Eric W Deutsch

List of Publications by Year
in descending order

135 papers	22,536 citations	18465 62 h-index	10152 140 g-index
162 all docs	162 docs citations	162 times ranked	27766 citing authors

#	Article	IF	Citations
1	A cross-platform toolkit for mass spectrometry and proteomics. Nature Biotechnology, 2012, 30, 918-920.	9.4	2,794
2	ProteomeXchange provides globally coordinated proteomics data submission and dissemination. Nature Biotechnology, 2014, 32, 223-226.	9.4	2,505
3	The ProteomeXchange consortium in 2017: supporting the cultural change in proteomics public data deposition. Nucleic Acids Research, 2017, 45, D1100-D1106.	6.5	860
4	The PeptideAtlas project. Nucleic Acids Research, 2006, 34, D655-D658.	6.5	733
5	A common open representation of mass spectrometry data and its application to proteomics research. Nature Biotechnology, 2004, 22, 1459-1466.	9.4	724
6	A guided tour of the Trans–Proteomic Pipeline. Proteomics, 2010, 10, 1150-1159.	1.3	710
7	The minimum information about a proteomics experiment (MIAPE). Nature Biotechnology, 2007, 25, 887-893.	9.4	694
8	mzML—a Community Standard for Mass Spectrometry Data. Molecular and Cellular Proteomics, 2011, 10, R110.000133.	2.5	555
9	PeptideAtlas: a resource for target selection for emerging targeted proteomics workflows. EMBO Reports, 2008, 9, 429-434.	2.0	516
10	The ProteomeXchange consortium in 2020: enabling 'big data' approaches in proteomics. Nucleic Acids Research, 2020, 48, D1145-D1152.	6.5	491
11	iProphet: Multi-level Integrative Analysis of Shotgun Proteomic Data Improves Peptide and Protein Identification Rates and Error Estimates. Molecular and Cellular Proteomics, 2011, 10, M111.007690.	2.5	490
12	Development and validation of a spectral library searching method for peptide identification from MS/MS. Proteomics, 2007, 7, 655-667.	1.3	487
13	Proteome-wide cellular protein concentrations of the human pathogen Leptospira interrogans. Nature, 2009, 460, 762-765.	13.7	402
14	A High-Confidence Human Plasma Proteome Reference Set with Estimated Concentrations in PeptideAtlas. Molecular and Cellular Proteomics, 2011, 10, M110.006353.	2.5	381
15	A repository of assays to quantify 10,000 human proteins by SWATH-MS. Scientific Data, 2014, 1, 140031.	2.4	370
16	Design and implementation of microarray gene expression markup language (MAGE-ML). Genome Biology, 2002, 3, RESEARCH0046.	3.8	350
17	Trans–Proteomic Pipeline, a standardized data processing pipeline for large–scale reproducible proteomics informatics. Proteomics - Clinical Applications, 2015, 9, 745-754.	0.8	319
18	A complete mass-spectrometric map of the yeast proteome applied to quantitative trait analysis. Nature, 2013, 494, 266-270.	13.7	307

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19	Human SRMAtlas: A Resource of Targeted Assays to Quantify the Complete Human Proteome. Cell, 2016, 166, 766-778.	13.5	295
20	The Human Proteome Project: Current State and Future Direction. Molecular and Cellular Proteomics, 2011, 10, M111.009993.	2.5	294
21	The Chromosome-Centric Human Proteome Project for cataloging proteins encoded in the genome. Nature Biotechnology, 2012, 30, 221-223.	9.4	281
22	Building consensus spectral libraries for peptide identification in proteomics. Nature Methods, 2008, 5, 873-875.	9.0	255
23	Integration with the human genome of peptide sequences obtained by high-throughput mass spectrometry. Genome Biology, 2004, 6, R9.	13.9	252
24	Reproducible Quantification of Cancer-Associated Proteins in Body Fluids Using Targeted Proteomics. Science Translational Medicine, 2012, 4, 142ra94.	5.8	236
25	A database of mass spectrometric assays for the yeast proteome. Nature Methods, 2008, 5, 913-914.	9.0	205
26	PASSEL: The PeptideAtlas SRM experiment library. Proteomics, 2012, 12, 1170-1175.	1.3	200
27	Targeted Quantitative Analysis of Streptococcus pyogenes Virulence Factors by Multiple Reaction Monitoring. Molecular and Cellular Proteomics, 2008, 7, 1489-1500.	2.5	189
28	The Human Plasma Proteome Draft of 2017: Building on the Human Plasma PeptideAtlas from Mass Spectrometry and Complementary Assays. Journal of Proteome Research, 2017, 16, 4299-4310.	1.8	185
29	Building ProteomeTools based on a complete synthetic human proteome. Nature Methods, 2017, 14, 259-262.	9.0	182
30	The mzIdentML Data Standard for Mass Spectrometry-Based Proteomics Results. Molecular and Cellular Proteomics, 2012, 11, M111.014381-1-M111.014381-10.	2.5	175
31	Discovering and linking public omics data sets using the Omics Discovery Index. Nature Biotechnology, 2017, 35, 406-409.	9.4	159
32	mzML: A single, unifying data format for mass spectrometer output. Proteomics, 2008, 8, 2776-2777.	1.3	158
33	Human Proteome Project Mass Spectrometry Data Interpretation Guidelines 2.1. Journal of Proteome Research, 2016, 15, 3961-3970.	1.8	158
34	Combining Results of Multiple Search Engines in Proteomics. Molecular and Cellular Proteomics, 2013, 12, 2383-2393.	2.5	154
35	A high-stringency blueprint of the human proteome. Nature Communications, 2020, 11, 5301.	5.8	152
36	Data analysis and bioinformatics tools for tandem mass spectrometry in proteomics. Physiological Genomics, 2008, 33, 18-25.	1.0	137

