

# Shabaz Mohammed

## List of Publications by Year in descending order

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178  
papers

19,054  
citations

15466

65  
h-index

12910

131  
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192  
all docs

192  
docs citations

192  
times ranked

28278  
citing authors

#	ARTICLE	IF	CITATIONS
1	The CRAPome: a contaminant repository for affinity purification-mass spectrometry data. <i>Nature Methods</i> , 2013, 10, 730-736.	9.0	1,353
2	Multiplex peptide stable isotope dimethyl labeling for quantitative proteomics. <i>Nature Protocols</i> , 2009, 4, 484-494.	5.5	1,247
3	Lgr5 homologues associate with Wnt receptors and mediate R-spondin signalling. <i>Nature</i> , 2011, 476, 293-297.	13.7	1,096
4	Tumour suppressor RNF43 is a stem-cell E3 ligase that induces endocytosis of Wnt receptors. <i>Nature</i> , 2012, 488, 665-669.	13.7	791
5	Wnt Signaling through Inhibition of $\beta$ -Catenin Degradation in an Intact Axin1 Complex. <i>Cell</i> , 2012, 149, 1245-1256.	13.5	747
6	Quantitative Phosphoproteomics Applied to the Yeast Pheromone Signaling Pathway. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 310-327.	2.5	708
7	The Lgr5 intestinal stem cell signature: robust expression of proposed quiescent $\beta$ -catenin cell markers. <i>EMBO Journal</i> , 2012, 31, 3079-3091.	3.5	634
8	Quantitative Phosphoproteomics of Early Elicitor Signaling in Arabidopsis. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 1198-1214.	2.5	614
9	Regulation of retromer recruitment to endosomes by sequential action of Rab5 and Rab7. <i>Journal of Cell Biology</i> , 2008, 183, 513-526.	2.3	395
10	Toward a Comprehensive Characterization of a Human Cancer Cell Phosphoproteome. <i>Journal of Proteome Research</i> , 2013, 12, 260-271.	1.8	363
11	Phosphopeptide fragmentation and analysis by mass spectrometry. <i>Journal of Mass Spectrometry</i> , 2009, 44, 861-878.	0.7	349
12	Robust phosphoproteome enrichment using monodisperse microsphere-based immobilized titanium (IV) ion affinity chromatography. <i>Nature Protocols</i> , 2013, 8, 461-480.	5.5	340
13	Improved Peptide Identification by Targeted Fragmentation Using CID, HCD and ETD on an LTQ-Orbitrap Velos. <i>Journal of Proteome Research</i> , 2011, 10, 2377-2388.	1.8	277
14	hnRNPK Recruits PCGF3/5-PRC1 to the Xist RNA B-Repeat to Establish Polycomb-Mediated Chromosomal Silencing. <i>Molecular Cell</i> , 2017, 68, 955-969.e10.	4.5	255
15	Lys-N and Trypsin Cover Complementary Parts of the Phosphoproteome in a Refined SCX-Based Approach. <i>Analytical Chemistry</i> , 2009, 81, 4493-4501.	3.2	251
16	Posttranslational mutagenesis: A chemical strategy for exploring protein side-chain diversity. <i>Science</i> , 2016, 354, .	6.0	247
17	A systematic approach to modeling, capturing, and disseminating proteomics experimental data. <i>Nature Biotechnology</i> , 2003, 21, 247-254.	9.4	246
18	Toward Full Peptide Sequence Coverage by Dual Fragmentation Combining Electron-Transfer and Higher-Energy Collision Dissociation Tandem Mass Spectrometry. <i>Analytical Chemistry</i> , 2012, 84, 9668-9673.	3.2	246

