

Juergen Cox

List of Publications by Year in descending order

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145
papers

65,968
citations

5248

83
h-index

8835

145
g-index

162
all docs

162
docs citations

162
times ranked

70128
citing authors

#	ARTICLE	IF	CITATIONS
1	MaxQuant enables high peptide identification rates, individualized p.p.b.-range mass accuracies and proteome-wide protein quantification. <i>Nature Biotechnology</i> , 2008, 26, 1367-1372.	9.4	12,966
2	The PRIDE database and related tools and resources in 2019: improving support for quantification data. <i>Nucleic Acids Research</i> , 2019, 47, D442-D450.	6.5	6,449
3	The Perseus computational platform for comprehensive analysis of (prote)omics data. <i>Nature Methods</i> , 2016, 13, 731-740.	9.0	6,181
4	Andromeda: A Peptide Search Engine Integrated into the MaxQuant Environment. <i>Journal of Proteome Research</i> , 2011, 10, 1794-1805.	1.8	4,935
5	Accurate Proteome-wide Label-free Quantification by Delayed Normalization and Maximal Peptide Ratio Extraction, Termed MaxLFQ. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2513-2526.	2.5	4,178
6	The MaxQuant computational platform for mass spectrometry-based shotgun proteomics. <i>Nature Protocols</i> , 2016, 11, 2301-2319.	5.5	3,353
7	Quantitative Phosphoproteomics Reveals Widespread Full Phosphorylation Site Occupancy During Mitosis. <i>Science Signaling</i> , 2010, 3, ra3.	1.6	1,319
8	A Human Interactome in Three Quantitative Dimensions Organized by Stoichiometries and Abundances. <i>Cell</i> , 2015, 163, 712-723.	13.5	1,132
9	Deep proteome and transcriptome mapping of a human cancer cell line. <i>Molecular Systems Biology</i> , 2011, 7, 548.	3.2	878
10	Ultradeep Human Phosphoproteome Reveals a Distinct Regulatory Nature of Tyr and Ser/Thr-Based Signaling. <i>Cell Reports</i> , 2014, 8, 1583-1594.	2.9	839
11	Comprehensive mass-spectrometry-based proteome quantification of haploid versus diploid yeast. <i>Nature</i> , 2008, 455, 1251-1254.	13.7	835
12	A practical guide to the MaxQuant computational platform for SILAC-based quantitative proteomics. <i>Nature Protocols</i> , 2009, 4, 698-705.	5.5	769
13	A Proteome-wide, Quantitative Survey of In Vivo Ubiquitylation Sites Reveals Widespread Regulatory Roles. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.013284.	2.5	754
14	Mass Spectrometry-based Proteomics Using Q Exactive, a High-performance Benchtop Quadrupole Orbitrap Mass Spectrometer. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.011015.	2.5	701
15	Comparative Proteomic Analysis of Eleven Common Cell Lines Reveals Ubiquitous but Varying Expression of Most Proteins. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.014050.	2.5	701
16	Quantitative, High-Resolution Proteomics for Data-Driven Systems Biology. <i>Annual Review of Biochemistry</i> , 2011, 80, 273-299.	5.0	630
17	Direct identification of clinically relevant neoepitopes presented on native human melanoma tissue by mass spectrometry. <i>Nature Communications</i> , 2016, 7, 13404.	5.8	613
18	Online Parallel Accumulation-Serial Fragmentation (PASEF) with a Novel Trapped Ion Mobility Mass Spectrometer. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 2534-2545.	2.5	602

