

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
g-index

192
all docs

192
docs citations

192
times ranked

28278
citing authors

#	ARTICLE	IF	CITATIONS
1	Uncovering viral RNA–host cell interactions on a proteome-wide scale. Trends in Biochemical Sciences, 2022, 47, 23-38.	3.7	20
2	RNA-binding protein Mub1 and the nuclear RNA exosome act to fine-tune environmental stress response. Life Science Alliance, 2022, 5, e202101111.	1.3	1
3	Reductive site-selective atypical C, Z -type/N2-C2 cleavage allows C-terminal protein amidation. Science Advances, 2022, 8, eabl8675.	4.7	1
4	Broad-range metalloprotease profiling in plants uncovers immunity provided by defence-related metalloenzyme. New Phytologist, 2022, 235, 1287-1301.	3.5	3
5	Global analysis of RNA-binding protein dynamics by comparative and enhanced RNA interactome capture. Nature Protocols, 2021, 16, 27-60.	5.5	31
6	NeissLock provides an inducible protein anhydride for covalent targeting of endogenous proteins. Nature Communications, 2021, 12, 717.	5.8	2
7	Global analysis of protein-RNA interactions in SARS-CoV-2-infected cells reveals key regulators of infection. Molecular Cell, 2021, 81, 2851-2867.e7.	4.5	108
8	LanCLs add glutathione to dehydroamino acids generated at phosphorylated sites in the proteome. Cell, 2021, 184, 2680-2695.e26.	13.5	34
9	Structural characterization of KKT4, an unconventional microtubule-binding kinetochore protein. Structure, 2021, 29, 1014-1028.e8.	1.6	9
10	Colicin-Mediated Transport of DNA through the Iron Transporter FepA. MBio, 2021, 12, e0178721.	1.8	7
11	Post-translational insertion of boron in proteins to probe and modulate function. Nature Chemical Biology, 2021, 17, 1245-1261.	3.9	15
12	Proteomics as a tool for live attenuated influenza vaccine characterisation. Vaccine, 2020, 38, 868-877.	1.7	6
13	Quantitative MS-Based Proteomics: Comparing the MCF7 Cellular Response to Hypoxia and a Oxoglutarate Analogue. ChemBioChem, 2020, 21, 1647-1655.	1.3	9
14	Chemical Proteomics and Phenotypic Profiling Identifies the Aryl Hydrocarbon Receptor as a Molecular Target of the Utrophin Modulator Ezutromid. Angewandte Chemie, 2020, 132, 2441-2449.	1.6	1
15	Chemical Proteomics and Phenotypic Profiling Identifies the Aryl Hydrocarbon Receptor as a Molecular Target of the Utrophin Modulator Ezutromid. Angewandte Chemie - International Edition, 2020, 59, 2420-2428.	7.2	31
16	Light-driven post-translational installation of reactive protein side chains. Nature, 2020, 585, 530-537.	13.7	100
17	Discovering the RNA-Binding Proteome of Plant Leaves with an Improved RNA Interactome Capture Method. Biomolecules, 2020, 10, 661.	1.8	63
18	System-wide analyses of the fission yeast poly(A) ⁺ RNA interactome reveal insights into organization and function of RNA–protein complexes. Genome Research, 2020, 30, 1012-1026.	2.4	6

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19	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
20	Threonine Phosphorylation of Î²BÎ¶ Mediates Inhibition of Selective Proinflammatory Target Genes. <i>Journal of Investigative Dermatology</i> , 2020, 140, 1805-1814.e6.	0.3	4
21	Comparative Poly(A)+ RNA Interactome Capture of RNA Surveillance Mutants. <i>Methods in Molecular Biology</i> , 2020, 2062, 255-276.	0.4	6
22	The role of the Xist 5â€™ m6A region and RBM15 in X chromosome inactivation. <i>Wellcome Open Research</i> , 2020, 5, 31.	0.9	37
23	Ordered dephosphorylation initiated by the selective proteolysis of cyclin B drives mitotic exit. <i>ELife</i> , 2020, 9, .	2.8	22
24	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
25	Triazine Probes Target Ascorbate Peroxidases in Plants. <i>Plant Physiology</i> , 2019, 180, 1848-1859.	2.3	5
26	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
27	Synthetic post-translational modification of histones. <i>Current Opinion in Chemical Biology</i> , 2018, 45, 35-47.	2.8	53
28	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
29	YcfDRM is a thermophilic oxygen-dependent ribosomal protein uL16 oxygenase. <i>Extremophiles</i> , 2018, 22, 553-562.	0.9	6
30	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
31	Elongation/Termination Factor Exchange Mediated by PP1 Phosphatase Orchestrates Transcription Termination. <i>Cell Reports</i> , 2018, 25, 259-269.e5.	2.9	58
32	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
33	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
34	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
35	Toward an Optimized Workflow for Middle-Down Proteomics. <i>Analytical Chemistry</i> , 2017, 89, 3318-3325.	3.2	91
36	Quantitative Map of Proteome Dynamics during Neuronal Differentiation. <i>Cell Reports</i> , 2017, 18, 1527-1542.	2.9	79

