

Shabaz Mohammed

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

180
papers

15,368
citations

61
h-index

122
g-index

192
ext. papers

17,713
ext. citations

9.6
avg, IF

6.29
L-index

#	Paper	IF	Citations
180	Reductive site-selective atypical, γ -type/N2-C2 cleavage allows C-terminal protein amidation.. <i>Science Advances</i> , 2022 , 8, eabl8675	14.3	0
179	Post-translational insertion of boron in proteins to probe and modulate function. <i>Nature Chemical Biology</i> , 2021 , 17, 1245-1261	11.7	4
178	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	17.6	27
177	LanCLs add glutathione to dehydroamino acids generated at phosphorylated sites in the proteome. <i>Cell</i> , 2021 , 184, 2680-2695.e26	56.2	6
176	Global analysis of RNA-binding protein dynamics by comparative and enhanced RNA interactome capture. <i>Nature Protocols</i> , 2021 , 16, 27-60	18.8	13
175	NeissLock provides an inducible protein anhydride for covalent targeting of endogenous proteins. <i>Nature Communications</i> , 2021 , 12, 717	17.4	2
174	Structural characterization of KKT4, an unconventional microtubule-binding kinetochore protein. <i>Structure</i> , 2021 , 29, 1014-1028.e8	5.2	2
173	Colicin-Mediated Transport of DNA through the Iron Transporter FepA. <i>MBio</i> , 2021 , 12, e0178721	7.8	1
172	Uncovering viral RNA-host cell interactions on a proteome-wide scale. <i>Trends in Biochemical Sciences</i> , 2021 ,	10.3	1
171	Discovering the RNA-Binding Proteome of Plant Leaves with an Improved RNA Interactome Capture Method. <i>Biomolecules</i> , 2020 , 10,	5.9	22
170	System-wide analyses of the fission yeast poly(A) RNA interactome reveal insights into organization and function of RNA-protein complexes. <i>Genome Research</i> , 2020 , 30, 1012-1026	9.7	3
169	A receptor for the complement regulator factor H increases transmission of trypanosomes to tsetse flies. <i>Nature Communications</i> , 2020 , 11, 1326	17.4	8
168	Threonine Phosphorylation of IB β Mediates Inhibition of Selective Proinflammatory Target Genes. <i>Journal of Investigative Dermatology</i> , 2020 , 140, 1805-1814.e6	4.3	1
167	The role of the Xist 5Tm6A region and RBM15 in X chromosome inactivation. <i>Wellcome Open Research</i> , 2020 , 5, 31	4.8	18
166	Ordered dephosphorylation initiated by the selective proteolysis of cyclin B drives mitotic exit. <i>ELife</i> , 2020 , 9,	8.9	7
165	Comparative Poly(A)+ RNA Interactome Capture of RNA Surveillance Mutants. <i>Methods in Molecular Biology</i> , 2020 , 2062, 255-276	1.4	1
164	Proteomics as a tool for live attenuated influenza vaccine characterisation. <i>Vaccine</i> , 2020 , 38, 868-877	4.1	6

