

Eric W Deutsch

List of Publications by Year in descending order

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Version: 2024-02-01

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	A cross-platform toolkit for mass spectrometry and proteomics. <i>Nature Biotechnology</i> , 2012, 30, 918-920.	9.4	2,794
2	ProteomeXchange provides globally coordinated proteomics data submission and dissemination. <i>Nature Biotechnology</i> , 2014, 32, 223-226.	9.4	2,505
3	The ProteomeXchange consortium in 2017: supporting the cultural change in proteomics public data deposition. <i>Nucleic Acids Research</i> , 2017, 45, D1100-D1106.	6.5	860
4	The PeptideAtlas project. <i>Nucleic Acids Research</i> , 2006, 34, D655-D658.	6.5	733
5	A common open representation of mass spectrometry data and its application to proteomics research. <i>Nature Biotechnology</i> , 2004, 22, 1459-1466.	9.4	724
6	A guided tour of the Trans-Proteomic Pipeline. <i>Proteomics</i> , 2010, 10, 1150-1159.	1.3	710
7	The minimum information about a proteomics experiment (MIAPE). <i>Nature Biotechnology</i> , 2007, 25, 887-893.	9.4	694
8	mzML—a Community Standard for Mass Spectrometry Data. <i>Molecular and Cellular Proteomics</i> , 2011, 10, R110.000133.	2.5	555
9	PeptideAtlas: a resource for target selection for emerging targeted proteomics workflows. <i>EMBO Reports</i> , 2008, 9, 429-434.	2.0	516
10	The ProteomeXchange consortium in 2020: enabling “big data” approaches in proteomics. <i>Nucleic Acids Research</i> , 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. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.007690.	2.5	490
12	Development and validation of a spectral library searching method for peptide identification from MS/MS. <i>Proteomics</i> , 2007, 7, 655-667.	1.3	487
13	Proteome-wide cellular protein concentrations of the human pathogen <i>Leptospira interrogans</i> . <i>Nature</i> , 2009, 460, 762-765.	13.7	402
14	A High-Confidence Human Plasma Proteome Reference Set with Estimated Concentrations in PeptideAtlas. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.006353.	2.5	381
15	A repository of assays to quantify 10,000 human proteins by SWATH-MS. <i>Scientific Data</i> , 2014, 1, 140031.	2.4	370
16	Design and implementation of microarray gene expression markup language (MAGE-ML). <i>Genome Biology</i> , 2002, 3, RESEARCH0046.	3.8	350
17	Trans-Proteomic Pipeline, a standardized data processing pipeline for large-scale reproducible proteomics informatics. <i>Proteomics - Clinical Applications</i> , 2015, 9, 745-754.	0.8	319
18	A complete mass-spectrometric map of the yeast proteome applied to quantitative trait analysis. <i>Nature</i> , 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. <i>Cell</i> , 2016, 166, 766-778.	13.5	295
20	The Human Proteome Project: Current State and Future Direction. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.009993.	2.5	294
21	The Chromosome-Centric Human Proteome Project for cataloging proteins encoded in the genome. <i>Nature Biotechnology</i> , 2012, 30, 221-223.	9.4	281
22	Building consensus spectral libraries for peptide identification in proteomics. <i>Nature Methods</i> , 2008, 5, 873-875.	9.0	255
23	Integration with the human genome of peptide sequences obtained by high-throughput mass spectrometry. <i>Genome Biology</i> , 2004, 6, R9.	13.9	252
24	Reproducible Quantification of Cancer-Associated Proteins in Body Fluids Using Targeted Proteomics. <i>Science Translational Medicine</i> , 2012, 4, 142ra94.	5.8	236
25	A database of mass spectrometric assays for the yeast proteome. <i>Nature Methods</i> , 2008, 5, 913-914.	9.0	205
26	<scp>PASSEL</scp>: The <scp>P</scp>eptide<scp>A</scp>tlas <scp>SRM</scp>experiment library. <i>Proteomics</i> , 2012, 12, 1170-1175.	1.3	200
27	Targeted Quantitative Analysis of <i>Streptococcus pyogenes</i> Virulence Factors by Multiple Reaction Monitoring. <i>Molecular and Cellular Proteomics</i> , 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. <i>Journal of Proteome Research</i> , 2017, 16, 4299-4310.	1.8	185
29	Building ProteomeTools based on a complete synthetic human proteome. <i>Nature Methods</i> , 2017, 14, 259-262.	9.0	182
30	The mzIdentML Data Standard for Mass Spectrometry-Based Proteomics Results. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.014381-1-M111.014381-10.	2.5	175
31	Discovering and linking public omics data sets using the Omics Discovery Index. <i>Nature Biotechnology</i> , 2017, 35, 406-409.	9.4	159
32	mzML: A single, unifying data format for mass spectrometer output. <i>Proteomics</i> , 2008, 8, 2776-2777.	1.3	158
33	Human Proteome Project Mass Spectrometry Data Interpretation Guidelines 2.1. <i>Journal of Proteome Research</i> , 2016, 15, 3961-3970.	1.8	158
34	Combining Results of Multiple Search Engines in Proteomics. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2383-2393.	2.5	154
35	A high-stringency blueprint of the human proteome. <i>Nature Communications</i> , 2020, 11, 5301.	5.8	152
36	Data analysis and bioinformatics tools for tandem mass spectrometry in proteomics. <i>Physiological Genomics</i> , 2008, 33, 18-25.	1.0	137