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19	Hydrophilic interaction liquid chromatography (HILIC) in proteomics. <i>Analytical and Bioanalytical Chemistry</i> , 2008, 391, 151-159.	1.9	234
20	The Generating Function of CID, ETD, and CID/ETD Pairs of Tandem Mass Spectra: Applications to Database Search. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 2840-2852.	2.5	226
21	An optimized protocol for metabolome analysis in yeast using direct infusion electrospray mass spectrometry. <i>Phytochemistry</i> , 2003, 62, 929-937.	1.4	207
22	Polyamines Control eIF5A Hypusination, TFEB Translation, and Autophagy to Reverse B Cell Senescence. <i>Molecular Cell</i> , 2019, 76, 110-125.e9.	4.5	205
23	Nuclear PtdIns5P as a Transducer of Stress Signaling: An In Vivo Role for PIP4Kbeta. <i>Molecular Cell</i> , 2006, 23, 685-695.	4.5	194
24	Triplex protein quantification based on stable isotope labeling by peptide dimethylation applied to cell and tissue lysates. <i>Proteomics</i> , 2008, 8, 4624-4632.	1.3	192
25	Evaluation and Optimization of ZIC-HILIC-RP as an Alternative MudPIT Strategy. <i>Journal of Proteome Research</i> , 2007, 6, 937-946.	1.8	182
26	The kinase TNIK is an essential activator of Wnt target genes. <i>EMBO Journal</i> , 2009, 28, 3329-3340.	3.5	169
27	Cross-talk between phosphorylation and lysine acetylation in a genome-reduced bacterium. <i>Molecular Systems Biology</i> , 2012, 8, 571.	3.2	169
28	Highly Robust, Automated, and Sensitive Online TiO <sub>2</sub> -Based Phosphoproteomics Applied To Study Endogenous Phosphorylation in <i>Drosophila melanogaster</i> . <i>Journal of Proteome Research</i> , 2008, 7, 687-697.	1.8	165
29	A large synthetic peptide and phosphopeptide reference library for mass spectrometry-based proteomics. <i>Nature Biotechnology</i> , 2013, 31, 557-564.	9.4	164
30	A PP2A-B55 recognition signal controls substrate dephosphorylation kinetics during mitotic exit. <i>Journal of Cell Biology</i> , 2016, 214, 539-554.	2.3	164
31	Unambiguous Phosphosite Localization using Electron-Transfer/Higher-Energy Collision Dissociation (ETHcD). <i>Journal of Proteome Research</i> , 2013, 12, 1520-1525.	1.8	145
32	Recent advances in peptide separation by multidimensional liquid chromatography for proteome analysis. <i>Journal of Proteomics</i> , 2012, 75, 3791-3813.	1.2	141
33	System-wide Profiling of RNA-Binding Proteins Uncovers Key Regulators of Virus Infection. <i>Molecular Cell</i> , 2019, 74, 196-211.e11.	4.5	137
34	Activation of FoxM1 during G <sub>2</sub> Requires Cyclin A/Cdk-Dependent Relief of Autorepression by the FoxM1 N-Terminal Domain. <i>Molecular and Cellular Biology</i> , 2008, 28, 3076-3087.	1.1	131
35	Zwitterionic Hydrophilic Interaction Liquid Chromatography (ZIC-HILIC and ZIC-cHILIC) Provide High Resolution Separation and Increase Sensitivity in Proteome Analysis. <i>Analytical Chemistry</i> , 2011, 83, 3440-3447.	3.2	128
36	Personalized Proteome Profiles of Healthy and Tumor Human Colon Organoids Reveal Both Individual Diversity and Basic Features of Colorectal Cancer. <i>Cell Reports</i> , 2017, 18, 263-274.	2.9	126