163	Quantitative MS-Based Proteomics: Comparing the MCF-7 Cellular Response to Hypoxia and a 2-Oxoglutarate Analogue. <i>ChemBioChem</i> , 2020 , 21, 1647-1655	3.8	5
162	Chemical Proteomics and Phenotypic Profiling Identifies the Aryl Hydrocarbon Receptor as a Molecular Target of the Utrophin Modulator Ezutromid. <i>Angewandte Chemie</i> , 2020 , 132, 2441-2449	3.6	
161	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	16.4	17
160	Light-driven post-translational installation of reactive protein side chains. <i>Nature</i> , 2020 , 585, 530-537	50.4	40
159	Polyamines Control eIF5A Hypusination, TFEB Translation, and Autophagy to Reverse B Cell Senescence. <i>Molecular Cell</i> , 2019 , 76, 110-125.e9	17.6	93
158	Triazine Probes Target Ascorbate Peroxidases in Plants. <i>Plant Physiology</i> , 2019 , 180, 1848-1859	6.6	1
157	Quantitative Proteomics for Differential Protein Expression Profiling 2019 , 1-27		2
156	System-wide Profiling of RNA-Binding Proteins Uncovers Key Regulators of Virus Infection. <i>Molecular Cell</i> , 2019 , 74, 196-211.e11	17.6	67
155	Synthetic post-translational modification of histones. <i>Current Opinion in Chemical Biology</i> , 2018 , 45, 35-43	7.7	37
154	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	7.6	13
153	YcFD is a thermophilic oxygen-dependent ribosomal protein uL16 oxygenase. <i>Extremophiles</i> , 2018 , 22, 553-562	3	5
152	Protein Syndesmos is a novel RNA-binding protein that regulates primary cilia formation. <i>Nucleic Acids Research</i> , 2018 , 46, 12067-12086	20.1	12
151	Elongation/Termination Factor Exchange Mediated by PP1 Phosphatase Orchestrates Transcription Termination. <i>Cell Reports</i> , 2018 , 25, 259-269.e5	10.6	32
150	Genetic Incorporation of Olefin Cross-Metathesis Reaction Tags for Protein Modification. <i>Journal of the American Chemical Society</i> , 2018 , 140, 14599-14603	16.4	30
149	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	10.6	96
148	Acetylation and phosphorylation control both local and global stability of the chloroplast F ₁ F ₀ ATP synthase. <i>Scientific Reports</i> , 2017 , 7, 44068	4.9	14
147	Toward an Optimized Workflow for Middle-Down Proteomics. <i>Analytical Chemistry</i> , 2017 , 89, 3318-3325	7.8	67
146	Quantitative Map of Proteome Dynamics during Neuronal Differentiation. <i>Cell Reports</i> , 2017 , 18, 1527-1542	14.2	47

145	Ligand binding to a G protein-coupled receptor captured in a mass spectrometer. <i>Science Advances</i> , 2017 , 3, e1701016	14.3	39
144	Monitoring the Disassembly of Virus-like Particles by F-NMR. <i>Journal of the American Chemical Society</i> , 2017 , 139, 5277-5280	16.4	14
143	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	11.5	48
142	hnRNP K 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	17.6	152
141	Nuclear phosphorylated Dicer processes double-stranded RNA in response to DNA damage. <i>Journal of Cell Biology</i> , 2017 , 216, 2373-2389	7.3	48
140	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	5.6	7
139	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	11.5	33
138	A PP2A-B55 recognition signal controls substrate dephosphorylation kinetics during mitotic exit. <i>Journal of Cell Biology</i> , 2016 , 214, 539-54	7.3	105
137	On the Statistical Significance of Compressed Ratios in Isobaric Labeling: A Cross-Platform Comparison. <i>Journal of Proteome Research</i> , 2016 , 15, 3029-38	5.6	11
136	Selective Metal-Site-Guided Arylation of Proteins. <i>Journal of the American Chemical Society</i> , 2016 , 138, 8678-81	16.4	68
135	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, 1412-23	7.6	48
134	Nicotinamide Cofactors Suppress Active-Site Labeling of Aldehyde Dehydrogenases. <i>ACS Chemical Biology</i> , 2016 , 11, 1578-86	4.9	6
133	Synthetic Nucleosomes Reveal that GlcNAcylation Modulates Direct Interaction with the FACT Complex. <i>Angewandte Chemie</i> , 2016 , 128, 9064-9068	3.6	4
132	Synthetic Nucleosomes Reveal that GlcNAcylation Modulates Direct Interaction with the FACT Complex. <i>Angewandte Chemie - International Edition</i> , 2016 , 55, 8918-22	16.4	29
131	Optimal Synthetic Glycosylation of a Therapeutic Antibody. <i>Angewandte Chemie - International Edition</i> , 2016 , 55, 2361-7	16.4	92
130	Dimer interface of bovine cytochrome c 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, 8230-5	11.5	30
129	The anti-sigma factor RsrA responds to oxidative stress by reburying its hydrophobic core. <i>Nature Communications</i> , 2016 , 7, 12194	17.4	16
128	Posttranslational mutagenesis: A chemical strategy for exploring protein side-chain diversity. <i>Science</i> , 2016 , 354,	33.3	182