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19	More than 100,000 Detectable Peptide Species Elute in Single Shotgun Proteomics Runs but the Majority is Inaccessible to Data-Dependent LC-MS/MS. <i>Journal of Proteome Research</i> , 2011, 10, 1785-1793.	1.8	595
20	Quantitative Proteomics Reveals Subset-Specific Viral Recognition in Dendritic Cells. <i>Immunity</i> , 2010, 32, 279-289.	6.6	544
21	1D and 2D annotation enrichment: a statistical method integrating quantitative proteomics with complementary high-throughput data. <i>BMC Bioinformatics</i> , 2012, 13, S12.	1.2	542
22	A "Proteomic Ruler" for Protein Copy Number and Concentration Estimation without Spike-in Standards. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3497-3506.	2.5	530
23	Super-SILAC mix for quantitative proteomics of human tumor tissue. <i>Nature Methods</i> , 2010, 7, 383-385.	9.0	480
24	Global, quantitative and dynamic mapping of protein subcellular localization. <i>ELife</i> , 2016, 5, .	2.8	469
25	Quantitative proteomics combined with BAC TransgeneOmics reveals in vivo protein interactions. <i>Journal of Cell Biology</i> , 2010, 189, 739-754.	2.3	427
26	System-Wide Changes to SUMO Modifications in Response to Heat Shock. <i>Science Signaling</i> , 2009, 2, ra24.	1.6	415
27	Is Proteomics the New Genomics?. <i>Cell</i> , 2007, 130, 395-398.	13.5	410
28	PHOSIDA (phosphorylation site database): management, structural and evolutionary investigation, and prediction of phosphosites. <i>Genome Biology</i> , 2007, 8, R250.	13.9	410
29	Perseus: A Bioinformatics Platform for Integrative Analysis of Proteomics Data in Cancer Research. <i>Methods in Molecular Biology</i> , 2018, 1711, 133-148.	0.4	389
30	Global analysis of genome, transcriptome and proteome reveals the response to aneuploidy in human cells. <i>Molecular Systems Biology</i> , 2012, 8, 608.	3.2	379
31	In-Vivo Quantitative Proteomics Reveals a Key Contribution of Post-Transcriptional Mechanisms to the Circadian Regulation of Liver Metabolism. <i>PLoS Genetics</i> , 2014, 10, e1004047.	1.5	358
32	System-wide Perturbation Analysis with Nearly Complete Coverage of the Yeast Proteome by Single-shot Ultra HPLC Runs on a Bench Top Orbitrap. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.013722.	2.5	350
33	The nucleolus functions as a phase-separated protein quality control compartment. <i>Science</i> , 2019, 365, 342-347.	6.0	348
34	The Coming Age of Complete, Accurate, and Ubiquitous Proteomes. <i>Molecular Cell</i> , 2013, 49, 583-590.	4.5	329
35	Defining the transcriptome and proteome in three functionally different human cell lines. <i>Molecular Systems Biology</i> , 2010, 6, 450.	3.2	324
36	Deep and Highly Sensitive Proteome Coverage by LC-MS/MS Without Prefractionation. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.003699.	2.5	311

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37	Ultra High Resolution Linear Ion Trap Orbitrap Mass Spectrometer (Orbitrap Elite) Facilitates Top Down LC MS/MS and Versatile Peptide Fragmentation Modes. <i>Molecular and Cellular Proteomics</i> , 2012, 11, O111.013698.	2.5	303
38	BoxCar acquisition method enables single-shot proteomics at a depth of 10,000 proteins in 100 minutes. <i>Nature Methods</i> , 2018, 15, 440-448.	9.0	303
39	Mislocalized Activation of Oncogenic RTKs Switches Downstream Signaling Outcomes. <i>Molecular Cell</i> , 2009, 36, 326-339.	4.5	278
40	Iodoacetamide-induced artifact mimics ubiquitination in mass spectrometry. <i>Nature Methods</i> , 2008, 5, 459-460.	9.0	268
41	Use of stable isotope labeling by amino acids in cell culture as a spike-in standard in quantitative proteomics. <i>Nature Protocols</i> , 2011, 6, 147-157.	5.5	265
42	Stable Isotope Labeling by Amino Acids in Cell Culture (SILAC) and Proteome Quantitation of Mouse Embryonic Stem Cells to a Depth of 5,111 Proteins. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 672-683.	2.5	261
43	Proteomic maps of breast cancer subtypes. <i>Nature Communications</i> , 2016, 7, 10259.	5.8	256
44	Visualization of LC-MS/MS proteomics data in MaxQuant. <i>Proteomics</i> , 2015, 15, 1453-1456.	1.3	248
45	MSQuant, an Open Source Platform for Mass Spectrometry-Based Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2010, 9, 393-403.	1.8	237
46	Acetylation site specificities of lysine deacetylase inhibitors in human cells. <i>Nature Biotechnology</i> , 2015, 33, 415-423.	9.4	237
47	Guidelines for Genome-Scale Analysis of Biological Rhythms. <i>Journal of Biological Rhythms</i> , 2017, 32, 380-393.	1.4	237
48	Deep Proteomics of Mouse Skeletal Muscle Enables Quantitation of Protein Isoforms, Metabolic Pathways, and Transcription Factors*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 841-853.	2.5	234
49	Proteomics on an Orbitrap Benchtop Mass Spectrometer Using All-ion Fragmentation. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 2252-2261.	2.5	213
50	Initial Quantitative Proteomic Map of 28 Mouse Tissues Using the SILAC Mouse. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 1709-1722.	2.5	204
51	High-quality MS/MS spectrum prediction for data-dependent and data-independent acquisition data analysis. <i>Nature Methods</i> , 2019, 16, 519-525.	9.0	194
52	Proteomics reveals dynamic assembly of repair complexes during bypass of DNA cross-links. <i>Science</i> , 2015, 348, 1253671.	6.0	183
53	Sleep-wake cycles drive daily dynamics of synaptic phosphorylation. <i>Science</i> , 2019, 366, .	6.0	181
54	Ultra-deep and quantitative saliva proteome reveals dynamics of the oral microbiome. <i>Genome Medicine</i> , 2016, 8, 44.	3.6	170