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37	Optimal Synthetic Glycosylation of a Therapeutic Antibody. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 2361-2367.	7.2	122
38	Identification of ischemia-regulated phosphorylation sites in connexin43: A possible target for the antiarrhythmic peptide analogue rotigaptide (ZP123). <i>Journal of Molecular and Cellular Cardiology</i> , 2006, 40, 790-798.	0.9	118
39	Straightforward ladder sequencing of peptides using a Lys-N metalloendopeptidase. <i>Nature Methods</i> , 2008, 5, 405-407.	9.0	116
40	Profiling of N-Acetylated Protein Termini Provides In-depth Insights into the N-terminal Nature of the Proteome. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 928-939.	2.5	113
41	Quantitative and Qualitative Proteome Characteristics Extracted from In-Depth Integrated Genomics and Proteomics Analysis. <i>Cell Reports</i> , 2013, 5, 1469-1478.	2.9	113
42	Benchmarking stable isotope labeling based quantitative proteomics. <i>Journal of Proteomics</i> , 2013, 88, 14-26.	1.2	112
43	Modification-Specific Proteomics of Plasma Membrane Proteins: Identification and Characterization of Glycosylphosphatidylinositol-Anchored Proteins Released upon Phospholipase D Treatment. <i>Journal of Proteome Research</i> , 2006, 5, 935-943.	1.8	111
44	Global analysis of protein-RNA interactions in SARS-CoV-2-infected cells reveals key regulators of infection. <i>Molecular Cell</i> , 2021, 81, 2851-2867.e7.	4.5	108
45	Light-driven post-translational installation of reactive protein side chains. <i>Nature</i> , 2020, 585, 530-537.	13.7	100
46	Quantitative Phosphoproteomics after Auxin-stimulated Lateral Root Induction Identifies an SNX1 Protein Phosphorylation Site Required for Growth. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 1158-1169.	2.5	95
47	Targeted Analysis of Protein Termini. <i>Journal of Proteome Research</i> , 2007, 6, 4634-4645.	1.8	93
48	Selective Metal-Site-Guided Arylation of Proteins. <i>Journal of the American Chemical Society</i> , 2016, 138, 8678-8681.	6.6	92
49	Toward an Optimized Workflow for Middle-Down Proteomics. <i>Analytical Chemistry</i> , 2017, 89, 3318-3325.	3.2	91
50	Improving SRM Assay Development: A Global Comparison between Triple Quadrupole, Ion Trap, and Higher Energy CID Peptide Fragmentation Spectra. <i>Journal of Proteome Research</i> , 2011, 10, 4334-4341.	1.8	90
51	The Tyrosine Phosphatase Shp2 Interacts with NPM-ALK and Regulates Anaplastic Lymphoma Cell Growth and Migration. <i>Cancer Research</i> , 2007, 67, 4278-4286.	0.4	86
52	Enhancing the Identification of Phosphopeptides from Putative Basophilic Kinase Substrates Using Ti (IV) Based IMAC Enrichment. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.006452.	2.5	81
53	Protease bias in absolute protein quantitation. <i>Nature Methods</i> , 2012, 9, 524-525.	9.0	80
54	Sampling From the Proteome to the Human Leukocyte Antigen-DR (HLA-DR) Ligandome Proceeds Via High Specificity. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1412-1423.	2.5	80

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55	Strong cation exchange (SCX) based analytical methods for the targeted analysis of protein post-translational modifications. <i>Current Opinion in Biotechnology</i> , 2011, 22, 9-16.	3.3	79
56	Quantitative Map of Proteome Dynamics during Neuronal Differentiation. <i>Cell Reports</i> , 2017, 18, 1527-1542.	2.9	79
57	The Leukemia-Associated Mllt10/Af10-Dot1l Are Tcf4/ $\beta$ -Catenin Coactivators Essential for Intestinal Homeostasis. <i>PLoS Biology</i> , 2010, 8, e1000539.	2.6	78
58	Perturbation of the yeast N-acetyltransferase NatB induces elevation of protein phosphorylation levels. <i>BMC Genomics</i> , 2010, 11, 685.	1.2	77
59	Coupled Activation and Degradation of eEF2K Regulates Protein Synthesis in Response to Genotoxic Stress. <i>Science Signaling</i> , 2012, 5, ra40.	1.6	76
60	Exploitation of an iron transporter for bacterial protein antibiotic import. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 12051-12056.	3.3	76
61	Highly Efficient Depletion Strategy for the Two Most Abundant Erythrocyte Soluble Proteins Improves Proteome Coverage Dramatically. <i>Journal of Proteome Research</i> , 2008, 7, 3060-3063.	1.8	74
62	Exploring the Human Leukocyte Phosphoproteome Using a Microfluidic Reversed-Phase <sup>2</sup> TiO <sub>2</sub> Reversed-Phase High-Performance Liquid Chromatography Phosphochip Coupled to a Quadrupole Time-of-Flight Mass Spectrometer. <i>Analytical Chemistry</i> , 2010, 82, 824-832.	3.2	74
63	Online Automated <i>in Vivo</i> Zebrafish Phosphoproteomics: From Large-Scale Analysis Down to a Single Embryo. <i>Journal of Proteome Research</i> , 2008, 7, 1555-1564.	1.8	73
64	Nuclear phosphorylated Dicer processes double-stranded RNA in response to DNA damage. <i>Journal of Cell Biology</i> , 2017, 216, 2373-2389.	2.3	73
65	p130Cas mediates the transforming properties of the anaplastic lymphoma kinase. <i>Blood</i> , 2005, 106, 3907-3916.	0.6	72
66	Strong Cation Exchange-based Fractionation of Lys-N-generated Peptides Facilitates the Targeted Analysis of Post-translational Modifications. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 190-200.	2.5	69
67	Genetic and proteomic evidences support the localization of yeast enolase in the cell surface. <i>Proteomics</i> , 2006, 6, S107-S118.	1.3	68
68	Automated Online Sequential Isotope Labeling for Protein Quantitation Applied to Proteasome Tissue-specific Diversity. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 1755-1762.	2.5	66
69	Chip-Based Enrichment and NanoLC <sup>2</sup> MS/MS Analysis of Phosphopeptides from Whole Lysates. <i>Journal of Proteome Research</i> , 2008, 7, 1565-1571.	1.8	63
70	Discovering the RNA-Binding Proteome of Plant Leaves with an Improved RNA Interactome Capture Method. <i>Biomolecules</i> , 2020, 10, 661.	1.8	63
71	Applications of stable isotope dimethyl labeling in quantitative proteomics. <i>Analytical and Bioanalytical Chemistry</i> , 2012, 404, 991-1009.	1.9	61
72	Highly Sensitive Proteome Analysis of FACS-Sorted Adult Colon Stem Cells. <i>Journal of Proteome Research</i> , 2011, 10, 3814-3819.	1.8	60

