

Juergen Cox

List of Publications by Year in Descending Order

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

153
papers

44,960
citations

76
h-index

162
g-index

162
ext. papers

58,844
ext. citations

12.6
avg, IF

7.94
L-index

#	Paper	IF	Citations
153	Benchmarking differential expression, imputation and quantification methods for proteomics data.. <i>Briefings in Bioinformatics</i> , 2022 ,	13.4	1
152	Tracing back variations in archaeal ESCRT-based cell division to protein domain architectures.. <i>PLoS ONE</i> , 2022 , 17, e0266395	3.7	0
151	Perseus plugin "Metis" for metabolic-pathway-centered quantitative multi-omics data analysis for static and time-series experimental designs.. <i>Cell Reports Methods</i> , 2022 , 2, 100198		
150	Deubiquitinating enzymes and the proteasome regulate preferential sets of ubiquitin substrates.. <i>Nature Communications</i> , 2022 , 13, 2736	17.4	4
149	MaxQuant Module for the Identification of Genomic Variants Propagated into Peptides. <i>Methods in Molecular Biology</i> , 2022 , 339-347	1.4	0
148	Redirected nuclear glutamate dehydrogenase supplies Tet3 with α -ketoglutarate in neurons. <i>Nature Communications</i> , 2021 , 12, 4100	17.4	1
147	MaxDIA enables library-based and library-free data-independent acquisition proteomics. <i>Nature Biotechnology</i> , 2021 ,	44.5	24
146	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	11.5	15
145	MaxQuant Software for Ion Mobility Enhanced Shotgun Proteomics. <i>Molecular and Cellular Proteomics</i> , 2020 , 19, 1058-1069	7.6	49
144	The dental proteome of Homo antecessor. <i>Nature</i> , 2020 , 580, 235-238	50.4	47
143	Defining the Adult Neural Stem Cell Niche Proteome Identifies Key Regulators of Adult Neurogenesis. <i>Cell Stem Cell</i> , 2020 , 26, 277-293.e8	18	54
142	Expanding the Perseus Software for Omics Data Analysis With Custom Plugins. <i>Current Protocols in Bioinformatics</i> , 2020 , 71, e105	24.2	4
141	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	5.6	16
140	High-quality MS/MS spectrum prediction for data-dependent and data-independent acquisition data analysis. <i>Nature Methods</i> , 2019 , 16, 519-525	21.6	116
139	First Community-Wide, Comparative Cross-Linking Mass Spectrometry Study. <i>Analytical Chemistry</i> , 2019 , 91, 6953-6961	7.8	57
138	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	5.6	32
137	The nucleolus functions as a phase-separated protein quality control compartment. <i>Science</i> , 2019 , 365, 342-347	33.3	185

136	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	17.6	36
135	Sleep-wake cycles drive daily dynamics of synaptic phosphorylation. <i>Science</i> , 2019 , 366,	33.3	82
134	MaxQuant.Live Enables Global Targeting of More Than 25,000 Peptides. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, 982-994	7.6	54
133	Enamel proteome shows that Gigantopithecus was an early diverging pongine. <i>Nature</i> , 2019 , 576, 262-265.	5.4	41
132	The PRIDE database and related tools and resources in 2019: improving support for quantification data. <i>Nucleic Acids Research</i> , 2019 , 47, D442-D450	20.1	3856
131	Perseus: A Bioinformatics Platform for Integrative Analysis of Proteomics Data in Cancer Research. <i>Methods in Molecular Biology</i> , 2018 , 1711, 133-148	1.4	200
130	Multiplexed proteome analysis with neutron-encoded stable isotope labeling in cells and mice. <i>Nature Protocols</i> , 2018 , 13, 293-306	18.8	22
129	Ancient Biomolecules and Evolutionary Inference. <i>Annual Review of Biochemistry</i> , 2018 , 87, 1029-1060	29.1	47
128	The Proteome of Prostate Cancer Bone Metastasis Reveals Heterogeneity with Prognostic Implications. <i>Clinical Cancer Research</i> , 2018 , 24, 5433-5444	12.9	44
127	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	21.6	198
126	Computational Methods for Understanding Mass Spectrometry-Based Shotgun Proteomics Data. <i>Annual Review of Biomedical Data Science</i> , 2018 , 1, 207-234	5.6	82
125	EASI-tag enables accurate multiplexed and interference-free MS2-based proteome quantification. <i>Nature Methods</i> , 2018 , 15, 527-530	21.6	55
124	Online Parallel Accumulation-Serial Fragmentation (PASEF) with a Novel Trapped Ion Mobility Mass Spectrometer. <i>Molecular and Cellular Proteomics</i> , 2018 , 17, 2534-2545	7.6	280
123	Organellar Proteomics and Phospho-Proteomics Reveal Subcellular Reorganization in Diet-Induced Hepatic Steatosis. <i>Developmental Cell</i> , 2018 , 47, 205-221.e7	10.2	70
122	MaxQuant goes Linux. <i>Nature Methods</i> , 2018 , 15, 401	21.6	24
121	The ER membrane protein complex interacts cotranslationally to enable biogenesis of multipass membrane proteins. <i>ELife</i> , 2018 , 7,	8.9	92
120	What computational non-targeted mass spectrometry-based metabolomics can gain from shotgun proteomics. <i>Current Opinion in Biotechnology</i> , 2017 , 43, 141-146	11.4	7
119	Lysine acetylome profiling uncovers novel histone deacetylase substrate proteins in. <i>Molecular Systems Biology</i> , 2017 , 13, 949	12.2	74