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55	A large synthetic peptide and phosphopeptide reference library for mass spectrometry-based proteomics. <i>Nature Biotechnology</i> , 2013, 31, 557-564.	9.4	164
56	The ER membrane protein complex interacts cotranslationally to enable biogenesis of multipass membrane proteins. <i>ELife</i> , 2018, 7, .	2.8	160
57	Super-SILAC Allows Classification of Diffuse Large B-cell Lymphoma Subtypes by Their Protein Expression Profiles. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 77-89.	2.5	155
58	Thermalization of quantum fields from time-reversal invariant evolution equations. <i>Physics Letters, Section B: Nuclear, Elementary Particle and High-Energy Physics</i> , 2001, 517, 369-374.	1.5	151
59	The Impact II, a Very High-Resolution Quadrupole Time-of-Flight Instrument (QTOF) for Deep Shotgun Proteomics *. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2014-2029.	2.5	150
60	Feasibility of Large-Scale Phosphoproteomics with Higher Energy Collisional Dissociation Fragmentation. <i>Journal of Proteome Research</i> , 2010, 9, 6786-6794.	1.8	149
61	Analysis of High Accuracy, Quantitative Proteomics Data in the MaxQB Database. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.014068.	2.5	147
62	The Ubiquitin-Proteasome System Is a Key Component of the SUMO-2/3 Cycle. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 2107-2122.	2.5	143
63	Cell-Type-Resolved Quantitative Proteomics of Murine Liver. <i>Cell Metabolism</i> , 2014, 20, 1076-1087.	7.2	143
64	Proteomics strategy for quantitative protein interaction profiling in cell extracts. <i>Nature Methods</i> , 2009, 6, 741-744.	9.0	141
65	Lysine acetylome profiling uncovers novel histone deacetylase substrate proteins in <i>Arabidopsis</i> . <i>Molecular Systems Biology</i> , 2017, 13, 949.	3.2	141
66	Software Lock Mass by Two-Dimensional Minimization of Peptide Mass Errors. <i>Journal of the American Society for Mass Spectrometry</i> , 2011, 22, 1373-1380.	1.2	138
67	Solid Tumor Proteome and Phosphoproteome Analysis by High Resolution Mass Spectrometry. <i>Journal of Proteome Research</i> , 2008, 7, 5314-5326.	1.8	132
68	High-accuracy identification and bioinformatic analysis of <i>in vivo</i> protein phosphorylation sites in yeast. <i>Proteomics</i> , 2009, 9, 4642-4652.	1.3	132
69	Organellar Proteomics and Phospho-Proteomics Reveal Subcellular Reorganization in Diet-Induced Hepatic Steatosis. <i>Developmental Cell</i> , 2018, 47, 205-221.e7.	3.1	132
70	The mzTab Data Exchange Format: Communicating Mass-spectrometry-based Proteomics and Metabolomics Experimental Results to a Wider Audience. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2765-2775.	2.5	130
71	MaxQuant Software for Ion Mobility Enhanced Shotgun Proteomics. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1058-1069.	2.5	128
72	Proteomic Changes Resulting from Gene Copy Number Variations in Cancer Cells. <i>PLoS Genetics</i> , 2010, 6, e1001090.	1.5	126