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73	Elongation/Termination Factor Exchange Mediated by PP1 Phosphatase Orchestrates Transcription Termination. <i>Cell Reports</i> , 2018, 25, 259-269.e5.	2.9	58
74	Novel Protein Phosphorylation Site Identification in Spinach Stroma Membranes by Titanium Dioxide Microcolumns and Tandem Mass Spectrometry. <i>Journal of Proteome Research</i> , 2006, 5, 973-982.	1.8	57
75	Phosphopeptide quantitation using amine-reactive isobaric tagging reagents and tandem mass spectrometry: application to proteins isolated by gel electrophoresis. <i>Rapid Communications in Mass Spectrometry</i> , 2006, 20, 1127-1134.	0.7	57
76	Cleavage specificities of the brother and sister proteases Lys-C and Lys-N. <i>Chemical Communications</i> , 2010, 46, 8827.	2.2	55
77	Probing Genuine Strong Interactions and Post-translational Modifications in the Heterogeneous Yeast Exosome Protein Complex. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 1581-1592.	2.5	53
78	Comparative Phosphoproteomics of Zebrafish Fyn/Yes Morpholino Knockdown Embryos. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 2176-2187.	2.5	53
79	Synthetic post-translational modification of histones. <i>Current Opinion in Chemical Biology</i> , 2018, 45, 35-47.	2.8	53
80	Ligand binding to a G protein-coupled receptor captured in a mass spectrometer. <i>Science Advances</i> , 2017, 3, e1701016.	4.7	52
81	Generation of a synthetic GlcNAcylated nucleosome reveals regulation of stability by H2A-Thr101 GlcNAcylation. <i>Nature Communications</i> , 2015, 6, 7978.	5.8	51
82	Serum protein profiling by miniaturized solid-phase extraction and matrix-assisted laser desorption/ionization mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2005, 19, 1578-1586.	0.7	50
83	Recovery from a DNA damage-induced G2 arrest requires Cdk-dependent activation of FoxM1. <i>EMBO Reports</i> , 2010, 11, 452-458.	2.0	50
84	Peptide Orientation Affects Selectivity in Ion-Exchange Chromatography. <i>Analytical Chemistry</i> , 2010, 82, 5253-5259.	3.2	49
85	Improving Depth in Phosphoproteomics by Using a Strong Cation Exchange-Weak Anion Exchange-Reversed Phase Multidimensional Separation Approach. <i>Analytical Chemistry</i> , 2011, 83, 7137-7143.	3.2	49
86	A systems-wide screen identifies substrates of the SCF <sup>TrCP</sup> ubiquitin ligase. <i>Science Signaling</i> , 2014, 7, rs8.	1.6	49
87	Atorvastatin modulates the profile of proteins released by human atherosclerotic plaques. <i>European Journal of Pharmacology</i> , 2007, 562, 119-129.	1.7	48
88	Interdomain conformational flexibility underpins the activity of UGGT, the eukaryotic glycoprotein secretion checkpoint. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 8544-8549.	3.3	48
89	Synthetic Phosphorylation of p38 <sup>±</sup> Recapitulates Protein Kinase Activity. <i>Journal of the American Chemical Society</i> , 2014, 136, 1698-1701.	6.6	46
90	Ultra Acidic Strong Cation Exchange Enabling the Efficient Enrichment of Basic Phosphopeptides. <i>Analytical Chemistry</i> , 2012, 84, 1804-1808.	3.2	45