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37	Ligand binding to a G protein-coupled receptor captured in a mass spectrometer. <i>Science Advances</i> , 2017, 3, e1701016.	4.7	52
38	Monitoring the Disassembly of Virus-like Particles by ¹⁹ F-NMR. <i>Journal of the American Chemical Society</i> , 2017, 139, 5277-5280.	6.6	23
39	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
40	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
41	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
42	Combining Deep Sequencing, Proteomics, Phosphoproteomics, and Functional Screens To Discover Novel Regulators of Sphingolipid Homeostasis. <i>Journal of Proteome Research</i> , 2017, 16, 571-582.	1.8	11
43	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
44	Synthetic Nucleosomes Reveal that GlcNAcylation Modulates Direct Interaction with the FACT Complex. <i>Angewandte Chemie</i> , 2016, 128, 9064-9068.	1.6	4
45	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
46	Optimal Synthetic Glycosylation of a Therapeutic Antibody. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 2361-2367.	7.2	122
47	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
48	The anti-sigma factor RsrA responds to oxidative stress by reburying its hydrophobic core. <i>Nature Communications</i> , 2016, 7, 12194.	5.8	26
49	Posttranslational mutagenesis: A chemical strategy for exploring protein side-chain diversity. <i>Science</i> , 2016, 354, .	6.0	247
50	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
51	On the Statistical Significance of Compressed Ratios in Isobaric Labeling: A Cross-Platform Comparison. <i>Journal of Proteome Research</i> , 2016, 15, 3029-3038.	1.8	13
52	Selective Metal-Site-Guided Arylation of Proteins. <i>Journal of the American Chemical Society</i> , 2016, 138, 8678-8681.	6.6	92
53	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
54	Nicotinamide Cofactors Suppress Active-Site Labeling of Aldehyde Dehydrogenases. <i>ACS Chemical Biology</i> , 2016, 11, 1578-1586.	1.6	6

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55	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
56	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
57	Rapid Analyses of Proteomes and Interactomes Using an Integrated Solid-Phase Extraction“Liquid Chromatography“MS/MS System. <i>Journal of Proteome Research</i> , 2015, 14, 977-985.	1.8	6
58	Datasets from an interaction proteomics screen for substrates of the SCF $\hat{\text{I}}^2\text{TrCP}$ ubiquitin ligase. <i>Data in Brief</i> , 2015, 4, 229-234.	0.5	0
59	De novo sequencing of two novel peptides homologous to calcitonin-like peptides, from skin secretion of the Chinese Frog, <i>Odorrana schmackeri</i> . <i>EuPA Open Proteomics</i> , 2015, 8, 157-166.	2.5	3
60	Generation of a synthetic GlcNAcylated nucleosome reveals regulation of stability by H2A-Thr101 GlcNAcylation. <i>Nature Communications</i> , 2015, 6, 7978.	5.8	51
61	A systems-wide screen identifies substrates of the SCF $\hat{\text{I}}^2\text{TrCP}$ ubiquitin ligase. <i>Science Signaling</i> , 2014, 7, rs8.	1.6	49
62	USP17- and SCF $\hat{\text{I}}^2\text{TrCP}$ -Regulated Degradation of DEC1 Controls the DNA Damage Response. <i>Molecular and Cellular Biology</i> , 2014, 34, 4177-4185.	1.1	30
63	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
64	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
65	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
66	Synthetic Phosphorylation of p38 $\hat{\text{I}}^{\pm}$ Recapitulates Protein Kinase Activity. <i>Journal of the American Chemical Society</i> , 2014, 136, 1698-1701.	6.6	46
67	Characterization of Biases in Phosphopeptide Enrichment by Ti ⁴⁺ -Immobilized Metal Affinity Chromatography and TiO ₂ Using a Massive Synthetic Library and Human Cell Digests. <i>Analytical Chemistry</i> , 2014, 86, 8312-8320.	3.2	43
68	Phosphoproteomics. <i>Analytical Chemistry</i> , 2014, 86, 1313-1313.	3.2	9
69	The CRAPome: a contaminant repository for affinity purification“mass spectrometry data. <i>Nature Methods</i> , 2013, 10, 730-736.	9.0	1,353
70	Profiling of Diet-Induced Neuropeptide Changes in Rat Brain by Quantitative Mass Spectrometry. <i>Analytical Chemistry</i> , 2013, 85, 4594-4604.	3.2	24
71	Toward a Comprehensive Characterization of a Human Cancer Cell Phosphoproteome. <i>Journal of Proteome Research</i> , 2013, 12, 260-271.	1.8	363
72	Control of Epithelial Cell Migration and Invasion by the IKK $\hat{\text{I}}^2$ - and CK1 $\hat{\text{I}}^{\pm}$ -Mediated Degradation of RAPGEF2. <i>Developmental Cell</i> , 2013, 27, 574-585.	3.1	30

