

Michael Lund Nielsen

List of Publications by Year in descending order

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14,375
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44069
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107
times ranked

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#	ARTICLE	IF	CITATIONS
1	Lysine Acetylation Targets Protein Complexes and Co-Regulates Major Cellular Functions. <i>Science</i> , 2009, 325, 834-840.	12.6	3,883
2	Comprehensive mass-spectrometry-based proteome quantification of haploid versus diploid yeast. <i>Nature</i> , 2008, 455, 1251-1254.	27.8	835
3	A Proteome-wide, Quantitative Survey of In Vivo Ubiquitylation Sites Reveals Widespread Regulatory Roles. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.013284.	3.8	754
4	Liquid demixing of intrinsically disordered proteins is seeded by poly(ADP-ribose). <i>Nature Communications</i> , 2015, 6, 8088.	12.8	463
5	An Optimized Shotgun Strategy for the Rapid Generation of Comprehensive Human Proteomes. <i>Cell Systems</i> , 2017, 4, 587-599.e4.	6.2	413
6	A Dual Pressure Linear Ion Trap Orbitrap Instrument with Very High Sequencing Speed. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 2759-2769.	3.8	398
7	Citrullination regulates pluripotency and histone H1 binding to chromatin. <i>Nature</i> , 2014, 507, 104-108.	27.8	358
8	Jmjd6 Catalyses Lysyl-Hydroxylation of U2AF65, a Protein Associated with RNA Splicing. <i>Science</i> , 2009, 325, 90-93.	12.6	356
9	Proteome-wide Identification of Poly(ADP-Ribosyl)ation Targets in Different Genotoxic Stress Responses. <i>Molecular Cell</i> , 2013, 52, 272-285.	9.7	315
10	Site-specific mapping of the human SUMO proteome reveals co-modification with phosphorylation. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 325-336.	8.2	283
11	Mass Spectrometric Analysis of Lysine Ubiquitylation Reveals Promiscuity at Site Level. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.003590.	3.8	275
12	Optimized Fast and Sensitive Acquisition Methods for Shotgun Proteomics on a Quadrupole Orbitrap Mass Spectrometer. <i>Journal of Proteome Research</i> , 2012, 11, 3487-3497.	3.7	270
13	Iodoacetamide-induced artifact mimics ubiquitination in mass spectrometry. <i>Nature Methods</i> , 2008, 5, 459-460.	19.0	268
14	Proteomic Analyses Reveal Divergent Ubiquitylation Site Patterns in Murine Tissues. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1578-1585.	3.8	244
15	Proteome-wide analysis of arginine monomethylation reveals widespread occurrence in human cells. <i>Science Signaling</i> , 2016, 9, rs9.	3.6	241
16	Systems-wide analysis of ubiquitylation dynamics reveals a key role for PAF15 ubiquitylation in DNA-damage bypass. <i>Nature Cell Biology</i> , 2012, 14, 1089-1098.	10.3	234
17	Glutamine methylation in histone H2A is an RNA-polymerase-I-dedicated modification. <i>Nature</i> , 2014, 505, 564-568.	27.8	186
18	De Novo Peptide Sequencing and Identification with Precision Mass Spectrometry. <i>Journal of Proteome Research</i> , 2007, 6, 114-123.	3.7	185

