.1
L-index

#	Paper	IF	Citations
115	Skyline: an open source document editor for creating and analyzing targeted proteomics experiments. <i>Bioinformatics</i> , 2010 , 26, 966-8	7.2	2910
114	A cross-platform toolkit for mass spectrometry and proteomics. <i>Nature Biotechnology</i> , 2012 , 30, 918-20	44.5	1583
113	DTASelect and Contrast: tools for assembling and comparing protein identifications from shotgun proteomics. <i>Journal of Proteome Research</i> , 2002 , 1, 21-6	5.6	1156
112	A proteomic view of the Plasmodium falciparum life cycle. <i>Nature</i> , 2002 , 419, 520-6	50.4	1066
111	Proteogenomic characterization of human colon and rectal cancer. <i>Nature</i> , 2014 , 513, 382-7	50.4	900
110	Multi-site assessment of the precision and reproducibility of multiple reaction monitoring-based measurements of proteins in plasma. <i>Nature Biotechnology</i> , 2009 , 27, 633-41	44.5	859
109	Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. <i>Cell</i> , 2016 , 166, 755-765	56.2	544
108	MyriMatch: highly accurate tandem mass spectral peptide identification by multivariate hypergeometric analysis. <i>Journal of Proteome Research</i> , 2007 , 6, 654-61	5.6	458
107	Repeatability and reproducibility in proteomic identifications by liquid chromatography-tandem mass spectrometry. <i>Journal of Proteome Research</i> , 2010 , 9, 761-76	5.6	377
106	MS1, MS2, and SQT-three unified, compact, and easily parsed file formats for the storage of shotgun proteomic spectra and identifications. <i>Rapid Communications in Mass Spectrometry</i> , 2004 , 18, 2162-8	2.2	295
105	IDPicker 2.0: Improved protein assembly with high discrimination peptide identification filtering. <i>Journal of Proteome Research</i> , 2009 , 8, 3872-81	5.6	274
104	Cleavage N-terminal to proline: analysis of a database of peptide tandem mass spectra. <i>Analytical Chemistry</i> , 2003 , 75, 1963-71	7.8	274
103	Proteomic parsimony through bipartite graph analysis improves accuracy and transparency. <i>Journal of Proteome Research</i> , 2007 , 6, 3549-57	5.6	266
102	GutenTag: high-throughput sequence tagging via an empirically derived fragmentation model. <i>Analytical Chemistry</i> , 2003 , 75, 6415-21	7.8	240
101	Proteogenomic Analysis of Human Colon Cancer Reveals New Therapeutic Opportunities. <i>Cell</i> , 2019 , 177, 1035-1049.e19	56.2	237
100	Statistical characterization of ion trap tandem mass spectra from doubly charged tryptic peptides. <i>Analytical Chemistry</i> , 2003 , 75, 1155-63	7.8	232
99	The enterocyte microvillus is a vesicle-generating organelle. <i>Journal of Cell Biology</i> , 2009 , 185, 1285-98	7.3	165

98	Efficient and specific trypsin digestion of microgram to nanogram quantities of proteins in organic-aqueous solvent systems. <i>Analytical Chemistry</i> , 2006 , 78, 125-34	7.8	157
97	Validation of tandem mass spectrometry database search results using DTASelect. <i>Current Protocols in Bioinformatics</i> , 2007 , Chapter 13, Unit 13.4	24.2	153
96	Performance metrics for liquid chromatography-tandem mass spectrometry systems in proteomics analyses. <i>Molecular and Cellular Proteomics</i> , 2010 , 9, 225-41	7.6	147
95	Similarity among tandem mass spectra from proteomic experiments: detection, significance, and utility. <i>Analytical Chemistry</i> , 2003 , 75, 2470-7	7.8	143
94	Identification of proteins at active, stalled, and collapsed replication forks using isolation of proteins on nascent DNA (iPOND) coupled with mass spectrometry. <i>Journal of Biological Chemistry</i> , 2013 , 288, 31458-67	5.4	140
93	Large-scale protein identification using mass spectrometry. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2003 , 1646, 1-10	4	137
