

Michael Lund Nielsen

List of Publications by Year in descending order

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98
papers

14,375
citations

44069
48
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33894
99
g-index

107
all docs

107
docs citations

107
times ranked

20106
citing authors

#	ARTICLE	IF	CITATIONS
1	ADP-ribosyltransferases, an update on function and nomenclature. FEBS Journal, 2022, 289, 7399-7410.	4.7	150
2	Waves of sumoylation support transcription dynamics during adipocyte differentiation. Nucleic Acids Research, 2022, 50, 1351-1369.	14.5	8
3	SCAI promotes error-free repair of DNA interstrand crosslinks via the Fanconi anemia pathway. EMBO Reports, 2022, 23, e53639.	4.5	12
4	The ubiquitin ligase RFWD3 is required for translesion DNA synthesis. Molecular Cell, 2021, 81, 442-458.e9.	9.7	43
5	Chemical genetics and proteome-wide site mapping reveal cysteine MArlylation by PARP-7 on immune-relevant protein targets. ELife, 2021, 10, .	6.0	43
6	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
7	Identification of Protein Direct Interactome with Genetic Code Expansion and Search Engine OpenUaa. Advanced Biology, 2021, 5, e2000308.	2.5	10
8	Unrestrained poly-ADP-ribosylation provides insights into chromatin regulation and human disease. Molecular Cell, 2021, 81, 2640-2655.e8.	9.7	52
9	DNAJC9 integrates heat shock molecular chaperones into the histone chaperone network. Molecular Cell, 2021, 81, 2533-2548.e9.	9.7	31
10	Serine-linked PARP1 auto-modification controls PARP inhibitor response. Nature Communications, 2021, 12, 4055.	12.8	51
11	Mechanism and function of DNA replication-independent DNA-protein crosslink repair via the SUMO-RNF4 pathway. EMBO Journal, 2021, 40, e107413.	7.8	32
12	The regulatory landscape of the human HPF1- and ARH3-dependent ADP-ribosylome. Nature Communications, 2021, 12, 5893.	12.8	45
13	Applicability of Small-Molecule Inhibitors in the Study of Peptidyl Arginine Deiminase 2 (PAD2) and PAD4. Frontiers in Immunology, 2021, 12, 716250.	4.8	16
14	Temporal and Site-Specific ADP-Ribosylation Dynamics upon Different Genotoxic Stresses. Cells, 2021, 10, 2927.	4.1	12
15	Treacle controls the nucleolar response to rDNA breaks via TOPBP1 recruitment and ATR activation. Nature Communications, 2020, 11, 123.	12.8	53
16	Extensive SUMO Modification of Repressive Chromatin Factors Distinguishes Pluripotent from Somatic Cells. Cell Reports, 2020, 32, 108146.	6.4	33
17	Mapping Physiological ADP-Ribosylation Using Activated Ion Electron Transfer Dissociation. Cell Reports, 2020, 32, 108176.	6.4	75
18	Multisite SUMOylation restrains DNA polymerase β interactions with DNA damage sites. Journal of Biological Chemistry, 2020, 295, 8350-8362.	3.4	17

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19	Interaction of Sox2 with RNA binding proteins in mouse embryonic stem cells. <i>Experimental Cell Research</i> , 2019, 381, 129-138.	2.6	10
20	PAD2-Mediated Citrullination Contributes to Efficient Oligodendrocyte Differentiation and Myelination. <i>Cell Reports</i> , 2019, 27, 1090-1102.e10.	6.4	59
21	Regulation of GLI1 by cis DNA elements and epigenetic marks. <i>DNA Repair</i> , 2019, 79, 10-21.	2.8	18
22	SUMOylation promotes protective responses to DNA-protein crosslinks. <i>EMBO Journal</i> , 2019, 38, .	7.8	73
23	Citrullination of HP1 ³ chromodomain affects association with chromatin. <i>Epigenetics and Chromatin</i> , 2019, 12, 21.	3.9	19
24	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
25	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
26	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
27	Site-specific characterization of endogenous SUMOylation across species and organs. <i>Nature Communications</i> , 2018, 9, 2456.	12.8	139
28	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
29	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.	3.7	11
30	An Optimized Shotgun Strategy for the Rapid Generation of Comprehensive Human Proteomes. <i>Cell Systems</i> , 2017, 4, 587-599.e4.	6.2	413
31	Bub1 positions Mad1 close to KNL1 MELT repeats to promote checkpoint signalling. <i>Nature Communications</i> , 2017, 8, 15822.	12.8	84
32	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
33	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
34	Proteome-wide analysis of arginine monomethylation reveals widespread occurrence in human cells. <i>Science Signaling</i> , 2016, 9, rs9.	3.6	241
35	Proteome-wide identification of the endogenous ADP-ribosylome of mammalian cells and tissue. <i>Nature Communications</i> , 2016, 7, 12917.	12.8	172
36	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