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19	ModifiComb, a New Proteomic Tool for Mapping Substoichiometric Post-translational Modifications, Finding Novel Types of Modifications, and Fingerprinting Complex Protein Mixtures. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 935-948.	3.8	178
20	Proteome-wide identification of the endogenous ADP-ribosylome of mammalian cells and tissue. <i>Nature Communications</i> , 2016, 7, 12917.	12.8	172
21	ADP-ribosyltransferases, an update on function and nomenclature. <i>FEBS Journal</i> , 2022, 289, 7399-7410.	4.7	150
22	Proteomics-Grade de Novo Sequencing Approach. <i>Journal of Proteome Research</i> , 2005, 4, 2348-2354.	3.7	147
23	Site-specific characterization of endogenous SUMOylation across species and organs. <i>Nature Communications</i> , 2018, 9, 2456.	12.8	139
24	Improving Protein Identification Using Complementary Fragmentation Techniques in Fourier Transform Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 835-845.	3.8	128
25	The NBS1-Treacle complex controls ribosomal RNA transcription in response to DNA damage. <i>Nature Cell Biology</i> , 2014, 16, 792-803.	10.3	127
26	Systems-wide Analysis of Serine ADP-Ribosylation Reveals Widespread Occurrence and Site-Specific Overlap with Phosphorylation. <i>Cell Reports</i> , 2018, 24, 2493-2505.e4.	6.4	123
27	Hydrogen rearrangement to and from radical z fragments in electron capture dissociation of peptides. <i>Journal of the American Society for Mass Spectrometry</i> , 2007, 18, 113-120.	2.8	120
28	A new cellular stress response that triggers centriolar satellite reorganization and ciliogenesis. <i>EMBO Journal</i> , 2013, 32, 3029-3040.	7.8	115
29	An Advanced Strategy for Comprehensive Profiling of ADP-ribosylation Sites Using Mass Spectrometry-based Proteomics*. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1010a-1026.	3.8	113
30	Advantages of External Accumulation for Electron Capture Dissociation in Fourier Transform Mass Spectrometry. <i>Analytical Chemistry</i> , 2001, 73, 2998-3005.	6.5	106
31	The RBCC GeneRFP2(Leu5) Encodes a Novel Transmembrane E3 Ubiquitin Ligase Involved in ERAD. <i>Molecular Biology of the Cell</i> , 2007, 18, 1670-1682.	2.1	97
32	Extent of Modifications in Human Proteome Samples and Their Effect on Dynamic Range of Analysis in Shotgun Proteomics. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 2384-2391.	3.8	93
33	HysTag-A Novel Proteomic Quantification Tool Applied to Differential Display Analysis of Membrane Proteins From Distinct Areas of Mouse Brain. <i>Molecular and Cellular Proteomics</i> , 2004, 3, 82-92.	3.8	88
34	New Data Base-independent, Sequence Tag-based Scoring of Peptide MS/MS Data Validates Mowse Scores, Recovers Below Threshold Data, Singles Out Modified Peptides, and Assesses the Quality of MS/MS Techniques. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 1180-1188.	3.8	88
35	Bub1 positions Mad1 close to KNL1 MELT repeats to promote checkpoint signalling. <i>Nature Communications</i> , 2017, 8, 15822.	12.8	84
36	Proteomic Analysis of Arginine Methylation Sites in Human Cells Reveals Dynamic Regulation During Transcriptional Arrest. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2072-2088.	3.8	81

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37	Complementary Sequence Preferences of Electron-Capture Dissociation and Vibrational Excitation in Fragmentation of Polypeptide Polycations. <i>Angewandte Chemie - International Edition</i> , 2006, 45, 5301-5303.	13.8	79
38	Integrative Characterization of the R6/2 Mouse Model of Huntington's Disease Reveals Dysfunctional Astrocyte Metabolism. <i>Cell Reports</i> , 2018, 23, 2211-2224.	6.4	79
39	Specificity and Commonality of the Phosphoinositide-Binding Proteome Analyzed by Quantitative Mass Spectrometry. <i>Cell Reports</i> , 2014, 6, 578-591.	6.4	75
40	Mapping Physiological ADP-Ribosylation Using Activated Ion Electron Transfer Dissociation. <i>Cell Reports</i> , 2020, 32, 108176.	6.4	75
41	Liquid Chromatography at Critical Conditions: A Comprehensive Approach to Sequence-Dependent Retention Time Prediction. <i>Analytical Chemistry</i> , 2006, 78, 7770-7777.	6.5	73
42	SUMOylation promotes protective responses to DNA-protein crosslinks. <i>EMBO Journal</i> , 2019, 38, .	7.8	73
43	Side-Chain Losses in Electron Capture Dissociation To Improve Peptide Identification. <i>Analytical Chemistry</i> , 2007, 79, 2296-2302.	6.5	68
44	CDK-mediated activation of the SCF ^{FBXO} ubiquitin ligase promotes MYC-driven transcription and tumorigenesis and predicts poor survival in breast cancer. <i>EMBO Molecular Medicine</i> , 2013, 5, 1067-1086.	6.9	61
45	The SOCS2 Ubiquitin Ligase Complex Regulates Growth Hormone Receptor Levels. <i>PLoS ONE</i> , 2011, 6, e25358.	2.5	60
46	PAD2-Mediated Citrullination Contributes to Efficient Oligodendrocyte Differentiation and Myelination. <i>Cell Reports</i> , 2019, 27, 1090-1102.e10.	6.4	59
47	Intramolecular hydrogen atom transfer in hydrogen-deficient polypeptide radical cations. <i>Chemical Physics Letters</i> , 2000, 330, 558-562.	2.6	58
48	Experiences and perspectives of MALDI MS and MS/MS in proteomic research. <i>International Journal of Mass Spectrometry</i> , 2003, 226, 223-237.	1.5	54
49	Tousled-like kinases phosphorylate Asf1 to promote histone supply during DNA replication. <i>Nature Communications</i> , 2014, 5, 3394.	12.8	54
50	Advances in characterizing ubiquitylation sites by mass spectrometry. <i>Current Opinion in Chemical Biology</i> , 2013, 17, 49-58.	6.1	53
51	Treacle controls the nucleolar response to rDNA breaks via TOPBP1 recruitment and ATR activation. <i>Nature Communications</i> , 2020, 11, 123.	12.8	53
52	Immunoaffinity Enrichments Followed by Mass Spectrometric Detection for Studying Global Protein Tyrosine Phosphorylation. <i>Journal of Proteome Research</i> , 2008, 7, 2897-2910.	3.7	52
53	Unrestrained poly-ADP-ribosylation provides insights into chromatin regulation and human disease. <i>Molecular Cell</i> , 2021, 81, 2640-2655.e8.	9.7	52
54	Serine-linked PARP1 auto-modification controls PARP inhibitor response. <i>Nature Communications</i> , 2021, 12, 4055.	12.8	51