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73	Proteomic Portrait of Human Breast Cancer Progression Identifies Novel Prognostic Markers. <i>Cancer Research</i> , 2012, 72, 2428-2439.	0.4	124
74	The Proteome of Primary Prostate Cancer. <i>European Urology</i> , 2016, 69, 942-952.	0.9	122
75	MaxDIA enables library-based and library-free data-independent acquisition proteomics. <i>Nature Biotechnology</i> , 2021, 39, 1563-1573.	9.4	115
76	Defining the Adult Neural Stem Cell Niche Proteome Identifies Key Regulators of Adult Neurogenesis. <i>Cell Stem Cell</i> , 2020, 26, 277-293.e8.	5.2	109
77	Computational Methods for Understanding Mass Spectrometry-Based Shotgun Proteomics Data. <i>Annual Review of Biomedical Data Science</i> , 2018, 1, 207-234.	2.8	108
78	Spatiotemporal Proteomic Profiling of Huntington's Disease Inclusions Reveals Widespread Loss of Protein Function. <i>Cell Reports</i> , 2017, 21, 2291-2303.	2.9	107
79	A Mass Spectrometry-Based Approach for Mapping Protein Subcellular Localization Reveals the Spatial Proteome of Mouse Primary Neurons. <i>Cell Reports</i> , 2017, 20, 2706-2718.	2.9	105
80	First Community-Wide, Comparative Cross-Linking Mass Spectrometry Study. <i>Analytical Chemistry</i> , 2019, 91, 6953-6961.	3.2	100
81	The dental proteome of Homo antecessor. <i>Nature</i> , 2020, 580, 235-238.	13.7	100
82	A Systematic Investigation into the Nature of Tryptic HCD Spectra. <i>Journal of Proteome Research</i> , 2012, 11, 5479-5491.	1.8	96
83	Combined Use of RNAi and Quantitative Proteomics to Study Gene Function in Drosophila. <i>Molecular Cell</i> , 2008, 31, 762-772.	4.5	93
84	Quantitative Proteomics Reveals That Hsp90 Inhibition Preferentially Targets Kinases and the DNA Damage Response. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.014654.	2.5	91
85	MaxQuant.Live Enables Global Targeting of More Than 25,000 Peptides. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 982a-994.	2.5	91
86	In Vivo SILAC-Based Proteomics Reveals Phosphoproteome Changes during Mouse Skin Carcinogenesis. <i>Cell Reports</i> , 2013, 3, 552-566.	2.9	90
87	EASI-tag enables accurate multiplexed and interference-free MS2-based proteome quantification. <i>Nature Methods</i> , 2018, 15, 527-530.	9.0	88
88	Systematic Detection of Amino Acid Substitutions in Proteomes Reveals Mechanistic Basis of Ribosome Errors and Selection for Translation Fidelity. <i>Molecular Cell</i> , 2019, 75, 427-441.e5.	4.5	84
89	Analysis of the Mouse Liver Proteome Using Advanced Mass Spectrometry. <i>Journal of Proteome Research</i> , 2007, 6, 2963-2972.	1.8	83
90	Enamel proteome shows that Gigantopithecus was an early diverging pongine. <i>Nature</i> , 2019, 576, 262-265.	13.7	82