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91	Universal Quantitative Kinase Assay Based on Diagonal SCX Chromatography and Stable Isotope Dimethyl Labeling Provides High-definition Kinase Consensus Motifs for PKA and Human Mps1. <i>Journal of Proteome Research</i> , 2013, 12, 2214-2224.	1.8	45
92	Quantitative Proteomics Identifies Gemin5, A Scaffolding Protein Involved in Ribonucleoprotein Assembly, as a Novel Partner for Eukaryotic Initiation Factor 4E. <i>Journal of Proteome Research</i> , 2006, 5, 1367-1378.	1.8	44
93	A Role for PtdIns(4,5)P <sub>2</sub> and PIP5K $\hat{\pm}$ in Regulating Stress-Induced Apoptosis. <i>Current Biology</i> , 2006, 16, 1850-1856.	1.8	44
94	In-house construction of a UHPLC system enabling the identification of over 4000 protein groups in a single analysis. <i>Analyst</i> , The, 2012, 137, 3541.	1.7	43
95	Characterization of Biases in Phosphopeptide Enrichment by Ti <sup>4+</sup> -Immobilized Metal Affinity Chromatography and TiO <sub>2</sub> Using a Massive Synthetic Library and Human Cell Digests. <i>Analytical Chemistry</i> , 2014, 86, 8312-8320.	3.2	43
96	Straightforward and de Novo Peptide Sequencing by MALDI-MS/MS Using a Lys-N Metalloendopeptidase. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 650-660.	2.5	42
97	Comparative Assessment of Site Assignments in CID and Electron Transfer Dissociation Spectra of Phosphopeptides Discloses Limited Relocation of Phosphate Groups. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 2140-2148.	2.5	42
98	Multiplexed Proteomics Mapping of Yeast RNA Polymerase II and III Allows Near-Complete Sequence Coverage and Reveals Several Novel Phosphorylation Sites. <i>Analytical Chemistry</i> , 2008, 80, 3584-3592.	3.2	40
99	Î²2-Syntrophin Is a Cdk5 Substrate That Restrains the Motility of Insulin Secretory Granules. <i>PLoS ONE</i> , 2010, 5, e12929.	1.1	40
100	Dimer interface of bovine cytochrome <i>c</i> oxidase is influenced by local posttranslational modifications and lipid binding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 8230-8235.	3.3	40
101	Selectivity in Enrichment of cAMP-dependent Protein Kinase Regulatory Subunits Type I and Type II and Their Interactors Using Modified cAMP Affinity Resins. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 1016-1028.	2.5	39
102	A three-way proteomics strategy allows differential analysis of yeast mitochondrial membrane protein complexes under anaerobic and aerobic conditions. <i>Proteomics</i> , 2009, 9, 4787-4798.	1.3	39
103	Effect of Chemical Modifications on Peptide Fragmentation Behavior upon Electron Transfer Induced Dissociation. <i>Analytical Chemistry</i> , 2009, 81, 7814-7822.	3.2	38
104	Genetic Incorporation of Olefin Cross-Metathesis Reaction Tags for Protein Modification. <i>Journal of the American Chemical Society</i> , 2018, 140, 14599-14603.	6.6	38
105	Guanidination chemistry for qualitative and quantitative proteomics. <i>Rapid Communications in Mass Spectrometry</i> , 2006, 20, 3245-3256.	0.7	37
106	The role of the Xist 5' m <sup>6</sup> A region and RBM15 in X chromosome inactivation. <i>Wellcome Open Research</i> , 2020, 5, 31.	0.9	37
107	Evaluation of Metalloendopeptidase Lys-N Protease Performance under Different Sample Handling Conditions. <i>Journal of Proteome Research</i> , 2010, 9, 4282-4288.	1.8	36
108	LanCLs add glutathione to dehydroamino acids generated at phosphorylated sites in the proteome. <i>Cell</i> , 2021, 184, 2680-2695.e26.	13.5	34