127	Datasets from an interaction proteomics screen for substrates of the SCF(β TrCP) ubiquitin ligase. <i>Data in Brief</i> , 2015 , 4, 229-34	1.2	
126	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	0.1	3
125	Generation of a synthetic GlcNAcylated nucleosome reveals regulation of stability by H2A-Thr101 GlcNAcylation. <i>Nature Communications</i> , 2015 , 6, 7978	17.4	40
124	eIF2 interactions with initiator tRNA and eIF2B are regulated by post-translational modifications and conformational dynamics. <i>Cell Discovery</i> , 2015 , 1, 15020	22.3	18
123	Signal Transduction Reaction Monitoring Deciphers Site-Specific PI3K-mTOR/MAPK Pathway Dynamics in Oncogene-Induced Senescence. <i>Journal of Proteome Research</i> , 2015 , 14, 2906-14	5.6	27
122	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, 977-85	5.6	5
121	Proteasome-dependent degradation of transcription factor activating enhancer-binding protein 4 (TFAP4) controls mitotic division. <i>Journal of Biological Chemistry</i> , 2014 , 289, 7730-7	5.4	18
120	Characterization and usage of the EASY-spray technology as part of an online 2D SCX-RP ultra-high pressure system. <i>Analyst, The</i> , 2014 , 139, 6520-8	5	14
119	Proteome adaptation of <i>Saccharomyces cerevisiae</i> to severe calorie restriction in Retentostat cultures. <i>Journal of Proteome Research</i> , 2014 , 13, 3542-53	5.6	14
118	Synthetic phosphorylation of p38 β recapitulates protein kinase activity. <i>Journal of the American Chemical Society</i> , 2014 , 136, 1698-701	16.4	40
117	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, 8312-20	7.8	35
116	A systems-wide screen identifies substrates of the SCF β TrCP ubiquitin ligase. <i>Science Signaling</i> , 2014 , 7, rs8	8.8	35
115	USP17- and SCF β TrCP--regulated degradation of DEC1 controls the DNA damage response. <i>Molecular and Cellular Biology</i> , 2014 , 34, 4177-85	4.8	18
114	The CRAPome: a contaminant repository for affinity purification-mass spectrometry data. <i>Nature Methods</i> , 2013 , 10, 730-6	21.6	894
113	Profiling of diet-induced neuropeptide changes in rat brain by quantitative mass spectrometry. <i>Analytical Chemistry</i> , 2013 , 85, 4594-604	7.8	21
112	Toward a comprehensive characterization of a human cancer cell phosphoproteome. <i>Journal of Proteome Research</i> , 2013 , 12, 260-71	5.6	276
111	Control of epithelial cell migration and invasion by the IKK β and CK1 β -mediated degradation of RAPGEF2. <i>Developmental Cell</i> , 2013 , 27, 574-85	10.2	22
110	Quantitative and qualitative proteome characteristics extracted from in-depth integrated genomics and proteomics analysis. <i>Cell Reports</i> , 2013 , 5, 1469-78	10.6	96

