

Michael Lund Nielsen

List of Publications by Year in descending order

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98
papers

14,375
citations

50566

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docs citations

107
times ranked

22346
citing authors

#	ARTICLE	IF	CITATIONS
1	Lysine Acetylation Targets Protein Complexes and Co-Regulates Major Cellular Functions. <i>Science</i> , 2009, 325, 834-840.	6.0	3,883
2	Comprehensive mass-spectrometry-based proteome quantification of haploid versus diploid yeast. <i>Nature</i> , 2008, 455, 1251-1254.	13.7	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.	2.5	754
4	Liquid demixing of intrinsically disordered proteins is seeded by poly(ADP-ribose). <i>Nature Communications</i> , 2015, 6, 8088.	5.8	463
5	An Optimized Shotgun Strategy for the Rapid Generation of Comprehensive Human Proteomes. <i>Cell Systems</i> , 2017, 4, 587-599.e4.	2.9	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.	2.5	398
7	Citrullination regulates pluripotency and histone H1 binding to chromatin. <i>Nature</i> , 2014, 507, 104-108.	13.7	358
8	Jmjd6 Catalyses Lysyl-Hydroxylation of U2AF65, a Protein Associated with RNA Splicing. <i>Science</i> , 2009, 325, 90-93.	6.0	356
9	Proteome-wide Identification of Poly(ADP-Ribosyl)ation Targets in Different Genotoxic Stress Responses. <i>Molecular Cell</i> , 2013, 52, 272-285.	4.5	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.	3.6	283
11	Mass Spectrometric Analysis of Lysine Ubiquitylation Reveals Promiscuity at Site Level. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.003590.	2.5	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.	1.8	270
13	Iodoacetamide-induced artifact mimics ubiquitination in mass spectrometry. <i>Nature Methods</i> , 2008, 5, 459-460.	9.0	268
14	Proteomic Analyses Reveal Divergent Ubiquitylation Site Patterns in Murine Tissues. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1578-1585.	2.5	244
15	Proteome-wide analysis of arginine monomethylation reveals widespread occurrence in human cells. <i>Science Signaling</i> , 2016, 9, rs9.	1.6	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.	4.6	234
17	Glutamine methylation in histone H2A is an RNA-polymerase-I-dedicated modification. <i>Nature</i> , 2014, 505, 564-568.	13.7	186
18	De Novo Peptide Sequencing and Identification with Precision Mass Spectrometry. <i>Journal of Proteome Research</i> , 2007, 6, 114-123.	1.8	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.	2.5	178
20	Proteome-wide identification of the endogenous ADP-ribosylome of mammalian cells and tissue. <i>Nature Communications</i> , 2016, 7, 12917.	5.8	172
21	ADP-ribosyltransferases, an update on function and nomenclature. <i>FEBS Journal</i> , 2022, 289, 7399-7410.	2.2	150
22	Proteomics-Grade de Novo Sequencing Approach. <i>Journal of Proteome Research</i> , 2005, 4, 2348-2354.	1.8	147
23	Site-specific characterization of endogenous SUMOylation across species and organs. <i>Nature Communications</i> , 2018, 9, 2456.	5.8	139
24	Improving Protein Identification Using Complementary Fragmentation Techniques in Fourier Transform Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 835-845.	2.5	128
25	The NBS1-Treacle complex controls ribosomal RNA transcription in response to DNA damage. <i>Nature Cell Biology</i> , 2014, 16, 792-803.	4.6	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.	2.9	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.	1.2	120
28	A new cellular stress response that triggers centriolar satellite reorganization and ciliogenesis. <i>EMBO Journal</i> , 2013, 32, 3029-3040.	3.5	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.	2.5	113
30	Advantages of External Accumulation for Electron Capture Dissociation in Fourier Transform Mass Spectrometry. <i>Analytical Chemistry</i> , 2001, 73, 2998-3005.	3.2	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.	0.9	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.	2.5	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.	2.5	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.	2.5	88
35	Bub1 positions Mad1 close to KNL1 MELT repeats to promote checkpoint signalling. <i>Nature Communications</i> , 2017, 8, 15822.	5.8	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.	2.5	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.	7.2	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.	2.9	79
39	Specificity and Commonality of the Phosphoinositide-Binding Proteome Analyzed by Quantitative Mass Spectrometry. <i>Cell Reports</i> , 2014, 6, 578-591.	2.9	75
40	Mapping Physiological ADP-Ribosylation Using Activated Ion Electron Transfer Dissociation. <i>Cell Reports</i> , 2020, 32, 108176.	2.9	75
41	Liquid Chromatography at Critical Conditions: A Comprehensive Approach to Sequence-Dependent Retention Time Prediction. <i>Analytical Chemistry</i> , 2006, 78, 7770-7777.	3.2	73
42	SUMOylation promotes protective responses to DNA-protein crosslinks. <i>EMBO Journal</i> , 2019, 38, .	3.5	73
43	Side-Chain Losses in Electron Capture Dissociation To Improve Peptide Identification. <i>Analytical Chemistry</i> , 2007, 79, 2296-2302.	3.2	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.	3.3	61
45	The SOCS2 Ubiquitin Ligase Complex Regulates The Growth Hormone Receptor Levels. <i>PLoS ONE</i> , 2011, 6, e25358.	1.1	60
46	PAD2-Mediated Citrullination Contributes to Efficient Oligodendrocyte Differentiation and Myelination. <i>Cell Reports</i> , 2019, 27, 1090-1102.e10.	2.9	59
47	Intramolecular hydrogen atom transfer in hydrogen-deficient polypeptide radical cations. <i>Chemical Physics Letters</i> , 2000, 330, 558-562.	1.2	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.	0.7	54
49	Tousled-like kinases phosphorylate Asf1 to promote histone supply during DNA replication. <i>Nature Communications</i> , 2014, 5, 3394.	5.8	54
50	Advances in characterizing ubiquitylation sites by mass spectrometry. <i>Current Opinion in Chemical Biology</i> , 2013, 17, 49-58.	2.8	53
51	Treacle controls the nucleolar response to rDNA breaks via TOPBP1 recruitment and ATR activation. <i>Nature Communications</i> , 2020, 11, 123.	5.8	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.	1.8	52
53	Unrestrained poly-ADP-ribosylation provides insights into chromatin regulation and human disease. <i>Molecular Cell</i> , 2021, 81, 2640-2655.e8.	4.5	52
54	Serine-linked PARP1 auto-modification controls PARP inhibitor response. <i>Nature Communications</i> , 2021, 12, 4055.	5.8	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.	5.8	47
56	The regulatory landscape of the human HPF1- and ARH3-dependent ADP-ribosylome. <i>Nature Communications</i> , 2021, 12, 5893.	5.8	45
57	The ubiquitin ligase RFW3 is required for translesion DNA synthesis. <i>Molecular Cell</i> , 2021, 81, 442-458.e9.	4.5	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, .	2.8	43
59	Can relative cleavage frequencies in peptides provide additional sequence information?. <i>International Journal of Mass Spectrometry</i> , 2002, 219, 283-294.	0.7	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.	3.2	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.	1.8	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.	1.8	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.	6.5	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.	1.6	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.	1.8	37
66	Peptide End Sequencing by Orthogonal MALDI Tandem Mass Spectrometry. <i>Journal of Proteome Research</i> , 2002, 1, 63-71.	1.8	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.	0.7	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.	1.7	33
69	Identification of dominant signaling pathways from proteomics expression data. <i>Journal of Proteomics</i> , 2008, 71, 89-96.	1.2	33
70	Extensive SUMO Modification of Repressive Chromatin Factors Distinguishes Pluripotent from Somatic Cells. <i>Cell Reports</i> , 2020, 32, 108146.	2.9	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.	0.7	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.	3.5	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.	4.5	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.	1.8	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.	7.2	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.	0.4	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.	1.8	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.	2.0	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.	2.5	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.	1.6	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.	3.2	21
82	Citrullination of HP1 ³ chromodomain affects association with chromatin. <i>Epigenetics and Chromatin</i> , 2019, 12, 21.	1.8	19
83	Comprehensive profiling of proteome changes upon sequential deletion of deubiquitylating enzymes. <i>Journal of Proteomics</i> , 2012, 75, 3886-3897.	1.2	18
84	Regulation of GIL1 by cis DNA elements and epigenetic marks. <i>DNA Repair</i> , 2019, 79, 10-21.	1.3	18
85	Multisite SUMOylation restrains DNA polymerase β interactions with DNA damage sites. <i>Journal of Biological Chemistry</i> , 2020, 295, 8350-8362.	1.6	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.	1.1	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.	2.2	16
88	Self-hydroxylation of the splicing factor lysyl hydroxylase, JMJD6. <i>MedChemComm</i> , 2012, 3, 80-85.	3.5	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.	1.2	14
90	Temporal and Site-Specific ADP-Ribosylation Dynamics upon Different Genotoxic Stresses. <i>Cells</i> , 2021, 10, 2927.	1.8	12