92	Influence of basic residue content on fragment ion peak intensities in low-energy collision-induced dissociation spectra of peptides. <i>Analytical Chemistry</i> , 2004 , 76, 1243-8	7.8	136
91	Employing ProteoWizard to Convert Raw Mass Spectrometry Data. <i>Current Protocols in Bioinformatics</i> , 2014 , 46, 13.24.1-9	24.2	131
90	Interlaboratory study characterizing a yeast performance standard for benchmarking LC-MS platform performance. <i>Molecular and Cellular Proteomics</i> , 2010 , 9, 242-54	7.6	130
89	Proteomic analysis of Chinese hamster ovary cells. <i>Journal of Proteome Research</i> , 2012 , 11, 5265-76	5.6	128
88	Protein identification using customized protein sequence databases derived from RNA-Seq data. <i>Journal of Proteome Research</i> , 2012 , 11, 1009-17	5.6	128
87	Four-Gene Pan-African Blood Signature Predicts Progression to Tuberculosis. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2018 , 197, 1198-1208	10.2	125
86	The evolutionary imprint of domestication on genome variation and function of the filamentous fungus <i>Aspergillus oryzae</i> . <i>Current Biology</i> , 2012 , 22, 1403-9	6.3	122
85	A face in the crowd: recognizing peptides through database search. <i>Molecular and Cellular Proteomics</i> , 2011 , 10, R111.009522	7.6	106
84	TagRecon: high-throughput mutation identification through sequence tagging. <i>Journal of Proteome Research</i> , 2010 , 9, 1716-26	5.6	100
83	DirecTag: accurate sequence tags from peptide MS/MS through statistical scoring. <i>Journal of Proteome Research</i> , 2008 , 7, 3838-46	5.6	100
82	Recognizing millions of consistently unidentified spectra across hundreds of shotgun proteomics datasets. <i>Nature Methods</i> , 2016 , 13, 651-656	21.6	99
81	Host blood RNA signatures predict the outcome of tuberculosis treatment. <i>Tuberculosis</i> , 2017 , 107, 48-58.6		90

80	ProRata: A quantitative proteomics program for accurate protein abundance ratio estimation with confidence interval evaluation. <i>Analytical Chemistry</i> , 2006 , 78, 7121-31	7.8	86
79	Evaluation of strong cation exchange versus isoelectric focusing of peptides for multidimensional liquid chromatography-tandem mass spectrometry. <i>Journal of Proteome Research</i> , 2008 , 7, 5286-94	5.6	82
78	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, 1060-71	7.6	80
77	Characterization of the 70S Ribosome from <i>Rhodospseudomonas palustris</i> using an integrated "top-down" and "bottom-up" mass spectrometric approach. <i>Journal of Proteome Research</i> , 2004 , 3, 965-78	5.6	78
76	A bioinformatics workflow for variant peptide detection in shotgun proteomics. <i>Molecular and Cellular Proteomics</i> , 2011 , 10, M110.006536	7.6	73
75	The influence of histidine on cleavage C-terminal to acidic residues in doubly protonated tryptic peptides. <i>International Journal of Mass Spectrometry</i> , 2002 , 219, 233-244	1.9	72
74	Proteogenomic Landscape of Breast Cancer Tumorigenesis and Targeted Therapy. <i>Cell</i> , 2020 , 183, 1436-1456.e31	10.5	71
73	Determination and comparison of the baseline proteomes of the versatile microbe <i>Rhodospseudomonas palustris</i> under its major metabolic states. <i>Journal of Proteome Research</i> , 2006 , 5, 287-98	5.6	64
72	Proteomics Standards Initiative: Fifteen Years of Progress and Future Work. <i>Journal of Proteome Research</i> , 2017 , 16, 4288-4298	5.6	61
71	Proteomic analysis of the enterocyte brush border. <i>American Journal of Physiology - Renal Physiology</i> , 2011 , 300, G914-26	5.1	60
70	Quality assessment for clinical proteomics. <i>Clinical Biochemistry</i> , 2013 , 46, 411-20	3.5	53
69	Pepitome: evaluating improved spectral library search for identification complementarity and quality assessment. <i>Journal of Proteome Research</i> , 2012 , 11, 1686-95	5.6	52
