Eric W Deutsch

List of Publications by Year
in descending order

135 papers	22,536 citations

18436

62 h-index

10127

140 g-index

162 all docs	162 docs citations	162 times ranked	27766 citing authors

#	Article	IF	Citations
1	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
2	A Comprehensive Evaluation of Consensus Spectrum Generation Methods in Proteomics. Journal of Proteome Research, 2022, 21, 1566-1574.	1.8	2
3	Profiling the Human Phosphoproteome to Estimate the True Extent of Protein Phosphorylation. Journal of Proteome Research, 2022, 21, 1510-1524.	1.8	15
4	Method for Independent Estimation of the False Localization Rate for Phosphoproteomics. Journal of Proteome Research, 2022, 21, 1603-1615.	1.8	14
5	Standardized annotation of translated open reading frames. Nature Biotechnology, 2022, 40, 994-999.	9.4	86
6	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
7	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
8	Universal Spectrum Explorer: A Standalone (Web-)Application for Cross-Resource Spectrum Comparison. Journal of Proteome Research, 2021, 20, 3388-3394.	1.8	22
9	Universal Spectrum Identifier for mass spectra. Nature Methods, 2021, 18, 768-770.	9.0	47
10	The Arabidopsis PeptideAtlas: Harnessing worldwide proteomics data to create a comprehensive community proteomics resource. Plant Cell, 2021, 33, 3421-3453.	3.1	36
11	A proteomics sample metadata representation for multiomics integration and big data analysis. Nature Communications, 2021, 12, 5854.	5.8	45
12	Advances and Utility of the Human Plasma Proteome. Journal of Proteome Research, 2021, 20, 5241-5263.	1.8	86
13	Progress Identifying and Analyzing the Human Proteome: 2021 Metrics from the HUPO Human Proteome Project. Journal of Proteome Research, 2021, 20, 5227-5240.	1.8	30
14	The ProteomeXchange consortium in 2020: enabling 'big data' approaches in proteomics. Nucleic Acids Research, 2020, 48, D1145-D1152.	6.5	491
15	The Human Immunopeptidome Project: A Roadmap to Predict and Treat Immune Diseases. Molecular and Cellular Proteomics, 2020, 19, 31-49.	2.5	65
16	A high-stringency blueprint of the human proteome. Nature Communications, 2020, 11, 5301.	5.8	152
17	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
18	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

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19	BioHackathon 2015: Semantics of data for life sciences and reproducible research. F1000Research, 2020, 9, 136.	0.8	5
20	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
21	PTMProphet: Fast and Accurate Mass Modification Localization for the Trans-Proteomic Pipeline. Journal of Proteome Research, 2019, 18, 4262-4272.	1.8	80
22	Human Proteome Project Mass Spectrometry Data Interpretation Guidelines 3.0. Journal of Proteome Research, 2019, 18, 4108-4116.	1.8	82
23	Mass Spectrometry-Based Plasma Proteomics: Considerations from Sample Collection to Achieving Translational Data. Journal of Proteome Research, 2019, 18, 4085-4097.	1.8	128
24	Proteomics Standards Initiative Extended FASTA Format. Journal of Proteome Research, 2019, 18, 2686-2692.	1.8	22
25	Reproducible big data science: A case study in continuous FAIRness. PLoS ONE, 2019, 14, e0213013.	1.1	29
26	Advances in Identifying and Characterizing the Human Proteome. Journal of Proteome Research, 2019, 18, 4079-4084.	1.8	4
27	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
28	The SysteMHC Atlas project. Nucleic Acids Research, 2018, 46, D1237-D1247.	6.5	119
29	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
30	Expanding the Use of Spectral Libraries in Proteomics. Journal of Proteome Research, 2018, 17, 4051-4060.	1.8	47
31	Flexible and Fast Mapping of Peptides to a Proteome with ProteoMapper. Journal of Proteome Research, 2018, 17, 4337-4344.	1.8	15
32	The proBAM and proBed standard formats: enabling a seamless integration of genomics and proteomics data. Genome Biology, 2018, 19, 12.	3.8	21
33	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
34	A tissue-based draft map of the murine MHC class I immunopeptidome. Scientific Data, 2018, 5, 180157.	2.4	45
35	Building ProteomeTools based on a complete synthetic human proteome. Nature Methods, 2017, 14, 259-262.	9.0	182
36	The PeptideAtlas of the Domestic Laying Hen. Journal of Proteome Research, 2017, 16, 1352-1363.	1.8	9