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73	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
74	Benchmarking stable isotope labeling based quantitative proteomics. <i>Journal of Proteomics</i> , 2013, 88, 14-26.	1.2	112
75	Unambiguous Phosphosite Localization using Electron-Transfer/Higher-Energy Collision Dissociation (EThcD). <i>Journal of Proteome Research</i> , 2013, 12, 1520-1525.	1.8	145
76	Robust phosphoproteome enrichment using monodisperse microsphere-based immobilized titanium (IV) ion affinity chromatography. <i>Nature Protocols</i> , 2013, 8, 461-480.	5.5	340
77	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
78	Quantitative global phosphoproteomics of human umbilical vein endothelial cells after activation of the Rap signaling pathway. <i>Molecular BioSystems</i> , 2013, 9, 732.	2.9	8
79	A large synthetic peptide and phosphopeptide reference library for mass spectrometry-based proteomics. <i>Nature Biotechnology</i> , 2013, 31, 557-564.	9.4	164
80	Characterization of Electron Transfer Dissociation in the Orbitrap Velos HCD Cell. <i>Journal of the American Society for Mass Spectrometry</i> , 2013, 24, 1663-1670.	1.2	5
81	HGF signaling regulates Claudin-3 dynamics through its C-terminal tyrosine residues. <i>Tissue Barriers</i> , 2013, 1, e27425.	1.6	17
82	Comparative Phosphoproteomic Analysis of Checkpoint Recovery Identifies New Regulators of the DNA Damage Response. <i>Science Signaling</i> , 2013, 6, rs9.	1.6	18
83	Collaboration of AMPK and PKC to induce phosphorylation of Ser413 on PIP5K1B resulting in decreased kinase activity and reduced PtdIns(4,5)P ₂ synthesis in response to oxidative stress and energy restriction. <i>Biochemical Journal</i> , 2013, 455, 347-358.	1.7	10
84	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
85	Enhancing the Identification of Phosphopeptides from Putative Basophilic Kinase Substrates Using Ti (IV) Based IMAC Enrichment. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2673.	2.5	6
86	Coupled Activation and Degradation of eEF2K Regulates Protein Synthesis in Response to Genotoxic Stress. <i>Science Signaling</i> , 2012, 5, ra40.	1.6	76
87	Database independent proteomics analysis of the ostrich and human proteome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 407-412.	3.3	13
88	Cross-talk between phosphorylation and lysine acetylation in a genome-reduced bacterium. <i>Molecular Systems Biology</i> , 2012, 8, 571.	3.2	169
89	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
90	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

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91	Ultra Acidic Strong Cation Exchange Enabling the Efficient Enrichment of Basic Phosphopeptides. <i>Analytical Chemistry</i> , 2012, 84, 1804-1808.	3.2	45
92	The Lgr5 intestinal stem cell signature: robust expression of proposed quiescent β -catenin cell markers. <i>EMBO Journal</i> , 2012, 31, 3079-3091.	3.5	634
93	In-house construction of a UHPLC system enabling the identification of over 4000 protein groups in a single analysis. <i>Analyst</i> , 2012, 137, 3541.	1.7	43
94	Recent advances in peptide separation by multidimensional liquid chromatography for proteome analysis. <i>Journal of Proteomics</i> , 2012, 75, 3791-3813.	1.2	141
95	Wnt Signaling through Inhibition of β -Catenin Degradation in an Intact Axin1 Complex. <i>Cell</i> , 2012, 149, 1245-1256.	13.5	747
96	ZIC-CHILIC as a fractionation method for sensitive and powerful shotgun proteomics. <i>Nature Protocols</i> , 2012, 7, 2041-2055.	5.5	31
97	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
98	Applications of stable isotope dimethyl labeling in quantitative proteomics. <i>Analytical and Bioanalytical Chemistry</i> , 2012, 404, 991-1009.	1.9	61
99	Protease bias in absolute protein quantitation. <i>Nature Methods</i> , 2012, 9, 524-525.	9.0	80
100	Abstract 983: Wnt pathway activation involves inhibition of β -catenin ubiquitination within the endogenous Axin1 complex. , 2012, , .		0
101	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
102	RockerBox: Analysis and Filtering of Massive Proteomics Search Results. <i>Journal of Proteome Research</i> , 2011, 10, 1420-1424.	1.8	28
103	Exploring New Proteome Space: Combining Lys-N Proteolytic Digestion and Strong Cation Exchange (SCX) Separation in Peptide-Centric MS-Driven Proteomics. <i>Methods in Molecular Biology</i> , 2011, 753, 157-167.	0.4	5
104	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
105	Lgr5 homologues associate with Wnt receptors and mediate R-spondin signalling. <i>Nature</i> , 2011, 476, 293-297.	13.7	1,096
106	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
107	Highly Sensitive Proteome Analysis of FACS-Sorted Adult Colon Stem Cells. <i>Journal of Proteome Research</i> , 2011, 10, 3814-3819.	1.8	60
108	Deconvolution of overlapping isotopic clusters improves quantification of stable isotope 13 C labeled peptides. <i>Journal of Proteomics</i> , 2011, 74, 2204-2209.	1.2	20