118	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	10.6	68
117	Spatiotemporal Proteomic Profiling of Huntington's Disease Inclusions Reveals Widespread Loss of Protein Function. <i>Cell Reports</i> , 2017 , 21, 2291-2303	10.6	71
116	Guidelines for Genome-Scale Analysis of Biological Rhythms. <i>Journal of Biological Rhythms</i> , 2017 , 32, 380-393	3.2	127
115	Direct identification of clinically relevant neoepitopes presented on native human melanoma tissue by mass spectrometry. <i>Nature Communications</i> , 2016 , 7, 13404	17.4	386
114	Glucose-regulated and drug-perturbed phosphoproteome reveals molecular mechanisms controlling insulin secretion. <i>Nature Communications</i> , 2016 , 7, 13250	17.4	53
113	The MaxQuant computational platform for mass spectrometry-based shotgun proteomics. <i>Nature Protocols</i> , 2016 , 11, 2301-2319	18.8	1656
112	The Perseus computational platform for comprehensive analysis of (prote)omics data. <i>Nature Methods</i> , 2016 , 13, 731-40	21.6	3257
111	The Proteome of Primary Prostate Cancer. <i>European Urology</i> , 2016 , 69, 942-52	10.2	97
110	IKAP: A heuristic framework for inference of kinase activities from Phosphoproteomics data. <i>Bioinformatics</i> , 2016 , 32, 424-31	7.2	40
109	Homology-driven assembly of NON-redundant protein sequence sets (NOMESS) for mass spectrometry. <i>Bioinformatics</i> , 2016 , 32, 1417-9	7.2	8
108	Proteomic maps of breast cancer subtypes. <i>Nature Communications</i> , 2016 , 7, 10259	17.4	178
107	Author response: Global, quantitative and dynamic mapping of protein subcellular localization 2016		3
106	Global, quantitative and dynamic mapping of protein subcellular localization. <i>ELife</i> , 2016 , 5,	8.9	282
105	Ultra-deep and quantitative saliva proteome reveals dynamics of the oral microbiome. <i>Genome Medicine</i> , 2016 , 8, 44	14.4	122
104	Quantitative Cross-linking/Mass Spectrometry Using Isotope-labeled Cross-linkers and MaxQuant. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 2769-78	7.6	26
103	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, 2014-29	7.6	116
102	DNA repair. Proteomics reveals dynamic assembly of repair complexes during bypass of DNA cross-links. <i>Science</i> , 2015 , 348, 1253671	33.3	116
101	Acetylation site specificities of lysine deacetylase inhibitors in human cells. <i>Nature Biotechnology</i> , 2015 , 33, 415-23	44.5	186