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109	MAP3K1 functionally interacts with Axin1 in the canonical Wnt signalling pathway. <i>Biological Chemistry</i> , 2010, 391, 171-180.	1.2	33
110	Signal Transduction Reaction Monitoring Deciphers Site-Specific PI3K-mTOR/MAPK Pathway Dynamics in Oncogene-Induced Senescence. <i>Journal of Proteome Research</i> , 2015, 14, 2906-2914.	1.8	33
111	Synthetic Nucleosomes Reveal that GlcNAcylation Modulates Direct Interaction with the FACT Complex. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 8918-8922.	7.2	32
112	Protein Phosphatase 2A (B55 $\hat{1}$ ) Prevents Premature Activation of Forkhead Transcription Factor FoxM1 by Antagonizing Cyclin A/Cyclin-dependent Kinase-mediated Phosphorylation. <i>Journal of Biological Chemistry</i> , 2011, 286, 33029-33036.	1.6	31
113	ZIC-CHILIC as a fractionation method for sensitive and powerful shotgun proteomics. <i>Nature Protocols</i> , 2012, 7, 2041-2055.	5.5	31
114	Chemical Proteomics and Phenotypic Profiling Identifies the Aryl Hydrocarbon Receptor as a Molecular Target of the Utrophin Modulator Ezutromid. <i>Angewandte Chemie - International Edition</i> , 2020, 59, 2420-2428.	7.2	31
115	Global analysis of RNA-binding protein dynamics by comparative and enhanced RNA interactome capture. <i>Nature Protocols</i> , 2021, 16, 27-60.	5.5	31
116	Control of Epithelial Cell Migration and Invasion by the IKK $\hat{1}$ <sup>2</sup> - and CK1 $\hat{1}$ <sup>±</sup> -Mediated Degradation of RAPGEF2. <i>Developmental Cell</i> , 2013, 27, 574-585.	3.1	30
117	USP17- and SCF <sup>TrCP</sup> -Regulated Degradation of DEC1 Controls the DNA Damage Response. <i>Molecular and Cellular Biology</i> , 2014, 34, 4177-4185.	1.1	30
118	eIF2 interactions with initiator tRNA and eIF2B are regulated by post-translational modifications and conformational dynamics. <i>Cell Discovery</i> , 2015, 1, 15020.	3.1	29
119	RockerBox: Analysis and Filtering of Massive Proteomics Search Results. <i>Journal of Proteome Research</i> , 2011, 10, 1420-1424.	1.8	28
120	Evaluation of the Deuterium Isotope Effect in Zwitterionic Hydrophilic Interaction Liquid Chromatography Separations for Implementation in a Quantitative Proteomic Approach. <i>Analytical Chemistry</i> , 2011, 83, 8352-8356.	3.2	28
121	Doxorubicin-induced DNA Damage Causes Extensive Ubiquitination of Ribosomal Proteins Associated with a Decrease in Protein Translation*. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 2297-2308.	2.5	28
122	A unique residue in rab3c determines the interaction with novel binding protein Zwint $\hat{1}$ . <i>FEBS Letters</i> , 2008, 582, 2838-2842.	1.3	26
123	In-depth Quantitative Cardiac Proteomics Combining Electron Transfer Dissociation and the Metalloendopeptidase Lys-N with the SILAC Mouse. <i>Molecular and Cellular Proteomics</i> , 2011, 10, O111.008474.	2.5	26
124	The anti-sigma factor RsrA responds to oxidative stress by reburying its hydrophobic core. <i>Nature Communications</i> , 2016, 7, 12194.	5.8	26
125	Improved Identification of Endogenous Peptides from Murine Nervous Tissue by Multiplexed Peptide Extraction Methods and Multiplexed Mass Spectrometric Analysis. <i>Journal of Proteome Research</i> , 2009, 8, 870-876.	1.8	25
126	Dimethyl isotope labeling assisted de novo peptide sequencing. <i>Journal of the American Society for Mass Spectrometry</i> , 2010, 21, 1957-1965.	1.2	25