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37	Human Plasma PeptideAtlas. Proteomics, 2005, 5, 3497-3500.	1.3	132
38	Mass Spectrometry-Based Plasma Proteomics: Considerations from Sample Collection to Achieving Translational Data. Journal of Proteome Research, 2019, 18, 4085-4097.	1.8	128
39	Metrics for the Human Proteome Project 2013â€"2014 and Strategies for Finding Missing Proteins. Journal of Proteome Research, 2014, 13, 15-20.	1.8	124
40	The PeptideAtlas Project. Methods in Molecular Biology, 2010, 604, 285-296.	0.4	121
41	The SysteMHC Atlas project. Nucleic Acids Research, 2018, 46, D1237-D1247.	6.5	119
42	The State of the Human Proteome in 2012 as Viewed through PeptideAtlas. Journal of Proteome Research, 2013, 12, 162-171.	1.8	115
43	State of the Human Proteome in 2013 as Viewed through PeptideAtlas: Comparing the Kidney, Urine, and Plasma Proteomes for the Biology- and Disease-Driven Human Proteome Project. Journal of Proteome Research, 2014, 13, 60-75.	1.8	115
44	Minimum information specification for in situ hybridization and immunohistochemistry experiments (MISFISHIE). Nature Biotechnology, 2008, 26, 305-312.	9.4	111
45	An open-source computational and data resource to analyze digital maps of immunopeptidomes. ELife, 2015, 4, .	2.8	107
46	Artificial Decoy Spectral Libraries for False Discovery Rate Estimation in Spectral Library Searching in Proteomics. Journal of Proteome Research, 2010, 9, 605-610.	1.8	106
47	Predictive Big Data Analytics: A Study of Parkinsonâ€™s Disease Using Large, Complex, Heterogeneous, Incongruent, Multi-Source and Incomplete Observations. PLoS ONE, 2016, 11, e0157077.	1.1	94
48	Proteomics Standards Initiative: Fifteen Years of Progress and Future Work. Journal of Proteome Research, 2017, 16, 4288-4298.	1.8	87
49	Metrics for the Human Proteome Project 2015: Progress on the Human Proteome and Guidelines for High-Confidence Protein Identification. Journal of Proteome Research, 2015, 14, 3452-3460.	1.8	86
50	Advances and Utility of the Human Plasma Proteome. Journal of Proteome Research, 2021, 20, 5241-5263.	1.8	86
51	Standardized annotation of translated open reading frames. Nature Biotechnology, 2022, 40, 994-999.	9.4	86
52	Guidelines for reporting the use of mass spectrometry in proteomics. Nature Biotechnology, 2008, 26, 860-861.	9.4	82
53	Human Proteome Project Mass Spectrometry Data Interpretation Guidelines 3.0. Journal of Proteome Research, 2019, 18, 4108-4116.	1.8	82
54	MaRiMba: A Software Application for Spectral Library-Based MRM Transition List Assembly. Journal of Proteome Research, 2009, 8, 4396-4405.	1.8	80