100	Machine Learning-based Classification of Diffuse Large B-cell Lymphoma Patients by Their Protein Expression Profiles. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 2947-60	7.6	58
99	A human interactome in three quantitative dimensions organized by stoichiometries and abundances. <i>Cell</i> , 2015 , 163, 712-23	56.2	788
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, 4885-95	5.6	47
97	Visualization of LC-MS/MS proteomics data in MaxQuant. <i>Proteomics</i> , 2015 , 15, 1453-6	4.8	143
96	Deep proteomics of mouse skeletal muscle enables quantitation of protein isoforms, metabolic pathways, and transcription factors. <i>Molecular and Cellular Proteomics</i> , 2015 , 14, 841-53	7.6	162
95	A "proteomic ruler" for protein copy number and concentration estimation without spike-in standards. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 3497-506	7.6	324
94	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, 240-51	7.6	64
93	Ultradeep human phosphoproteome reveals a distinct regulatory nature of Tyr and Ser/Thr-based signaling. <i>Cell Reports</i> , 2014 , 8, 1583-94	10.6	616
92	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	6	260
91	Accurate proteome-wide label-free quantification by delayed normalization and maximal peptide ratio extraction, termed MaxLFQ. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 2513-26	7.6	2578
90	Cell-type-resolved quantitative proteomics of murine liver. <i>Cell Metabolism</i> , 2014 , 20, 1076-87	24.6	106
89	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, 2765-75	7.6	96
88	MaxQuant for in-depth analysis of large SILAC datasets. <i>Methods in Molecular Biology</i> , 2014 , 1188, 351-64.4		66
87	Comparison of SILAC and mTRAQ quantification for phosphoproteomics on a quadrupole orbitrap mass spectrometer. <i>Journal of Proteome Research</i> , 2013 , 12, 4089-100	5.6	28
86	Initial quantitative proteomic map of 28 mouse tissues using the SILAC mouse. <i>Molecular and Cellular Proteomics</i> , 2013 , 12, 1709-22	7.6	166
85	Proteomic Analysis of Cellular Systems 2013 , 3-25		13
84	The coming age of complete, accurate, and ubiquitous proteomes. <i>Molecular Cell</i> , 2013 , 49, 583-90	17.6	294
83	In vivo SILAC-based proteomics reveals phosphoproteome changes during mouse skin carcinogenesis. <i>Cell Reports</i> , 2013 , 3, 552-66	10.6	82

82	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, 2858-68	5.6	26
81	A large synthetic peptide and phosphopeptide reference library for mass spectrometry-based proteomics. <i>Nature Biotechnology</i> , 2013 , 31, 557-64	44.5	132
80	Computational proteomics pitfalls and challenges: HavanaBioinfo 2012 workshop report. <i>Journal of Proteomics</i> , 2013 , 87, 134-8	3.9	17
79	Phosphorylation variation during the cell cycle scales with structural propensities of proteins. <i>PLoS Computational Biology</i> , 2013 , 9, e1002842	5	48
78	Global analysis of genome, transcriptome and proteome reveals the response to aneuploidy in human cells. <i>Molecular Systems Biology</i> , 2012 , 8, 608	12.2	266
77	Expert system for computer-assisted annotation of MS/MS spectra. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, 1500-9	7.6	53
76	Correction to Feasibility of Large-Scale Phosphoproteomics with Higher Energy Collisional Dissociation Fragmentation. <i>Journal of Proteome Research</i> , 2012 , 11, 3506-3508	5.6	10
75	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	7.6	566
74	A systematic investigation into the nature of tryptic HCD spectra. <i>Journal of Proteome Research</i> , 2012 , 11, 5479-91	5.6	85
73	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	7.6	135
72	1D and 2D annotation enrichment: a statistical method integrating quantitative proteomics with complementary high-throughput data. <i>BMC Bioinformatics</i> , 2012 , 13 Suppl 16, S12	3.6	393
71	PhosphoSiteAnalyzer: a bioinformatic platform for deciphering phospho proteomes using kinase predictions retrieved from NetworKIN. <i>Journal of Proteome Research</i> , 2012 , 11, 3480-6	5.6	17
70	Quantitative proteomics reveals that Hsp90 inhibition preferentially targets kinases and the DNA damage response. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, M111.014654	7.6	77
69	Analysis of high accuracy, quantitative proteomics data in the MaxQB database. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, M111.014068	7.6	116
68	Proteomic portrait of human breast cancer progression identifies novel prognostic markers. <i>Cancer Research</i> , 2012 , 72, 2428-39	10.1	107
67	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	7.6	255
66	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 ³¹³	7.6	313
65	A framework for intelligent data acquisition and real-time database searching for shotgun proteomics. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, M111.013185	7.6	40