68	MS2Grouper: group assessment and synthetic replacement of duplicate proteomic tandem mass spectra. <i>Journal of the American Society for Mass Spectrometry</i> , 2005 , 16, 1250-61	3.5	51
67	What's driving false discovery rates?. <i>Journal of Proteome Research</i> , 2008 , 7, 45-6	5.6	50
66	Verification of automated peptide identifications from proteomic tandem mass spectra. <i>Nature Protocols</i> , 2006 , 1, 2213-22	18.8	50
65	Neurovascular unit on a chip: implications for translational applications. <i>Stem Cell Research and Therapy</i> , 2013 , 4 Suppl 1, S18	8.3	48
64	Network-assisted protein identification and data interpretation in shotgun proteomics. <i>Molecular Systems Biology</i> , 2009 , 5, 303	12.2	45
63	DBDigger: reorganized proteomic database identification that improves flexibility and speed. <i>Analytical Chemistry</i> , 2005 , 77, 2464-74	7.8	45

62	QuaMeter: multivendor performance metrics for LC-MS/MS proteomics instrumentation. <i>Analytical Chemistry</i> , 2012 , 84, 5845-50	7.8	44
61	MASPIC: intensity-based tandem mass spectrometry scoring scheme that improves peptide identification at high confidence. <i>Analytical Chemistry</i> , 2005 , 77, 7581-93	7.8	44
60	Quality control in mass spectrometry-based proteomics. <i>Mass Spectrometry Reviews</i> , 2018 , 37, 697-711	11	44
59	Comprehensive Characterization of Glycosylation and Hydroxylation of Basement Membrane Collagen IV by High-Resolution Mass Spectrometry. <i>Journal of Proteome Research</i> , 2016 , 15, 245-58	5.6	43
58	Greazy: Open-Source Software for Automated Phospholipid Tandem Mass Spectrometry Identification. <i>Analytical Chemistry</i> , 2016 , 88, 5733-41	7.8	43
57	In-depth analysis of protein inference algorithms using multiple search engines and well-defined metrics. <i>Journal of Proteomics</i> , 2017 , 150, 170-182	3.9	39
56	MS for identification of single nucleotide polymorphisms and MS/MS for discrimination of isomeric PCR products. <i>Analytical Chemistry</i> , 2000 , 72, 4033-40	7.8	38
55	Robust estimation of peptide abundance ratios and rigorous scoring of their variability and bias in quantitative shotgun proteomics. <i>Analytical Chemistry</i> , 2006 , 78, 7110-20	7.8	36
54	Reproducibility of Differential Proteomic Technologies in CPTAC Fractionated Xenografts. <i>Journal of Proteome Research</i> , 2016 , 15, 691-706	5.6	35
53	Differential localization and dynamics of class I myosins in the enterocyte microvillus. <i>Molecular Biology of the Cell</i> , 2010 , 21, 970-8	3.5	35
52	Integrated Proteomic and Glycoproteomic Characterization of Human High-Grade Serous Ovarian Carcinoma. <i>Cell Reports</i> , 2020 , 33, 108276	10.6	33
51	Use of fluorescence-activated vesicle sorting for isolation of Naked2-associated, basolaterally targeted exocytic vesicles for proteomics analysis. <i>Molecular and Cellular Proteomics</i> , 2008 , 7, 1651-67	7.6	32
50	QC metrics from CPTAC raw LC-MS/MS data interpreted through multivariate statistics. <i>Analytical Chemistry</i> , 2014 , 86, 2497-509	7.8	31
49	Identifying proteomic LC-MS/MS data sets with Bumbershoot and IDPicker. <i>Current Protocols in Bioinformatics</i> , 2012 , Chapter 13, Unit13.17	24.2	31
48	Obesity and altered glucose metabolism impact HDL composition in CETP transgenic mice: a role for ovarian hormones. <i>Journal of Lipid Research</i> , 2012 , 53, 379-389	6.3	31
47	The SEQUEST family tree. <i>Journal of the American Society for Mass Spectrometry</i> , 2015 , 26, 1814-9	3.5	30
46	Protein Identification by SEQUEST. <i>Principles and Practice</i> , 2001 , 125-142		29
45	Supporting tool suite for production proteomics. <i>Bioinformatics</i> , 2011 , 27, 3214-5	7.2	28