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55	File Formats Commonly Used in Mass Spectrometry Proteomics. Molecular and Cellular Proteomics, 2012, 11, 1612-1621.	2.5	80
56	PTMProphet: Fast and Accurate Mass Modification Localization for the Trans-Proteomic Pipeline. Journal of Proteome Research, 2019, 18, 4262-4272.	1.8	80
57	The HUPO proteomics standards initiative- mass spectrometry controlled vocabulary. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat009-bat009.	1.4	76
58	Data Standards for Omics Data: The Basis of Data Sharing and Reuse. Methods in Molecular Biology, 2011, 719, 31-69.	0.4	73
59	State of the Human Proteome in 2014/2015 As Viewed through PeptideAtlas: Enhancing Accuracy and Coverage through the AtlasProphet. Journal of Proteome Research, 2015, 14, 3461-3473.	1.8	72
60	Metrics for the Human Proteome Project 2016: Progress on Identifying and Characterizing the Human Proteome, Including Post-Translational Modifications. Journal of Proteome Research, 2016, 15, 3951-3960.	1.8	72
61	Big biomedical data as the key resource for discovery science. Journal of the American Medical Informatics Association: JAMIA, 2015, 22, 1126-1131.	2.2	70
62	ATAQS: A computational software tool for high throughput transition optimization and validation for selected reaction monitoring mass spectrometry. BMC Bioinformatics, 2011, 12, 78.	1.2	67
63	The mzQuantML Data Standard for Mass Spectrometry–based Quantitative Studies in Proteomics. Molecular and Cellular Proteomics, 2013, 12, 2332-2340.	2.5	66
64	TraML–A Standard Format for Exchange of Selected Reaction Monitoring Transition Lists. Molecular and Cellular Proteomics, 2012, 11, R111.015040.	2.5	65
65	The Human Immunopeptidome Project: A Roadmap to Predict and Treat Immune Diseases. Molecular and Cellular Proteomics, 2020, 19, 31-49.	2.5	65
66	Analysis of the Saccharomyces cerevisiae proteome with PeptideAtlas. Genome Biology, 2006, 7, R106.	13.9	60
67	Progress on Identifying and Characterizing the Human Proteome: 2018 Metrics from the HUPO Human Proteome Project. Journal of Proteome Research, 2018, 17, 4031-4041.	1.8	59
68	Progress on the HUPO Draft Human Proteome: 2017 Metrics of the Human Proteome Project. Journal of Proteome Research, 2017, 16, 4281-4287.	1.8	55
69	The mzIdentML Data Standard Version 1.2, Supporting Advances in Proteome Informatics. Molecular and Cellular Proteomics, 2017, 16, 1275-1285.	2.5	55
70	Development of data representation standards by the human proteome organization proteomics standards initiative. Journal of the American Medical Informatics Association: JAMIA, 2015, 22, 495-506.	2.2	54
71	Numerical Compression Schemes for Proteomics Mass Spectrometry Data. Molecular and Cellular Proteomics, 2014, 13, 1537-1542.	2.5	53
72	Quest for Missing Proteins: Update 2015 on Chromosome-Centric Human Proteome Project. Journal of Proteome Research, 2015, 14, 3415-3431.	1.8	53