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

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

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

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91	Mass Spectrometer Output File Format mzML. <i>Methods in Molecular Biology</i> , 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. <i>Proteomics</i> , 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. <i>Journal of Proteome Research</i> , 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: 2021 Metrics from the HUPO Human Proteome Project. <i>Journal of Proteome Research</i> , 2021, 20, 5227-5240.	1.8	30
96	Reproducible big data science: A case study in continuous FAIRness. <i>PLoS ONE</i> , 2019, 14, e0213013.	1.1	29
97	Data Management of Sensitive Human Proteomics Data: Current Practices, Recommendations, and Perspectives for the Future. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100071.	2.5	25
98	Tiered Human Integrated Sequence Search Databases for Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2016, 15, 4091-4100.	1.8	24
99	A mouse plasma PeptideAtlas as a resource for disease proteomics. <i>Genome Biology</i> , 2008, 9, R93.	13.9	22
100	Using the Human Plasma PeptideAtlas to Study Human Plasma Proteins. <i>Methods in Molecular Biology</i> , 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. <i>Journal of Proteome Research</i> , 2018, 17, 4023-4030.	1.8	22
102	Proteomics Standards Initiative Extended FASTA Format. <i>Journal of Proteome Research</i> , 2019, 18, 2686-2692.	1.8	22
103	Universal Spectrum Explorer: A Standalone (Web-)Application for Cross-Resource Spectrum Comparison. <i>Journal of Proteome Research</i> , 2021, 20, 3388-3394.	1.8	22
104	A <i>Candida albicans</i> PeptideAtlas. <i>Journal of Proteomics</i> , 2014, 97, 62-68.	1.2	21
105	Highlights of the Biology and Disease-driven Human Proteome Project, 2015-2016. <i>Journal of Proteome Research</i> , 2016, 15, 3979-3987.	1.8	21
106	The proBAM and proBed standard formats: enabling a seamless integration of genomics and proteomics data. <i>Genome Biology</i> , 2018, 19, 12.	3.8	21
107	Development of the Minimum Information Specification for In Situ Hybridization and Immunohistochemistry Experiments (MISFISHIE). <i>OMICS A Journal of Integrative Biology</i> , 2006, 10, 205-208.	1.0	19
108	jTraML: An Open Source Java API for TraML, the PSI Standard for Sharing SRM Transitions. <i>Journal of Proteome Research</i> , 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. <i>Molecular and Cellular Proteomics</i> , 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. <i>Proteomics</i> , 2020, 20, e1900362.	1.3	18
111	The Equine PeptideAtlas: A resource for developing proteomics-based veterinary research. <i>Proteomics</i> , 2014, 14, 763-773.	1.3	17
112	reSpect: Software for Identification of High and Low Abundance Ion Species in Chimeric Tandem Mass Spectra. <i>Journal of the American Society for Mass Spectrometry</i> , 2015, 26, 1837-1847.	1.2	17