109	Benchmarking stable isotope labeling based quantitative proteomics. <i>Journal of Proteomics</i> , 2013 , 88, 14-26	3.9	100
108	Unambiguous phosphosite localization using electron-transfer/higher-energy collision dissociation (ETHCD). <i>Journal of Proteome Research</i> , 2013 , 12, 1520-5	5.6	125
107	Robust phosphoproteome enrichment using monodisperse microsphere-based immobilized titanium (IV) ion affinity chromatography. <i>Nature Protocols</i> , 2013 , 8, 461-80	18.8	270
106	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, 2214-24	5.6	36
105	Quantitative global phosphoproteomics of human umbilical vein endothelial cells after activation of the Rap signaling pathway. <i>Molecular BioSystems</i> , 2013 , 9, 732-49		8
104	A large synthetic peptide and phosphopeptide reference library for mass spectrometry-based proteomics. <i>Nature Biotechnology</i> , 2013 , 31, 557-64	44.5	132
103	Characterization of electron transfer dissociation in the Orbitrap Velos HCD cell. <i>Journal of the American Society for Mass Spectrometry</i> , 2013 , 24, 1663-70	3.5	3
102	HGF signaling regulates Claudin-3 dynamics through its C-terminal tyrosine residues. <i>Tissue Barriers</i> , 2013 , 1, e27425	4.3	14
101	Comparative phosphoproteomic analysis of checkpoint recovery identifies new regulators of the DNA damage response. <i>Science Signaling</i> , 2013 , 6, rs9	8.8	11
100	Collaboration of AMPK and PKC to induce phosphorylation of Ser413 on PIP5K1B resulting in decreased kinase activity and reduced PtdIns(4,5)P2 synthesis in response to oxidative stress and energy restriction. <i>Biochemical Journal</i> , 2013 , 455, 347-58	3.8	8
99	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, 1158-69	7.6	76
98	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	7.6	5
97	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, 9668-73	7.8	203
96	Fully automated isotopic dimethyl labeling and phosphopeptide enrichment using a microfluidic HPLC phosphochip. <i>Analytical and Bioanalytical Chemistry</i> , 2012 , 404, 2507-12	4.4	15
95	Ultra acidic strong cation exchange enabling the efficient enrichment of basic phosphopeptides. <i>Analytical Chemistry</i> , 2012 , 84, 1804-8	7.8	45
94	The Lgr5 intestinal stem cell signature: robust expression of proposed quiescent T _H 4Tcell markers. <i>EMBO Journal</i> , 2012 , 31, 3079-91	13	523
93	In-house construction of a UHPLC system enabling the identification of over 4000 protein groups in a single analysis. <i>Analyst, The</i> , 2012 , 137, 3541-8	5	41
92	Recent advances in peptide separation by multidimensional liquid chromatography for proteome analysis. <i>Journal of Proteomics</i> , 2012 , 75, 3791-813	3.9	124

91	Wnt signaling through inhibition of β -catenin degradation in an intact Axin1 complex. <i>Cell</i> , 2012 , 149, 1245-56	56.2	619
90	ZIC-cHILIC as a fractionation method for sensitive and powerful shotgun proteomics. <i>Nature Protocols</i> , 2012 , 7, 2041-55	18.8	29
89	Tumour suppressor RNF43 is a stem-cell E3 ligase that induces endocytosis of Wnt receptors. <i>Nature</i> , 2012 , 488, 665-9	50.4	599
88	Applications of stable isotope dimethyl labeling in quantitative proteomics. <i>Analytical and Bioanalytical Chemistry</i> , 2012 , 404, 991-1009	4.4	57
87	Protease bias in absolute protein quantitation. <i>Nature Methods</i> , 2012 , 9, 524-5	21.6	67
86	Coupled activation and degradation of eEF2K regulates protein synthesis in response to genotoxic stress. <i>Science Signaling</i> , 2012 , 5, ra40	8.8	68
85	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, 407-12	11.5	12
84	Cross-talk between phosphorylation and lysine acetylation in a genome-reduced bacterium. <i>Molecular Systems Biology</i> , 2012 , 8, 571	12.2	144
83	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, 157-174	7.4	4
82	Improved peptide identification by targeted fragmentation using CID, HCD and ETD on an LTQ-Orbitrap Velos. <i>Journal of Proteome Research</i> , 2011 , 10, 2377-88	5.6	248
81	Lgr5 homologues associate with Wnt receptors and mediate R-spondin signalling. <i>Nature</i> , 2011 , 476, 293-7	50.4	903
80	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, 3440-7	7.8	117
79	Highly sensitive proteome analysis of FACS-sorted adult colon stem cells. <i>Journal of Proteome Research</i> , 2011 , 10, 3814-9	5.6	50
78	Deconvolution of overlapping isotopic clusters improves quantification of stable isotope-labeled peptides. <i>Journal of Proteomics</i> , 2011 , 74, 2204-9	3.9	19
77	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, 8352-6	7.8	25
76	Improving depth in phosphoproteomics by using a strong cation exchange-weak anion exchange-reversed phase multidimensional separation approach. <i>Analytical Chemistry</i> , 2011 , 83, 7137-43	7.8	46
75	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, 4334-41	5.6	77
74	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	11.4	67