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91	MaxQuant for In-Depth Analysis of Large SILAC Datasets. <i>Methods in Molecular Biology</i> , 2014, 1188, 351-364.	0.4	79
92	N-linked Glycosylation Enrichment for In-depth Cell Surface Proteomics of Diffuse Large B-cell Lymphoma Subtypes. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 240-251.	2.5	77
93	Ancient Biomolecules and Evolutionary Inference. <i>Annual Review of Biochemistry</i> , 2018, 87, 1029-1060.	5.0	76
94	Glucose-regulated and drug-perturbed phosphoproteome reveals molecular mechanisms controlling insulin secretion. <i>Nature Communications</i> , 2016, 7, 13250.	5.8	74
95	Machine Learning-based Classification of Diffuse Large B-cell Lymphoma Patients by Their Protein Expression Profiles. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2947-2960.	2.5	73
96	Will my protein crystallize? A sequence-based predictor. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 62, 343-355.	1.5	71
97	The Proteome of Prostate Cancer Bone Metastasis Reveals Heterogeneity with Prognostic Implications. <i>Clinical Cancer Research</i> , 2018, 24, 5433-5444.	3.2	68
98	Secretome Analysis of Lipid-Induced Insulin Resistance in Skeletal Muscle Cells by a Combined Experimental and Bioinformatics Workflow. <i>Journal of Proteome Research</i> , 2015, 14, 4885-4895.	1.8	66
99	Computational principles of determining and improving mass precision and accuracy for proteome measurements in an Orbitrap. <i>Journal of the American Society for Mass Spectrometry</i> , 2009, 20, 1477-1485.	1.2	65
100	IKAP: A heuristic framework for inference of kinase activities from Phosphoproteomics data. <i>Bioinformatics</i> , 2016, 32, 424-431.	1.8	62
101	Predicting post-translational lysine acetylation using support vector machines. <i>Bioinformatics</i> , 2010, 26, 1666-1668.	1.8	61
102	A Network Module for the Perseus Software for Computational Proteomics Facilitates Proteome Interaction Graph Analysis. <i>Journal of Proteome Research</i> , 2019, 18, 2052-2064.	1.8	60
103	Solution of the complex action problem in the Potts model for dense QCD. <i>Nuclear Physics B</i> , 2001, 602, 61-86.	0.9	59
104	Expert System for Computer-assisted Annotation of MS/MS Spectra. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1500-1509.	2.5	59
105	Isobaric Matching between Runs and Novel PSM-Level Normalization in MaxQuant Strongly Improve Reporter Ion-Based Quantification. <i>Journal of Proteome Research</i> , 2020, 19, 3945-3954.	1.8	55
106	Phosphorylation Variation during the Cell Cycle Scales with Structural Propensities of Proteins. <i>PLoS Computational Biology</i> , 2013, 9, e1002842.	1.5	54
107	A Framework for Intelligent Data Acquisition and Real-Time Database Searching for Shotgun Proteomics. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.013185.	2.5	50
108	Securin Is Not Required for Chromosomal Stability in Human Cells. <i>PLoS Biology</i> , 2005, 3, e416.	2.6	47

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109	High Performance Computational Analysis of Large-scale Proteome Data Sets to Assess Incremental Contribution to Coverage of the Human Genome. <i>Journal of Proteome Research</i> , 2013, 12, 2858-2868.	1.8	43
110	The proteogenomic subtypes of acute myeloid leukemia. <i>Cancer Cell</i> , 2022, 40, 301-317.e12.	7.7	43
111	MaxQuant goes Linux. <i>Nature Methods</i> , 2018, 15, 401-401.	9.0	41
112	Multiplexed proteome analysis with neutron-encoded stable isotope labeling in cells and mice. <i>Nature Protocols</i> , 2018, 13, 293-306.	5.5	35
113	Comparison of SILAC and mTRAQ Quantification for Phosphoproteomics on a Quadrupole Orbitrap Mass Spectrometer. <i>Journal of Proteome Research</i> , 2013, 12, 4089-4100.	1.8	30
114	How much peptide sequence information is contained in ion trap tandem mass spectra?. <i>Journal of the American Society for Mass Spectrometry</i> , 2008, 19, 1813-1820.	1.2	28
115	An Integrated Phosphoproteomics Work Flow Reveals Extensive Network Regulation in Early Lysophosphatidic Acid Signaling. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1047-1062.	2.5	28
116	Quantitative Cross-linking/Mass Spectrometry Using Isotope-labeled Cross-linkers and MaxQuant. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2769-2778.	2.5	28
117	Meron-cluster simulation of a chiral phase transition with staggered fermions. <i>Nuclear Physics B</i> , 2000, 576, 481-500.	0.9	27
118	A Novel Chromatographic Method Allows On-line Reanalysis of the Proteome. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 1452-1459.	2.5	27
119	Role for ribosome-associated quality control in sampling proteins for MHC class I-mediated antigen presentation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 4099-4108.	3.3	27
120	Deubiquitinating enzymes and the proteasome regulate preferential sets of ubiquitin substrates. <i>Nature Communications</i> , 2022, 13, 2736.	5.8	22
121	Gauge-ball spectrum of the four-dimensional pure U(1) gauge theory. <i>Nuclear Physics B</i> , 1997, 499, 371-408.	0.9	21
122	Expanding the Perseus Software for Omics Data Analysis With Custom Plugins. <i>Current Protocols in Bioinformatics</i> , 2020, 71, e105.	25.8	21
123	PhosphoSiteAnalyzer: A Bioinformatic Platform for Deciphering Phospho Proteomes Using Kinase Predictions Retrieved from NetworkKIN. <i>Journal of Proteome Research</i> , 2012, 11, 3480-3486.	1.8	19
124	Computational proteomics pitfalls and challenges: HavanaBioinfo 2012 Workshop report. <i>Journal of Proteomics</i> , 2013, 87, 134-138.	1.2	19
125	Accurate and Automated High-Coverage Identification of Chemically Cross-Linked Peptides with MaxLynx. <i>Analytical Chemistry</i> , 2022, 94, 1608-1617.	3.2	19
126	Benchmarking differential expression, imputation and quantification methods for proteomics data. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	16