64	Deep proteome and transcriptome mapping of a human cancer cell line. <i>Molecular Systems Biology</i> , 2011 , 7, 548	12.2	723
63	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, 147-57	18.8	232
62	Facing challenges in Proteomics today and in the coming decade: Report of Roundtable Discussions at the 4th EuPA Scientific Meeting, Portugal, Estoril 2010. <i>Journal of Proteomics</i> , 2011 , 75, 4-17	3.9	8
61	Quantitative, high-resolution proteomics for data-driven systems biology. <i>Annual Review of Biochemistry</i> , 2011 , 80, 273-99	29.1	550
60	A proteome-wide, quantitative survey of in vivo ubiquitylation sites reveals widespread regulatory roles. <i>Molecular and Cellular Proteomics</i> , 2011 , 10, M111.013284	7.6	644
59	Software lock mass by two-dimensional minimization of peptide mass errors. <i>Journal of the American Society for Mass Spectrometry</i> , 2011 , 22, 1373-80	3.5	103
58	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, 1785-93	5.6	486
57	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	7.6	614
56	Andromeda: a peptide search engine integrated into the MaxQuant environment. <i>Journal of Proteome Research</i> , 2011 , 10, 1794-805	5.6	3402
55	Deep and highly sensitive proteome coverage by LC-MS/MS without prefractionation. <i>Molecular and Cellular Proteomics</i> , 2011 , 10, M110.003699	7.6	264
54	Super-SILAC mix for quantitative proteomics of human tumor tissue. <i>Nature Methods</i> , 2010 , 7, 383-5	21.6	431
53	An integrated phosphoproteomics work flow reveals extensive network regulation in early lysophosphatidic acid signaling. <i>Molecular and Cellular Proteomics</i> , 2010 , 9, 1047-62	7.6	25
52	Defining the transcriptome and proteome in three functionally different human cell lines. <i>Molecular Systems Biology</i> , 2010 , 6, 450	12.2	269
51	Proteomics on an Orbitrap benchtop mass spectrometer using all-ion fragmentation. <i>Molecular and Cellular Proteomics</i> , 2010 , 9, 2252-61	7.6	189
50	Quantitative proteomics combined with BAC TransgeneOmics reveals in vivo protein interactions. <i>Journal of Cell Biology</i> , 2010 , 189, 739-54	7.3	341
49	Predicting post-translational lysine acetylation using support vector machines. <i>Bioinformatics</i> , 2010 , 26, 1666-8	7.2	52
48	MSQuant, an open source platform for mass spectrometry-based quantitative proteomics. <i>Journal of Proteome Research</i> , 2010 , 9, 393-403	5.6	225
47	Quantitative phosphoproteomics reveals widespread full phosphorylation site occupancy during mitosis. <i>Science Signaling</i> , 2010 , 3, ra3	8.8	1106

46	Feasibility of large-scale phosphoproteomics with higher energy collisional dissociation fragmentation. <i>Journal of Proteome Research</i> , 2010 , 9, 6786-94	5.6	139
45	Quantitative proteomics reveals subset-specific viral recognition in dendritic cells. <i>Immunity</i> , 2010 , 32, 279-89	32.3	435
44	Proteomic changes resulting from gene copy number variations in cancer cells. <i>PLoS Genetics</i> , 2010 , 6, e1001090	6	97
43	High-accuracy identification and bioinformatic analysis of in vivo protein phosphorylation sites in yeast. <i>Proteomics</i> , 2009 , 9, 4642-52	4.8	103
42	Proteomics strategy for quantitative protein interaction profiling in cell extracts. <i>Nature Methods</i> , 2009 , 6, 741-4	21.6	121
41	A practical guide to the MaxQuant computational platform for SILAC-based quantitative proteomics. <i>Nature Protocols</i> , 2009 , 4, 698-705	18.8	637
40	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, 1477-85	3.5	55
39	System-wide changes to SUMO modifications in response to heat shock. <i>Science Signaling</i> , 2009 , 2, ra24	8.8	367
38	Mislocalized activation of oncogenic RTKs switches downstream signaling outcomes. <i>Molecular Cell</i> , 2009 , 36, 326-39	17.6	245
37	Comprehensive mass-spectrometry-based proteome quantification of haploid versus diploid yeast. <i>Nature</i> , 2008 , 455, 1251-4	50.4	745
36	MaxQuant enables high peptide identification rates, individualized p.p.b.-range mass accuracies and proteome-wide protein quantification. <i>Nature Biotechnology</i> , 2008 , 26, 1367-72	44.5	9012
35	Iodoacetamide-induced artifact mimics ubiquitination in mass spectrometry. <i>Nature Methods</i> , 2008 , 5, 459-60	21.6	237
34	Solid tumor proteome and phosphoproteome analysis by high resolution mass spectrometry. <i>Journal of Proteome Research</i> , 2008 , 7, 5314-26	5.6	119
33	Combined use of RNAi and quantitative proteomics to study gene function in <i>Drosophila</i> . <i>Molecular Cell</i> , 2008 , 31, 762-72	17.6	87
32	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, 672-83	7.6	242
31	A novel chromatographic method allows on-line reanalysis of the proteome. <i>Molecular and Cellular Proteomics</i> , 2008 , 7, 1452-9	7.6	26
30	The ubiquitin-proteasome system is a key component of the SUMO-2/3 cycle. <i>Molecular and Cellular Proteomics</i> , 2008 , 7, 2107-22	7.6	124
29	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, 1813-20	3.5	26