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109	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
110	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
111	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
112	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
113	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
114	Protein Phosphatase 2A (B55 $\hat{\pm}$) 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
115	Protein phosphatase 2A (B55 $\hat{\pm}$) 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, 39674.	1.6	1
116	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
117	Identification of Salt-Tolerant <i>Sinorhizobium</i> sp. Strain BL3 Membrane Proteins Based on Proteomics. <i>Microbes and Environments</i> , 2010, 25, 275-280.	0.7	2
118	Perturbation of the yeast N-acetyltransferase NatB induces elevation of protein phosphorylation levels. <i>BMC Genomics</i> , 2010, 11, 685.	1.2	77
119	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
120	<i>LysNDeNovo</i> : An algorithm enabling <i>de novo</i> sequencing of Lys $\hat{\text{N}}$ generated peptides fragmented by electron transfer dissociation. <i>Proteomics</i> , 2010, 10, 1196-1201.	1.3	8
121	$\hat{2}$ -Syntrophin Is a Cdk5 Substrate That Restrains the Motility of Insulin Secretory Granules. <i>PLoS ONE</i> , 2010, 5, e12929.	1.1	40
122	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
123	MAP3K1 functionally interacts with Axin1 in the canonical Wnt signalling pathway. <i>Biological Chemistry</i> , 2010, 391, 171-180.	1.2	33
124	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
125	The Leukemia-Associated Mllt10/Af10-Dot1l Are Tcf4/ $\hat{2}$ -Catenin Coactivators Essential for Intestinal Homeostasis. <i>PLoS Biology</i> , 2010, 8, e1000539.	2.6	78
126	Exploring the Human Leukocyte Phosphoproteome Using a Microfluidic Reversed-Phase $\hat{2}$ 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

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127	Peptide Orientation Affects Selectivity in Ion-Exchange Chromatography. <i>Analytical Chemistry</i> , 2010, 82, 5253-5259.	3.2	49
128	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
129	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
130	Cleavage specificities of the brother and sister proteases Lys-C and Lys-N. <i>Chemical Communications</i> , 2010, 46, 8827.	2.2	55
131	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
132	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
133	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
134	Phosphopeptide fragmentation and analysis by mass spectrometry. <i>Journal of Mass Spectrometry</i> , 2009, 44, 861-878.	0.7	349
135	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
136	The kinase TNIK is an essential activator of Wnt target genes. <i>EMBO Journal</i> , 2009, 28, 3329-3340.	3.5	169
137	Multiplex peptide stable isotope dimethyl labeling for quantitative proteomics. <i>Nature Protocols</i> , 2009, 4, 484-494.	5.5	1,247
138	Effect of Chemical Modifications on Peptide Fragmentation Behavior upon Electron Transfer Induced Dissociation. <i>Analytical Chemistry</i> , 2009, 81, 7814-7822.	3.2	38
139	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
140	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
141	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
142	Assessing biological variation and protein processing in primary human leukocytes by automated multiplex stable isotope labeling coupled to 2 dimensional peptide separation. <i>Molecular BioSystems</i> , 2009, 5, 992.	2.9	10
143	Hydrophilic interaction liquid chromatography (HILIC) in proteomics. <i>Analytical and Bioanalytical Chemistry</i> , 2008, 391, 151-159.	1.9	234
144	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

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145	Straightforward ladder sequencing of peptides using a Lys-N metalloendopeptidase. <i>Nature Methods</i> , 2008, 5, 405-407.	9.0	116
146	A unique residue in rab3c determines the interaction with novel binding protein Zwiñtâ€¹. <i>FEBS Letters</i> , 2008, 582, 2838-2842.	1.3	26
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148	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
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