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127	Proteasome-dependent Degradation of Transcription Factor Activating Enhancer-binding Protein 4 (TFAP4) Controls Mitotic Division. <i>Journal of Biological Chemistry</i> , 2014, 289, 7730-7737.	1.6	25
128	Profiling of Diet-Induced Neuropeptide Changes in Rat Brain by Quantitative Mass Spectrometry. <i>Analytical Chemistry</i> , 2013, 85, 4594-4604.	3.2	24
129	Monitoring the Disassembly of Virus-like Particles by <sup>19</sup> F-NMR. <i>Journal of the American Chemical Society</i> , 2017, 139, 5277-5280.	6.6	23
130	A receptor for the complement regulator factor H increases transmission of trypanosomes to tsetse flies. <i>Nature Communications</i> , 2020, 11, 1326.	5.8	23
131	Ordered dephosphorylation initiated by the selective proteolysis of cyclin B drives mitotic exit. <i>ELife</i> , 2020, 9, .	2.8	22
132	A novel tandem quadrupole mass spectrometer allowing gaseous collisional activation and surface induced dissociation. <i>Journal of Mass Spectrometry</i> , 2001, 36, 1260-1268.	0.7	21
133	Deconvolution of overlapping isotopic clusters improves quantification of stable isotope <sup>15</sup> N labeled peptides. <i>Journal of Proteomics</i> , 2011, 74, 2204-2209.	1.2	20
134	Protein Syndesmos is a novel RNA-binding protein that regulates primary cilia formation. <i>Nucleic Acids Research</i> , 2018, 46, 12067-12086.	6.5	20
135	Uncovering viral RNA <sup>15</sup> N host cell interactions on a proteome-wide scale. <i>Trends in Biochemical Sciences</i> , 2022, 47, 23-38.	3.7	20
136	Comparative Phosphoproteomic Analysis of Checkpoint Recovery Identifies New Regulators of the DNA Damage Response. <i>Science Signaling</i> , 2013, 6, rs9.	1.6	18
137	Characterization and usage of the EASY-spray technology as part of an online 2D SCX-RP ultra-high pressure system. <i>Analyst</i> , The, 2014, 139, 6520-6528.	1.7	18
138	Acetylation and phosphorylation control both local and global stability of the chloroplast F1 ATP synthase. <i>Scientific Reports</i> , 2017, 7, 44068.	1.6	18
139	Fully automated isotopic dimethyl labeling and phosphopeptide enrichment using a microfluidic HPLC phosphochip. <i>Analytical and Bioanalytical Chemistry</i> , 2012, 404, 2507-2512.	1.9	17
140	HGF signaling regulates Claudin-3 dynamics through its C-terminal tyrosine residues. <i>Tissue Barriers</i> , 2013, 1, e27425.	1.6	17
141	Proteome Adaptation of <i>Saccharomyces cerevisiae</i> to Severe Calorie Restriction in Retentostat Cultures. <i>Journal of Proteome Research</i> , 2014, 13, 3542-3553.	1.8	17
142	Post-translational insertion of boron in proteins to probe and modulate function. <i>Nature Chemical Biology</i> , 2021, 17, 1245-1261.	3.9	15
143	Phosphorylation of Not4p Functions Parallel to BUR2 to Regulate Resistance to Cellular Stresses in <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , 2010, 5, e9864.	1.1	14
144	Targeted SCX Based Peptide Fractionation for Optimal Sequencing by Collision Induced, and Electron Transfer Dissociation. <i>Journal of Proteomics and Bioinformatics</i> , 2008, 01, 379-388.	0.4	14

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