28	Nanoelectrospray peptide mapping revisited: Composite survey spectra allow high dynamic range protein characterization without LCMS on an orbitrap mass spectrometer. <i>International Journal of Mass Spectrometry</i> , 2007 , 268, 158-167	1.9	8
27	Predicting experimental properties of proteins from sequence by machine learning techniques. <i>Current Protein and Peptide Science</i> , 2007 , 8, 121-33	2.8	12
26	Is proteomics the new genomics?. <i>Cell</i> , 2007 , 130, 395-8	56.2	350
25	PHOSIDA (phosphorylation site database): management, structural and evolutionary investigation, and prediction of phosphosites. <i>Genome Biology</i> , 2007 , 8, R250	18.3	376
24	Analysis of the mouse liver proteome using advanced mass spectrometry. <i>Journal of Proteome Research</i> , 2007 , 6, 2963-72	5.6	75
23	Will my protein crystallize? A sequence-based predictor. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 62, 343-55	4.2	65
22	Generation and Validation of a Reference System for Toxicogenomics DNA Microarray Experiments 2005 , 185-200		
21	Securin is not required for chromosomal stability in human cells. <i>PLoS Biology</i> , 2005 , 3, e416	9.7	45
20	Meron-cluster approach to systems of strongly correlated electrons. <i>Nuclear Physics B</i> , 2003 , 673, 405-436	3.8	9
19	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	4.2	143
18	Solution of the complex action problem in the Potts model for dense QCD. <i>Nuclear Physics B</i> , 2001 , 602, 61-86	2.8	50
17	Meron-cluster simulation of a chiral phase transition with staggered fermions. <i>Nuclear Physics B</i> , 2000 , 576, 481-500	2.8	25
16	Meron-cluster algorithms and chiral-symmetry breaking in a (2+1)D staggered fermion model. <i>Nuclear Physics B</i> , 2000 , 583, 331-346	2.8	13
15	Meron-Cluster Solution of Fermion and Other Sign Problems. <i>Nuclear Physics, Section B, Proceedings Supplements</i> , 2000 , 83-84, 777-791		2
14	Study of the order of the phase transition in pure U(1) gauge theory with Villain action. <i>Nuclear Physics, Section B, Proceedings Supplements</i> , 1999 , 73, 712-714		2
13	Universality of the gauge-ball spectrum of the four-dimensional pure U(1) gauge theory. <i>Nuclear Physics B</i> , 1999 , 545, 607-619	2.8	4
12	Strongly coupled compact lattice QED with staggered fermions. <i>Nuclear Physics B</i> , 1998 , 532, 315-336	2.8	6
11	Scaling of gauge balls and static potential in the confinement phase of the pure U(1) lattice gauge theory. <i>Nuclear Physics, Section B, Proceedings Supplements</i> , 1998 , 63, 691-693		5

10	Gauge-ball spectrum of the four-dimensional pure U(1) gauge theory. <i>Nuclear Physics B</i> , 1997 , 499, 371-408	21
9	Properties of the non-Gaussian fixed point in 4D compact U(1) lattice gauge theory. <i>Nuclear Physics, Section B, Proceedings Supplements</i> , 1997 , 53, 696-698	4
8	Isobaric matching between runs and novel PSM-level normalization in MaxQuant strongly improve reporter ion-based quantification	2
7	Quantitative cross-linking/mass spectrometry using isotope-labeled cross-linkers and MaxQuant	2
6	EASI-tag enables accurate multiplexed and interference-free MS2-based proteome quantification	2
5	Systematic detection of amino acid substitutions in proteome reveals a mechanistic basis of ribosome errors	4
4	Online parallel accumulation serial fragmentation (PASEF) with a novel trapped ion mobility mass spectrometer	7
3	MaxQuant.Live enables global targeting of more than 25,000 peptides	2
2	MaxQuant software for ion mobility enhanced shotgun proteomics	7
1	Accurate and automated high-coverage identification of chemically cross-linked peptides with MaxLynx	1