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37	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
38	Liquid demixing of intrinsically disordered proteins is seeded by poly(ADP-ribose). <i>Nature Communications</i> , 2015, 6, 8088.	12.8	463
39	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
40	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
41	Glutamine methylation in histone H2A is an RNA-polymerase-I-dedicated modification. <i>Nature</i> , 2014, 505, 564-568.	27.8	186
42	Citrullination regulates pluripotency and histone H1 binding to chromatin. <i>Nature</i> , 2014, 507, 104-108.	27.8	358
43	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
44	Tousled-like kinases phosphorylate Asf1 to promote histone supply during DNA replication. <i>Nature Communications</i> , 2014, 5, 3394.	12.8	54
45	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
46	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
47	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
48	Specificity and Commonality of the Phosphoinositide-Binding Proteome Analyzed by Quantitative Mass Spectrometry. <i>Cell Reports</i> , 2014, 6, 578-591.	6.4	75
49	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
50	CDK-mediated activation of the SCF ^{FBXO28} ubiquitin ligase promotes MYC-driven transcription and tumourigenesis and predicts poor survival in breast cancer. <i>EMBO Molecular Medicine</i> , 2013, 5, 1067-1086.	6.9	61
51	Advances in characterizing ubiquitylation sites by mass spectrometry. <i>Current Opinion in Chemical Biology</i> , 2013, 17, 49-58.	6.1	53
52	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
53	A new cellular stress response that triggers centriolar satellite reorganization and ciliogenesis. <i>EMBO Journal</i> , 2013, 32, 3029-3040.	7.8	115
54	Proteomic Analyses Reveal Divergent Ubiquitylation Site Patterns in Murine Tissues. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1578-1585.	3.8	244

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55	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
56	Self-hydroxylation of the splicing factor lysyl hydroxylase, JMJD6. <i>MedChemComm</i> , 2012, 3, 80-85.	3.4	15
57	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
58	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
59	Comprehensive profiling of proteome changes upon sequential deletion of deubiquitylating enzymes. <i>Journal of Proteomics</i> , 2012, 75, 3886-3897.	2.4	18
60	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
61	ATP Enhances Neuronal Differentiation of PC12 Cells by Activating PKC δ Interactions with Cytoskeletal Proteins. <i>Journal of Proteome Research</i> , 2011, 10, 529-540.	3.7	11
62	The SOCS2 Ubiquitin Ligase Complex Regulates Growth Hormone Receptor Levels. <i>PLoS ONE</i> , 2011, 6, e25358.	2.5	60
63	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
64	Mass Spectrometric Analysis of Lysine Ubiquitylation Reveals Promiscuity at Site Level. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.003590.	3.8	275
65	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
66	Lysine Acetylation Targets Protein Complexes and Co-Regulates Major Cellular Functions. <i>Science</i> , 2009, 325, 834-840.	12.6	3,883
67	Jmjd6 Catalyses Lysyl-Hydroxylation of U2AF65, a Protein Associated with RNA Splicing. <i>Science</i> , 2009, 325, 90-93.	12.6	356
68	Identification of dominant signaling pathways from proteomics expression data. <i>Journal of Proteomics</i> , 2008, 71, 89-96.	2.4	33
69	Comprehensive mass-spectrometry-based proteome quantification of haploid versus diploid yeast. <i>Nature</i> , 2008, 455, 1251-1254.	27.8	835
70	Iodoacetamide-induced artifact mimics ubiquitination in mass spectrometry. <i>Nature Methods</i> , 2008, 5, 459-460.	19.0	268
71	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
72	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

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73	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
74	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
75	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
76	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
77	Side-Chain Losses in Electron Capture Dissociation To Improve Peptide Identification. <i>Analytical Chemistry</i> , 2007, 79, 2296-2302.	6.5	68
78	De Novo Peptide Sequencing and Identification with Precision Mass Spectrometry. <i>Journal of Proteome Research</i> , 2007, 6, 114-123.	3.7	185
79	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
80	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
81	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
82	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
83	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
84	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
85	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
86	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
87	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
88	Proteomics-Grade de Novo Sequencing Approach. <i>Journal of Proteome Research</i> , 2005, 4, 2348-2354.	3.7	147
89	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
90	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

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91	Physicochemical Properties Determining the Detection Probability of Tryptic Peptides in Fourier Transform Mass Spectrometry. A Correlation Study. Analytical Chemistry, 2004, 76, 5872-5877.	6.5	21
92	Tandem MALDI/El ionization for tandem Fourier transform ion cyclotron resonance mass spectrometry of polypeptides. International Journal of Mass Spectrometry, 2003, 226, 181-187.	1.5	33
93	Experiences and perspectives of MALDI MS and MS/MS in proteomic research. International Journal of Mass Spectrometry, 2003, 226, 223-237.	1.5	54
94	Peptide End Sequencing by Orthogonal MALDI Tandem Mass Spectrometry. Journal of Proteome Research, 2002, 1, 63-71.	3.7	34
95	Can relative cleavage frequencies in peptides provide additional sequence information?. International Journal of Mass Spectrometry, 2002, 219, 283-294.	1.5	42
96	Advantages of External Accumulation for Electron Capture Dissociation in Fourier Transform Mass Spectrometry. Analytical Chemistry, 2001, 73, 2998-3005.	6.5	106
97	Comparison of electron capture dissociation and collisionally activated dissociation of polycations of peptide nucleic acids. Rapid Communications in Mass Spectrometry, 2001, 15, 969-974.	1.5	32
98	Intramolecular hydrogen atom transfer in hydrogen-deficient polypeptide radical cations. Chemical Physics Letters, 2000, 330, 558-562.	2.6	58