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37	Discovering and linking public omics data sets using the Omics Discovery Index. Nature Biotechnology, 2017, 35, 406-409.	9.4	159
38	Proteomics Standards Initiative: Fifteen Years of Progress and Future Work. Journal of Proteome Research, 2017, 16, 4288-4298.	1.8	87
39	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
40	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
41	A global Staphylococcus aureus proteome resource applied to the in vivo characterization of host-pathogen interactions. Scientific Reports, 2017, 7, 9718.	1.6	42
42	Progress and Future Direction of Chromosome-Centric Human Proteome Project. Journal of Proteome Research, 2017, 16, 4253-4258.	1.8	14
43	The mzIdentML Data Standard Version 1.2, Supporting Advances in Proteome Informatics. Molecular and Cellular Proteomics, 2017, 16, 1275-1285.	2.5	55
44	The ProteomeXchange consortium in 2017: supporting the cultural change in proteomics public data deposition. Nucleic Acids Research, 2017, 45, D1100-D1106.	6.5	860
45	Mapping genetic variations to three-dimensional protein structures to enhance variant interpretation: a proposed framework. Genome Medicine, 2017, 9, 113.	3.6	47
46	Predictive Big Data Analytics: A Study of Parkinson's Disease Using Large, Complex, Heterogeneous, Incongruent, Multi-Source and Incomplete Observations. PLoS ONE, 2016, 11, e0157077.	1.1	94
47	The Pig PeptideAtlas: A resource for systems biology in animal production and biomedicine. Proteomics, 2016, 16, 634-644.	1.3	47
48	I'll take that to go: Big data bags and minimal identifiers for exchange of large, complex datasets. , 2016, , .		33
49	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
50	Human Proteome Project Mass Spectrometry Data Interpretation Guidelines 2.1. Journal of Proteome Research, 2016, 15, 3961-3970.	1.8	158
51	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
52	Highlights of the Biology and Disease-driven Human Proteome Project, 2015–2016. Journal of Proteome Research, 2016, 15, 3979-3987.	1.8	21
53	Tiered Human Integrated Sequence Search Databases for Shotgun Proteomics. Journal of Proteome Research, 2016, 15, 4091-4100.	1.8	24
54	Human SRMAtlas: A Resource of Targeted Assays to Quantify the Complete Human Proteome. Cell, 2016, 166, 766-778.	13.5	295

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55	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
56	A comprehensive Candida albicans PeptideAtlas build enables deep proteome coverage. Journal of Proteomics, 2016, 131, 122-130.	1.2	8
57	Trans–Proteomic Pipeline, a standardized data processing pipeline for large–scale reproducible proteomics informatics. Proteomics - Clinical Applications, 2015, 9, 745-754.	0.8	319
58	Processing Shotgun Proteomics Data on the Amazon Cloud with the Trans-Proteomic Pipeline. Molecular and Cellular Proteomics, 2015, 14, 399-404.	2.5	19
59	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
60	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
61	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
62	Quest for Missing Proteins: Update 2015 on Chromosome-Centric Human Proteome Project. Journal of Proteome Research, 2015, 14, 3415-3431.	1.8	53
63	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
64	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
65	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
66	An open-source computational and data resource to analyze digital maps of immunopeptidomes. ELife, 2015, 4, .	2.8	107
67	The Equine PeptideAtlas: A resource for developing proteomics–based veterinary research. Proteomics, 2014, 14, 763-773.	1.3	17
68	A Candida albicans PeptideAtlas. Journal of Proteomics, 2014, 97, 62-68.	1.2	21
69	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
70	ProteomeXchange provides globally coordinated proteomics data submission and dissemination. Nature Biotechnology, 2014, 32, 223-226.	9.4	2,505
71	Metrics for the Human Proteome Project 2013–2014 and Strategies for Finding Missing Proteins. Journal of Proteome Research, 2014, 13, 15-20.	1.8	124
72	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