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55	Biotin starvation causes mitochondrial protein hyperacetylation and partial rescue by the SIRT3-like deacetylase Hst4p. <i>Nature Communications</i> , 2015, 6, 7726.	12.8	47
56	The regulatory landscape of the human HPF1- and ARH3-dependent ADP-ribosylome. <i>Nature Communications</i> , 2021, 12, 5893.	12.8	45
57	The ubiquitin ligase RFWD3 is required for translesion DNA synthesis. <i>Molecular Cell</i> , 2021, 81, 442-458.e9.	9.7	43
58	Chemical genetics and proteome-wide site mapping reveal cysteine MARYlation by PARP-7 on immune-relevant protein targets. <i>ELife</i> , 2021, 10, .	6.0	43
59	Can relative cleavage frequencies in peptides provide additional sequence information?. <i>International Journal of Mass Spectrometry</i> , 2002, 219, 283-294.	1.5	42
60	Analytical Utility of Small Neutral Losses from Reduced Species in Electron Capture Dissociation Studied Using SwedECD Database. <i>Analytical Chemistry</i> , 2008, 80, 8089-8094.	6.5	42
61	Using Guanidine-Hydrochloride for Fast and Efficient Protein Digestion and Single-step Affinity-purification Mass Spectrometry. <i>Journal of Proteome Research</i> , 2013, 12, 1020-1030.	3.7	41
62	PhosTShunter: A Fast and Reliable Tool to Detect Phosphorylated Peptides in Liquid Chromatography Fourier Transform Tandem Mass Spectrometry Data Sets. <i>Journal of Proteome Research</i> , 2006, 5, 659-668.	3.7	39
63	The molecular basis of ATM-dependent dimerization of the Mdc1 DNA damage checkpoint mediator. <i>Nucleic Acids Research</i> , 2012, 40, 3913-3928.	14.5	39
64	Protein Interaction Screening for the Ankyrin Repeats and Suppressor of Cytokine Signaling (SOCS) Box (ASB) Family Identify Asb11 as a Novel Endoplasmic Reticulum Resident Ubiquitin Ligase. <i>Journal of Biological Chemistry</i> , 2014, 289, 2043-2054.	3.4	37
65	Specifying RNA-Binding Regions in Proteins by Peptide Cross-Linking and Affinity Purification. <i>Journal of Proteome Research</i> , 2017, 16, 2762-2772.	3.7	37
66	Peptide End Sequencing by Orthogonal MALDI Tandem Mass Spectrometry. <i>Journal of Proteome Research</i> , 2002, 1, 63-71.	3.7	34
67	Tandem MALDI/EI ionization for tandem Fourier transform ion cyclotron resonance mass spectrometry of polypeptides. <i>International Journal of Mass Spectrometry</i> , 2003, 226, 181-187.	1.5	33
68	On studying protein phosphorylation patterns using bottom-up LC-MS/MS: the case of human β -casein. <i>Analyst</i> , 2007, 132, 768-776.	3.5	33
69	Identification of dominant signaling pathways from proteomics expression data. <i>Journal of Proteomics</i> , 2008, 71, 89-96.	2.4	33
70	Extensive SUMO Modification of Repressive Chromatin Factors Distinguishes Pluripotent from Somatic Cells. <i>Cell Reports</i> , 2020, 32, 108146.	6.4	33
71	Comparison of electron capture dissociation and collisionally activated dissociation of polycations of peptide nucleic acids. <i>Rapid Communications in Mass Spectrometry</i> , 2001, 15, 969-974.	1.5	32
72	Mechanism and function of DNA replication-independent DNA-protein crosslink repair via the SUMO-RNF4 pathway. <i>EMBO Journal</i> , 2021, 40, e107413.	7.8	32