44	Wavelet-based peak detection and a new charge inference procedure for MS/MS implemented in ProteoWizard's msConvert. <i>Journal of Proteome Research</i> , 2015 , 14, 1299-307	5.6	27
43	Determination of peptide and protein ion charge states by Fourier transformation of isotope-resolved mass spectra. <i>Journal of the American Society for Mass Spectrometry</i> , 2006 , 17, 903-915	3.5	27
42	Immunometabolic Signatures Predict Risk of Progression to Active Tuberculosis and Disease Outcome. <i>Frontiers in Immunology</i> , 2019 , 10, 527	8.4	26
41	Identification and validation of novel spinophilin-associated proteins in rodent striatum using an enhanced ex vivo shotgun proteomics approach. <i>Molecular and Cellular Proteomics</i> , 2010 , 9, 1243-59	7.6	26
40	Prostate cancer serum biomarker discovery through proteomic analysis of alpha-2 macroglobulin protein complexes. <i>Proteomics - Clinical Applications</i> , 2008 , 2, 1223	3.1	26
39	Sequence tagging reveals unexpected modifications in toxicoproteomics. <i>Chemical Research in Toxicology</i> , 2011 , 24, 204-16	4	24
38	A Serum Circulating miRNA Signature for Short-Term Risk of Progression to Active Tuberculosis Among Household Contacts. <i>Frontiers in Immunology</i> , 2018 , 9, 661	8.4	23
37	ScanRanker: Quality assessment of tandem mass spectra via sequence tagging. <i>Journal of Proteome Research</i> , 2011 , 10, 2896-904	5.6	23
36	The bis-electrophile diepoxybutane cross-links DNA to human histones but does not result in enhanced mutagenesis in recombinant systems. <i>Chemical Research in Toxicology</i> , 2009 , 22, 1069-76	4	23
35	Chronic intermittent alcohol disrupts the GluN2B-associated proteome and specifically regulates group I mGlu receptor-dependent long-term depression. <i>Addiction Biology</i> , 2017 , 22, 275-290	4.6	22
34	Advanced Proteogenomic Analysis Reveals Multiple Peptide Mutations and Complex Immunoglobulin Peptides in Colon Cancer. <i>Journal of Proteome Research</i> , 2015 , 14, 3555-67	5.6	22
33	proBAMsuite, a Bioinformatics Framework for Genome-Based Representation and Analysis of Proteomics Data. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 1164-75	7.6	20
32	Proteomic analysis of colon and rectal carcinoma using standard and customized databases. <i>Scientific Data</i> , 2015 , 2, 150022	8.2	20
31	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. <i>Chemical Research in Toxicology</i> , 2012 , 25, 2179-93	4	18
30	Informatics of protein and posttranslational modification detection via shotgun proteomics. <i>Methods in Molecular Biology</i> , 2013 , 1002, 167-79	1.4	18
29	Tandem mass spectrometry for the detection of plant pathogenic fungi and the effects of database composition on protein inferences. <i>Proteomics</i> , 2007 , 7, 3932-42	4.8	18
28	Sipros Ensemble improves database searching and filtering for complex metaproteomics. <i>Bioinformatics</i> , 2018 , 34, 795-802	7.2	17
27	IDPQuantify: combining precursor intensity with spectral counts for protein and peptide quantification. <i>Journal of Proteome Research</i> , 2013 , 12, 4111-21	5.6	16

26	A standardized framing for reporting protein identifications in mzIdentML 1.2. <i>Proteomics</i> , 2014 , 14, 2389-99	4.8	16
25	Proteogenomic Investigation of Strain Variation in Clinical Mycobacterium tuberculosis Isolates. <i>Journal of Proteome Research</i> , 2017 , 16, 3841-3851	5.6	15
24	Correcting systematic bias and instrument measurement drift with mzRefinery. <i>Bioinformatics</i> , 2015 , 31, 3838-40	7.2	15
23	A proteomics analysis of yeast Mot1p protein-protein associations: insights into mechanism. <i>Molecular and Cellular Proteomics</i> , 2008 , 7, 2090-106	7.6	15
22	Quality Assessments of Long-Term Quantitative Proteomic Analysis of Breast Cancer Xenograft Tissues. <i>Journal of Proteome Research</i> , 2017 , 16, 4523-4530	5.6	14