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73	Using PeptideAtlas, SRMAtlas, and PASSEL: Comprehensive Resources for Discovery and Targeted Proteomics. Current Protocols in Bioinformatics, 2014, 46, 13.25.1-28.	25.8	51
74	Hydra: a scalable proteomic search engine which utilizes the Hadoop distributed computing framework. BMC Bioinformatics, 2012, 13, 324.	1.2	48
75	The Pig PeptideAtlas: A resource for systems biology in animal production and biomedicine. Proteomics, 2016, 16, 634-644.	1.3	47
76	Mapping genetic variations to three-dimensional protein structures to enhance variant interpretation: a proposed framework. Genome Medicine, 2017, 9, 113.	3.6	47
77	Expanding the Use of Spectral Libraries in Proteomics. Journal of Proteome Research, 2018, 17, 4051-4060.	1.8	47
78	Universal Spectrum Identifier for mass spectra. Nature Methods, 2021, 18, 768-770.	9.0	47
79	SBEAMS-Microarray: database software supporting genomic expression analyses for systems biology. BMC Bioinformatics, 2006, 7, 286.	1.2	46
80	Halobacterium salinarum NRC-1 PeptideAtlas: Toward Strategies for Targeted Proteomics and Improved Proteome Coverage. Journal of Proteome Research, 2008, 7, 3755-3764.	1.8	46
81	A tissue-based draft map of the murine MHC class I immunopeptidome. Scientific Data, 2018, 5, 180157.	2.4	45
82	A proteomics sample metadata representation for multiomics integration and big data analysis. Nature Communications, 2021, 12, 5854.	5.8	45
83	A global Staphylococcus aureus proteome resource applied to the in vivo characterization of host-pathogen interactions. Scientific Reports, 2017, 7, 9718.	1.6	42
84	Progress on Identifying and Characterizing the Human Proteome: 2019 Metrics from the HUPO Human Proteome Project. Journal of Proteome Research, 2019, 18, 4098-4107.	1.8	41
85	Trans‐Proteomic Pipeline supports and improves analysis of electron transfer dissociation data sets. Proteomics, 2010, 10, 1190-1195.	1.3	39
86	Research on the Human Proteome Reaches a Major Milestone: >90% of Predicted Human Proteins Now Credibly Detected, According to the HUPO Human Proteome Project. Journal of Proteome Research, 2020, 19, 4735-4746.	1.8	38
87	The Drosophila melanogaster PeptideAtlas facilitates the use of peptide data for improved fly proteomics and genome annotation. BMC Bioinformatics, 2009, 10, 59.	1.2	37
88	The human proteome project: Current state and future direction. Molecular and Cellular Proteomics, 2011, , .	2.5	37
89	Controlled vocabularies and ontologies in proteomics: Overview, principles and practice. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 98-107.	1.1	36
90	The Arabidopsis PeptideAtlas: Harnessing worldwide proteomics data to create a comprehensive community proteomics resource. Plant Cell, 2021, 33, 3421-3453.	3.1	36

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91	Mass Spectrometer Output File Format mzML. Methods in Molecular Biology, 2010, 604, 319-331.	0.4	36
92	A <scp>B</scp>ovine <scp>P</scp>eptide<scp>A</scp>tlas of milk and mammary gland proteomes. Proteomics, 2012, 12, 2895-2899.	1.3	35
93	A Chromosome-centric Human Proteome Project (C-HPP) to Characterize the Sets of Proteins Encoded in Chromosome 17. Journal of Proteome Research, 2013, 12, 45-57.	1.8	35
94	I'll take that to go: Big data bags and minimal identifiers for exchange of large, complex datasets. , 2016, , .		33
95	Progress Identifying and Analyzing the Human Proteome: 2021ÂMetrics from the HUPO Human Proteome Project. Journal of Proteome Research, 2021, 20, 5227-5240.	1.8	30
96	Reproducible big data science: A case study in continuous FAIRness. PLoS ONE, 2019, 14, e0213013.	1.1	29
97	Data Management of Sensitive Human Proteomics Data: Current Practices, Recommendations, and Perspectives for the Future. Molecular and Cellular Proteomics, 2021, 20, 100071.	2.5	25
98	Tiered Human Integrated Sequence Search Databases for Shotgun Proteomics. Journal of Proteome Research, 2016, 15, 4091-4100.	1.8	24
99	A mouse plasma PeptideAtlas as a resource for disease proteomics. Genome Biology, 2008, 9, R93.	13.9	22
100	Using the Human Plasma PeptideAtlas to Study Human Plasma Proteins. Methods in Molecular Biology, 2011, 728, 349-374.	0.4	22
101	Toward Completion of the Human Proteome Parts List: Progress Uncovering Proteins That Are Missing or Have Unknown Function and Developing Analytical Methods. Journal of Proteome Research, 2018, 17, 4023-4030.	1.8	22
102	Proteomics Standards Initiative Extended FASTA Format. Journal of Proteome Research, 2019, 18, 2686-2692.	1.8	22
103	Universal Spectrum Explorer: A Standalone (Web-)Application for Cross-Resource Spectrum Comparison. Journal of Proteome Research, 2021, 20, 3388-3394.	1.8	22
104	A Candida albicans PeptideAtlas. Journal of Proteomics, 2014, 97, 62-68.	1.2	21
105	Highlights of the Biology and Disease-driven Human Proteome Project, 2015â€"2016. Journal of Proteome Research, 2016, 15, 3979-3987.	1.8	21
106	The proBAM and proBed standard formats: enabling a seamless integration of genomics and proteomics data. Genome Biology, 2018, 19, 12.	3.8	21
107	Development of the Minimum Information Specification forIn SituHybridization and Immunohistochemistry Experiments (MISFISHIE). OMICS A Journal of Integrative Biology, 2006, 10, 205-208.	1.0	19
108	jTraML: An Open Source Java API for TraML, the PSI Standard for Sharing SRM Transitions. Journal of Proteome Research, 2011, 10, 5260-5263.	1.8	19