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73	Numerical Compression Schemes for Proteomics Mass Spectrometry Data. Molecular and Cellular Proteomics, 2014, 13, 1537-1542.	2.5	53
74	Controlled vocabularies and ontologies in proteomics: Overview, principles and practice. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 98-107.	1.1	36
75	A repository of assays to quantify 10,000 human proteins by SWATH-MS. Scientific Data, 2014, 1, 140031.	2.4	370
76	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
77	Combining Results of Multiple Search Engines in Proteomics. Molecular and Cellular Proteomics, 2013, 12, 2383-2393.	2.5	154
78	A complete mass-spectrometric map of the yeast proteome applied to quantitative trait analysis. Nature, 2013, 494, 266-270.	13.7	307
79	The State of the Human Proteome in 2012 as Viewed through PeptideAtlas. Journal of Proteome Research, 2013, 12, 162-171.	1.8	115
80	The mzQuantML Data Standard for Mass Spectrometry–based Quantitative Studies in Proteomics. Molecular and Cellular Proteomics, 2013, 12, 2332-2340.	2.5	66
81	The HUPO proteomics standards initiative- mass spectrometry controlled vocabulary. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat009-bat009.	1.4	76
82	File Formats Commonly Used in Mass Spectrometry Proteomics. Molecular and Cellular Proteomics, 2012, 11, 1612-1621.	2.5	80
83	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
84	TraML—A Standard Format for Exchange of Selected Reaction Monitoring Transition Lists. Molecular and Cellular Proteomics, 2012, 11, R111.015040.	2.5	65
85	A cross-platform toolkit for mass spectrometry and proteomics. Nature Biotechnology, 2012, 30, 918-920.	9.4	2,794
86	Interfaces to PeptideAtlas: a case study of standard data access systems. Briefings in Bioinformatics, 2012, 13, 615-626.	3.2	1
87	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
88	Ten Years of Standardizing Proteomic Data: A Report on the HUPO–PSI Spring Workshop. Proteomics, 2012, 12, 2767-2772.	1.3	16
89	Hydra: a scalable proteomic search engine which utilizes the Hadoop distributed computing framework. BMC Bioinformatics, 2012, 13, 324.	1.2	48
90	Reproducible Quantification of Cancer-Associated Proteins in Body Fluids Using Targeted Proteomics. Science Translational Medicine, 2012, 4, 142ra94.	5.8	236