21	The Human Proteome Organization-Proteomics Standards Initiative Quality Control Working Group: Making Quality Control More Accessible for Biological Mass Spectrometry. <i>Analytical Chemistry</i> , 2017 , 89, 4474-4479	7.8	12
20	Site-Specific N-Glycosylation Characterization of Windmill Palm Tree Peroxidase Using Novel Tools for Analysis of Plant Glycopeptide Mass Spectrometry Data. <i>Journal of Proteome Research</i> , 2016 , 15, 2026-38	5.6	12
19	Targeted next-generation sequencing identifies novel variants in candidate genes for Parkinson's disease in Black South African and Nigerian patients. <i>BMC Medical Genetics</i> , 2020 , 21, 23	2.1	8
18	The 2012/2013 ABRF Proteomic Research Group Study: Assessing Longitudinal Intralaboratory Variability in Routine Peptide Liquid Chromatography Tandem Mass Spectrometry Analyses. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 3299-309	7.6	8
17	Proteomic analysis reveals that sulfamethoxazole induces oxidative stress in M. tuberculosis. <i>Tuberculosis</i> , 2018 , 111, 78-85	2.6	8
16	Open search unveils modification patterns in formalin-fixed, paraffin-embedded thermo HCD and SCIEX TripleTOF shotgun proteomes. <i>International Journal of Mass Spectrometry</i> , 2020 , 448, 116266	1.9	7
15	Refining comparative proteomics by spectral counting to account for shared peptides and multiple search engines. <i>Analytical and Bioanalytical Chemistry</i> , 2012 , 404, 1115-25	4.4	6
14	HI-bone: a scoring system for identifying phenylisothiocyanate-derivatized peptides based on precursor mass and high intensity fragment ions. <i>Analytical Chemistry</i> , 2013 , 85, 3515-20	7.8	6
13	MetaNovo: a probabilistic approach to peptide and polymorphism discovery in complex metaproteomic datasets		4
12	Microbial function and genital inflammation in young South African women at high risk of HIV infection. <i>Microbiome</i> , 2020 , 8, 165	16.6	4
11	Challenges and Opportunities for Biological Mass Spectrometry Core Facilities in the Developing World. <i>Journal of Biomolecular Techniques</i> , 2018 , 29, 4-15	1.1	4
10	Automated discrimination of polymerase chain reaction products with closely related sequences by software-based detection of characteristic peaks in product ion spectra. <i>Rapid Communications in Mass Spectrometry</i> , 2003 , 17, 2755-62	2.2	3
9	SWATH-MS based proteomic profiling of pancreatic ductal adenocarcinoma tumours reveals the interplay between the extracellular matrix and related intracellular pathways. <i>PLoS ONE</i> , 2020 , 15, e0240453	2.7	3

8	Dysregulated healing responses in diabetic wounds occur in the early stages postinjury. <i>Journal of Molecular Endocrinology</i> , 2021 , 66, 141-155	4.5	2
7	Characterization of Plant Glycoproteins: Analysis of Plant Glycopeptide Mass Spectrometry Data with plantGlycoMS, a Package in the R Statistical Computing Environment. <i>Methods in Molecular Biology</i> , 2018 , 1789, 205-220	1.4	1
6	Basophile: accurate fragment charge state prediction improves peptide identification rates. <i>Genomics, Proteomics and Bioinformatics</i> , 2013 , 11, 86-95	6.5	1
5	Gaussian process modelling for improved resolution in Faraday depth reconstruction. <i>Monthly Notices of the Royal Astronomical Society</i> , 2021 , 502, 5839-5853	4.3	1
4	Interrogating Fractionation and Other Sources of Variability in Shotgun Proteomes Using Quality Metrics. <i>Proteomics</i> , 2020 , 20, e1900382	4.8	0
3	Bioinformatics and Database Searching 2011 , 231-252		
2	Technologies for Large-Scale Proteomic Tandem Mass Spectrometry 2006 , 91-109		
1	Open search algorithms discover patterns of chemical modifications via LC-MS/MS 2022 , 95-125		