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127	Proteomic Analysis of Cellular Systems. , 2013, , 3-25.		15
128	Meron-cluster algorithms and chiral-symmetry breaking in a (2+1)D staggered fermion model. Nuclear Physics B, 2000, 583, 331-346.	0.9	13
129	Meron-cluster approach to systems of strongly correlated electrons. Nuclear Physics B, 2003, 673, 405-436.	0.9	13
130	Predicting Experimental Properties of Proteins from Sequence by Machine Learning Techniques. Current Protein and Peptide Science, 2007, 8, 121-133.	0.7	13
131	Correction to Feasibility of Large-Scale Phosphoproteomics with Higher Energy Collisional Dissociation Fragmentation. Journal of Proteome Research, 2012, 11, 3506-3508.	1.8	11
132	Nanoelectrospray peptide mapping revisited: Composite survey spectra allow high dynamic range protein characterization without LCMS on an orbitrap mass spectrometer. International Journal of Mass Spectrometry, 2007, 268, 158-167.	0.7	10
133	Homology-driven assembly of NON-redundant protein sequence sets (NOMESS) for mass spectrometry. Bioinformatics, 2016, 32, 1417-1419.	1.8	9
134	Tracing back variations in archaeal ESCRT-based cell division to protein domain architectures. PLoS ONE, 2022, 17, e0266395.	1.1	9
135	Strongly coupled compact lattice QED with staggered fermions. Nuclear Physics B, 1998, 532, 315-336.	0.9	8
136	Facing challenges in Proteomics today and in the coming decade: Report of Roundtable Discussions at the 4th EuPA Scientific Meeting, Portugal, Estoril 2010. Journal of Proteomics, 2011, 75, 4-17.	1.2	8
137	What computational non-targeted mass spectrometry-based metabolomics can gain from shotgun proteomics. Current Opinion in Biotechnology, 2017, 43, 141-146.	3.3	7
138	Redirected nuclear glutamate dehydrogenase supplies Tet3 with α -ketoglutarate in neurons. Nature Communications, 2021, 12, 4100.	5.8	7
139	Scaling of gauge balls and static potential in the confinement phase of the pure U(1) lattice gauge theory. Nuclear Physics, Section B, Proceedings Supplements, 1998, 63, 691-693.	0.5	5
140	Properties of the non-Gaussian fixed point in 4D compact U(1) lattice gauge theory. Nuclear Physics, Section B, Proceedings Supplements, 1997, 53, 696-698.	0.5	4
141	Universality of the gauge-ball spectrum of the four-dimensional pure U (1) gauge theory. Nuclear Physics B, 1999, 545, 607-619.	0.9	4
142	Study of the order of the phase transition in pure U(1) gauge theory with Villain action. Nuclear Physics, Section B, Proceedings Supplements, 1999, 73, 712-714.	0.5	3
143	Meron-Cluster Solution of Fermion and Other Sign Problems. Nuclear Physics, Section B, Proceedings Supplements, 2000, 83-84, 777-791.	0.5	2
144	1088 In-depth Analysis of Cancer HLA-I Peptidomes. European Journal of Cancer, 2012, 48, S262.	1.3	0

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145	Perseus plugin "Metis" for metabolic-pathway-centered quantitative multi-omics data analysis for static and time-series experimental designs. Cell Reports Methods, 2022, 2, 100198.	1.4	0