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109	Processing Shotgun Proteomics Data on the Amazon Cloud with the Trans-Proteomic Pipeline. Molecular and Cellular Proteomics, 2015, 14, 399-404.	2.5	19
110	Extending Comet for Global Amino Acid Variant and Post–Translational Modification Analysis Using the PSI Extended FASTA Format. Proteomics, 2020, 20, e1900362.	1.3	18
111	The Equine PeptideAtlas: A resource for developing proteomics–based veterinary research. Proteomics, 2014, 14, 763-773.	1.3	17
112	reSpect: Software for Identification of High and Low Abundance Ion Species in Chimeric Tandem Mass Spectra. Journal of the American Society for Mass Spectrometry, 2015, 26, 1837-1847.	1.2	17
113	Progress in the Chromosome-Centric Human Proteome Project as Highlighted in the Annual Special Issue IV. Journal of Proteome Research, 2016, 15, 3945-3950.	1.8	17
114	Ten Years of Standardizing Proteomic Data: A Report on the HUPO–PSI Spring Workshop. Proteomics, 2012, 12, 2767-2772.	1.3	16
115	Recent Advances in the Chromosome-Centric Human Proteome Project: Missing Proteins in the Spot Light. Journal of Proteome Research, 2015, 14, 3409-3414.	1.8	16
116	A Tandem Mass Spectrometry Sequence Database Search Method for Identification of O-Fucosylated Proteins by Mass Spectrometry. Journal of Proteome Research, 2019, 18, 652-663.	1.8	16
117	A honey bee (Apis mellifera L.) PeptideAtlas crossing castes and tissues. BMC Genomics, 2011, 12, 290.	1.2	15
118	Flexible and Fast Mapping of Peptides to a Proteome with ProteoMapper. Journal of Proteome Research, 2018, 17, 4337-4344.	1.8	15
119	Profiling the Human Phosphoproteome to Estimate the True Extent of Protein Phosphorylation. Journal of Proteome Research, 2022, 21, 1510-1524.	1.8	15
120	Progress and Future Direction of Chromosome-Centric Human Proteome Project. Journal of Proteome Research, 2017, 16, 4253-4258.	1.8	14
121	Proteomics Standards Initiative's ProForma 2.0: Unifying the Encoding of Proteoforms and Peptidoforms. Journal of Proteome Research, 2022, 21, 1189-1195.	1.8	14
122	Method for Independent Estimation of the False Localization Rate for Phosphoproteomics. Journal of Proteome Research, 2022, 21, 1603-1615.	1.8	14
123	mzMLb: A Future-Proof Raw Mass Spectrometry Data Format Based on Standards-Compliant mzML and Optimized for Speed and Storage Requirements. Journal of Proteome Research, 2021, 20, 172-183.	1.8	12
124	mspecLINE: bridging knowledge of human disease with the proteome. BMC Medical Genomics, 2010, 3, 7.	0.7	9
125	An Open Data Format for Visualization and Analysis of Cross-Linked Mass Spectrometry Results. Journal of the American Society for Mass Spectrometry, 2016, 27, 1728-1734.	1.2	9
126	The PeptideAtlas of the Domestic Laying Hen. Journal of Proteome Research, 2017, 16, 1352-1363.	1.8	9

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127	Optical Identification of the X-Ray Burster X1746âˇ370 in the Globular Cluster NGC 6441. Astronomical Journal, 2002, 123, 3255-3262.	1.9	9
128	A comprehensive Candida albicans PeptideAtlas build enables deep proteome coverage. Journal of Proteomics, 2016, 131, 122-130.	1.2	8
129	Tandem Mass Spectrometry Spectral Libraries and Library Searching. Methods in Molecular Biology, 2011, 696, 225-232.	0.4	8
130	BioHackathon 2015: Semantics of data for life sciences and reproducible research. F1000Research, 2020, 9, 136.	0.8	5
131	Advances in Identifying and Characterizing the Human Proteome. Journal of Proteome Research, 2019, 18, 4079-4084.	1.8	4
132	A Comprehensive Evaluation of Consensus Spectrum Generation Methods in Proteomics. Journal of Proteome Research, 2022, 21, 1566-1574.	1.8	2
133	Interfaces to PeptideAtlas: a case study of standard data access systems. Briefings in Bioinformatics, 2012, 13, 615-626.	3.2	1
134	Human Plasma PeptideAtlas. , 0, , 317-322.		0
135	Standards for Functional Genomics. , 2009, , 293-329.		0