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91	PASSEL: The PeptideAtlas SRM experiment library. Proteomics, 2012, 12, 1170-1175.	1.3	200
92	The Chromosome-Centric Human Proteome Project for cataloging proteins encoded in the genome. Nature Biotechnology, 2012, 30, 221-223.	9.4	281
93	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
94	Using the Human Plasma PeptideAtlas to Study Human Plasma Proteins. Methods in Molecular Biology, 2011, 728, 349-374.	0.4	22
95	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
96	Data Standards for Omics Data: The Basis of Data Sharing and Reuse. Methods in Molecular Biology, 2011, 719, 31-69.	0.4	73
97	A High-Confidence Human Plasma Proteome Reference Set with Estimated Concentrations in PeptideAtlas. Molecular and Cellular Proteomics, 2011, 10, M110.006353.	2.5	381
98	The Human Proteome Project: Current State and Future Direction. Molecular and Cellular Proteomics, 2011, 10, M111.009993.	2.5	294
99	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
100	A honey bee (Apis mellifera L.) PeptideAtlas crossing castes and tissues. BMC Genomics, 2011, 12, 290.	1.2	15
101	mzML—a Community Standard for Mass Spectrometry Data. Molecular and Cellular Proteomics, 2011, 10, R110.000133.	2.5	555
102	The human proteome project: Current state and future direction. Molecular and Cellular Proteomics, 2011, , .	2.5	37
103	Tandem Mass Spectrometry Spectral Libraries and Library Searching. Methods in Molecular Biology, 2011, 696, 225-232.	0.4	8
104	mspecLINE: bridging knowledge of human disease with the proteome. BMC Medical Genomics, 2010, 3, 7.	0.7	9
105	A guided tour of the Trans—Proteomic Pipeline. Proteomics, 2010, 10, 1150-1159.	1.3	710
106	Trans—Proteomic Pipeline supports and improves analysis of electron transfer dissociation data sets. Proteomics, 2010, 10, 1190-1195.	1.3	39
107	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
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109	Mass Spectrometer Output File Format mzML. Methods in Molecular Biology, 2010, 604, 319-331.	0.4	36
110	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
111	Proteome-wide cellular protein concentrations of the human pathogen Leptospira interrogans. Nature, 2009, 460, 762-765.	13.7	402
112	MaRiMba: A Software Application for Spectral Library-Based MRM Transition List Assembly. Journal of Proteome Research, 2009, 8, 4396-4405.	1.8	80
113	Standards for Functional Genomics. , 2009, , 293-329.		0
114	mzML: A single, unifying data format for mass spectrometer output. Proteomics, 2008, 8, 2776-2777.	1.3	158
115	PeptideAtlas: a resource for target selection for emerging targeted proteomics workflows. EMBO Reports, 2008, 9, 429-434.	2.0	516
116	Guidelines for reporting the use of mass spectrometry in proteomics. Nature Biotechnology, 2008, 26, 860-861.	9.4	82
117	Minimum information specification for in situ hybridization and immunohistochemistry experiments (MISFISHIE). Nature Biotechnology, 2008, 26, 305-312.	9.4	111
118	Building consensus spectral libraries for peptide identification in proteomics. Nature Methods, 2008, 5, 873-875.	9.0	255
119	A database of mass spectrometric assays for the yeast proteome. Nature Methods, 2008, 5, 913-914.	9.0	205
120	Data analysis and bioinformatics tools for tandem mass spectrometry in proteomics. Physiological Genomics, 2008, 33, 18-25.	1.0	137
121	A mouse plasma PeptideAtlas as a resource for disease proteomics. Genome Biology, 2008, 9, R93.	13.9	22
122	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
123	Targeted Quantitative Analysis of Streptococcus pyogenes Virulence Factors by Multiple Reaction Monitoring. Molecular and Cellular Proteomics, 2008, 7, 1489-1500.	2.5	189
124	Development and validation of a spectral library searching method for peptide identification from MS/MS. Proteomics, 2007, 7, 655-667.	1.3	487
125	The minimum information about a proteomics experiment (MIAPE). Nature Biotechnology, 2007, 25, 887-893.	9.4	694
126	Analysis of the Saccharomyces cerevisiae proteome with PeptideAtlas. Genome Biology, 2006, 7, R106.	13.9	60

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127	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
128	SBEAMS-Microarray: database software supporting genomic expression analyses for systems biology. BMC Bioinformatics, 2006, 7, 286.	1.2	46
129	The PeptideAtlas project. Nucleic Acids Research, 2006, 34, D655-D658.	6.5	733
130	Human Plasma PeptideAtlas. Proteomics, 2005, 5, 3497-3500.	1.3	132
131	A common open representation of mass spectrometry data and its application to proteomics research. Nature Biotechnology, 2004, 22, 1459-1466.	9.4	724
132	Integration with the human genome of peptide sequences obtained by high-throughput mass spectrometry. Genome Biology, 2004, 6, R9.	13.9	252
133	Design and implementation of microarray gene expression markup language (MAGE-ML). Genome Biology, 2002, 3, RESEARCH0046.	3.8	350
134	Optical Identification of the X-Ray Burster X1746â�’370 in the Globular Cluster NGC 6441. Astronomical Journal, 2002, 123, 3255-3262.	1.9	9
135	Human Plasma PeptideAtlas. , 0, , 317-322.		0