113	Progress in the Chromosome-Centric Human Proteome Project as Highlighted in the Annual Special Issue IV. <i>Journal of Proteome Research</i> , 2016, 15, 3945-3950.	1.8	17
114	Ten Years of Standardizing Proteomic Data: A Report on the HUPO-PSI Spring Workshop. <i>Proteomics</i> , 2012, 12, 2767-2772.	1.3	16
115	Recent Advances in the Chromosome-Centric Human Proteome Project: Missing Proteins in the Spot Light. <i>Journal of Proteome Research</i> , 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. <i>Journal of Proteome Research</i> , 2019, 18, 652-663.	1.8	16
117	A honey bee (<i>Apis mellifera</i> L.) PeptideAtlas crossing castes and tissues. <i>BMC Genomics</i> , 2011, 12, 290.	1.2	15
118	Flexible and Fast Mapping of Peptides to a Proteome with ProteoMapper. <i>Journal of Proteome Research</i> , 2018, 17, 4337-4344.	1.8	15
119	Profiling the Human Phosphoproteome to Estimate the True Extent of Protein Phosphorylation. <i>Journal of Proteome Research</i> , 2022, 21, 1510-1524.	1.8	15
120	Progress and Future Direction of Chromosome-Centric Human Proteome Project. <i>Journal of Proteome Research</i> , 2017, 16, 4253-4258.	1.8	14
121	Proteomics Standards Initiative's ProForma 2.0: Unifying the Encoding of Proteoforms and Peptidoforms. <i>Journal of Proteome Research</i> , 2022, 21, 1189-1195.	1.8	14
122	Method for Independent Estimation of the False Localization Rate for Phosphoproteomics. <i>Journal of Proteome Research</i> , 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. <i>Journal of Proteome Research</i> , 2021, 20, 172-183.	1.8	12
124	mspecLINE: bridging knowledge of human disease with the proteome. <i>BMC Medical Genomics</i> , 2010, 3, 7.	0.7	9
125	An Open Data Format for Visualization and Analysis of Cross-Linked Mass Spectrometry Results. <i>Journal of the American Society for Mass Spectrometry</i> , 2016, 27, 1728-1734.	1.2	9
126	The PeptideAtlas of the Domestic Laying Hen. <i>Journal of Proteome Research</i> , 2017, 16, 1352-1363.	1.8	9

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127	Optical Identification of the X-Ray Burster X1746â~370 in the Globular Cluster NGC 6441. <i>Astronomical Journal</i> , 2002, 123, 3255-3262.	1.9	9
128	A comprehensive <i>Candida albicans</i> PeptideAtlas build enables deep proteome coverage. <i>Journal of Proteomics</i> , 2016, 131, 122-130.	1.2	8
129	Tandem Mass Spectrometry Spectral Libraries and Library Searching. <i>Methods in Molecular Biology</i> , 2011, 696, 225-232.	0.4	8
130	BioHackathon 2015: Semantics of data for life sciences and reproducible research. <i>F1000Research</i> , 2020, 9, 136.	0.8	5
131	Advances in Identifying and Characterizing the Human Proteome. <i>Journal of Proteome Research</i> , 2019, 18, 4079-4084.	1.8	4
132	A Comprehensive Evaluation of Consensus Spectrum Generation Methods in Proteomics. <i>Journal of Proteome Research</i> , 2022, 21, 1566-1574.	1.8	2
133	Interfaces to PeptideAtlas: a case study of standard data access systems. <i>Briefings in Bioinformatics</i> , 2012, 13, 615-626.	3.2	1
134	Human Plasma PeptideAtlas. , 0, , 317-322.		0
135	Standards for Functional Genomics. , 2009, , 293-329.		0