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73	DNAJC9 integrates heat shock molecular chaperones into the histone chaperone network. <i>Molecular Cell</i> , 2021, 81, 2533-2548.e9.	9.7	31
74	SwedCAD, a Database of Annotated High-Mass Accuracy MS/MS Spectra of Tryptic Peptides. <i>Journal of Proteome Research</i> , 2007, 6, 4063-4067.	3.7	28
75	Backbone Carbonyl Group Basicities Are Related to Gas-Phase Fragmentation of Peptides and Protein Folding. <i>Angewandte Chemie - International Edition</i> , 2007, 46, 1481-1484.	13.8	25
76	Proteome-Wide Identification of In Vivo ADP-Ribose Acceptor Sites by Liquid Chromatography–Tandem Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2017, 1608, 149-162.	0.9	24
77	Relative Specificities of Water and Ammonia Losses from Backbone Fragments in Collision-Activated Dissociation. <i>Journal of Proteome Research</i> , 2007, 6, 2669-2673.	3.7	23
78	Age-related changes in nicotine response of cholinergic and non-cholinergic laterodorsal tegmental neurons: Implications for the heightened adolescent susceptibility to nicotine addiction. <i>Neuropharmacology</i> , 2014, 85, 263-283.	4.1	23
79	Analytical Utility of Mass Spectral Binning in Proteomic Experiments by Spectral Immonium Ion Detection (SPIID). <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1914-1924.	3.8	22
80	A Two-step Protein Quality Control Pathway for a Misfolded DJ-1 Variant in Fission Yeast. <i>Journal of Biological Chemistry</i> , 2015, 290, 21141-21153.	3.4	22
81	Physicochemical Properties Determining the Detection Probability of Tryptic Peptides in Fourier Transform Mass Spectrometry. A Correlation Study. <i>Analytical Chemistry</i> , 2004, 76, 5872-5877.	6.5	21
82	Citrullination of HP1 ¹³ chromodomain affects association with chromatin. <i>Epigenetics and Chromatin</i> , 2019, 12, 21.	3.9	19
83	Comprehensive profiling of proteome changes upon sequential deletion of deubiquitylating enzymes. <i>Journal of Proteomics</i> , 2012, 75, 3886-3897.	2.4	18
84	Regulation of GLI1 by cis DNA elements and epigenetic marks. <i>DNA Repair</i> , 2019, 79, 10-21.	2.8	18
85	Multisite SUMOylation restrains DNA polymerase β interactions with DNA damage sites. <i>Journal of Biological Chemistry</i> , 2020, 295, 8350-8362.	3.4	17
86	Pdx1 Is Post-Translationally Modified In vivo and Serine 61 Is the Principal Site of Phosphorylation. <i>PLoS ONE</i> , 2012, 7, e35233.	2.5	16
87	Applicability of Small-Molecule Inhibitors in the Study of Peptidyl Arginine Deiminase 2 (PAD2) and PAD4. <i>Frontiers in Immunology</i> , 2021, 12, 716250.	4.8	16
88	Self-hydroxylation of the splicing factor lysyl hydroxylase, JMJD6. <i>MedChemComm</i> , 2012, 3, 80-85.	3.4	15
89	Shifted-basis technique improves accuracy of peak position determination in Fourier transform mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2004, 15, 457-461.	2.8	14
90	Temporal and Site-Specific ADP-Ribosylation Dynamics upon Different Genotoxic Stresses. <i>Cells</i> , 2021, 10, 2927.	4.1	12

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91	SCAI promotes error-free repair of DNA interstrand crosslinks via the Fanconi anemia pathway. EMBO Reports, 2022, 23, e53639.	4.5	12
92	ATP Enhances Neuronal Differentiation of PC12 Cells by Activating PKC Interactions with Cytoskeletal Proteins. Journal of Proteome Research, 2011, 10, 529-540.	3.7	11
93	Improved Reversed Phase Chromatography of Hydrophilic Peptides from Spatial and Temporal Changes in Column Temperature. Journal of Proteome Research, 2017, 16, 2307-2317.	3.7	11
94	Interaction of Sox2 with RNA binding proteins in mouse embryonic stem cells. Experimental Cell Research, 2019, 381, 129-138.	2.6	10
95	Identification of Protein Direct Interactome with Genetic Code Expansion and Search Engine OpenUaa. Advanced Biology, 2021, 5, e2000308.	2.5	10
96	MaxQuant.Live Enables Enhanced Selectivity and Identification of Peptides Modified by Endogenous SUMO and Ubiquitin. Journal of Proteome Research, 2021, 20, 2042-2055.	3.7	9
97	Waves of sumoylation support transcription dynamics during adipocyte differentiation. Nucleic Acids Research, 2022, 50, 1351-1369.	14.5	8
98	Large-scale Identification of the Arginine Methylome by Mass Spectrometry. Current Protocols in Protein Science, 2015, 82, 24.7.1-24.7.17.	2.8	2