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91	SCAI promotes error-free repair of DNA interstrand crosslinks via the Fanconi anemia pathway. <i>EMBO Reports</i> , 2022, 23, e53639.	2.0	12
92	ATP Enhances Neuronal Differentiation of PC12 Cells by Activating PKC ζ Interactions with Cytoskeletal Proteins. <i>Journal of Proteome Research</i> , 2011, 10, 529-540.	1.8	11
93	Improved Reversed Phase Chromatography of Hydrophilic Peptides from Spatial and Temporal Changes in Column Temperature. <i>Journal of Proteome Research</i> , 2017, 16, 2307-2317.	1.8	11
94	Interaction of Sox2 with RNA binding proteins in mouse embryonic stem cells. <i>Experimental Cell Research</i> , 2019, 381, 129-138.	1.2	10
95	Identification of Protein Direct Interactome with Genetic Code Expansion and Search Engine OpenUaa. <i>Advanced Biology</i> , 2021, 5, e2000308.	1.4	10
96	MaxQuant.Live Enables Enhanced Selectivity and Identification of Peptides Modified by Endogenous SUMO and Ubiquitin. <i>Journal of Proteome Research</i> , 2021, 20, 2042-2055.	1.8	9
97	Waves of sumoylation support transcription dynamics during adipocyte differentiation. <i>Nucleic Acids Research</i> , 2022, 50, 1351-1369.	6.5	8
98	Large-scale Identification of the Arginine Methylome by Mass Spectrometry. <i>Current Protocols in Protein Science</i> , 2015, 82, 24.7.1-24.7.17.	2.8	2