73	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	7.6	77
72	RockerBox: analysis and filtering of massive proteomics search results. <i>Journal of Proteome Research</i> , 2011 , 10, 1420-4	5.6	28
71	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	7.6	25
70	Protein phosphatase 2A (B55) 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, 33029-36	5.4	30
69	Protein phosphatase 2A (B55) 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	5.4	78
68	β-Syntrophin is a Cdk5 substrate that restrains the motility of insulin secretory granules. <i>PLoS ONE</i> , 2010 , 5, e12929	3.7	32
67	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, 928-39	7.6	92
66	MAP3K1 functionally interacts with Axin1 in the canonical Wnt signalling pathway. <i>Biological Chemistry</i> , 2010 , 391, 171-180	4.5	29
65	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, 2840-52	7.6	193
64	The leukemia-associated Mllt10/Af10-Dot1l are Tcf4/βatenin coactivators essential for intestinal homeostasis. <i>PLoS Biology</i> , 2010 , 8, e1000539	9.7	70
63	Exploring the human leukocyte phosphoproteome using a microfluidic reversed-phase-TiO ₂ -reversed-phase high-performance liquid chromatography phosphochip coupled to a quadrupole time-of-flight mass spectrometer. <i>Analytical Chemistry</i> , 2010 , 82, 824-32	7.8	70
62	Peptide orientation affects selectivity in ion-exchange chromatography. <i>Analytical Chemistry</i> , 2010 , 82, 5253-9	7.8	45
61	Evaluation of metalloendopeptidase Lys-N protease performance under different sample handling conditions. <i>Journal of Proteome Research</i> , 2010 , 9, 4282-8	5.6	29
60	Recovery from a DNA-damage-induced G2 arrest requires Cdk-dependent activation of FoxM1. <i>EMBO Reports</i> , 2010 , 11, 452-8	6.5	44
59	Cleavage specificities of the brother and sister proteases Lys-C and Lys-N. <i>Chemical Communications</i> , 2010 , 46, 8827-9	5.8	44
58	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, 2140-8	7.6	36
57	Identification of salt-tolerant <i>Sinorhizobium</i> sp. strain BL3 membrane proteins based on proteomics. <i>Microbes and Environments</i> , 2010 , 25, 275-80	2.6	2
56	Perturbation of the yeast N-acetyltransferase NatB induces elevation of protein phosphorylation levels. <i>BMC Genomics</i> , 2010 , 11, 685	4.5	61

55	Dimethyl isotope labeling assisted de novo peptide sequencing. <i>Journal of the American Society for Mass Spectrometry</i> , 2010 , 21, 1957-65	3.5	22
54	LysNDeNovo: an algorithm enabling de novo sequencing of Lys-N generated peptides fragmented by electron transfer dissociation. <i>Proteomics</i> , 2010 , 10, 1196-201	4.8	8
53	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	3.7	13
52	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, 1016-28	7.6	37
51	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	7.6	64
50	Phosphopeptide fragmentation and analysis by mass spectrometry. <i>Journal of Mass Spectrometry</i> , 2009 , 44, 861-78	2.2	290
49	A three-way proteomics strategy allows differential analysis of yeast mitochondrial membrane protein complexes under anaerobic and aerobic conditions. <i>Proteomics</i> , 2009 , 9, 4787-98	4.8	33
48	The kinase TNIK is an essential activator of Wnt target genes. <i>EMBO Journal</i> , 2009 , 28, 3329-40	13	130
47	Multiplex peptide stable isotope dimethyl labeling for quantitative proteomics. <i>Nature Protocols</i> , 2009 , 4, 484-94	18.8	1072
46	Effect of chemical modifications on peptide fragmentation behavior upon electron transfer induced dissociation. <i>Analytical Chemistry</i> , 2009 , 81, 7814-22	7.8	37
45	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, 870-6	5.6	23
44	Straightforward and de novo peptide sequencing by MALDI-MS/MS using a Lys-N metalloendopeptidase. <i>Molecular and Cellular Proteomics</i> , 2009 , 8, 650-60	7.6	39
43	Lys-N and trypsin cover complementary parts of the phosphoproteome in a refined SCX-based approach. <i>Analytical Chemistry</i> , 2009 , 81, 4493-501	7.8	226
42	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, 992-1003		10
41	Straightforward ladder sequencing of peptides using a Lys-N metalloendopeptidase. <i>Nature Methods</i> , 2008 , 5, 405-7	21.6	103
40	A unique residue in rab3c determines the interaction with novel binding protein Zwint-1. <i>FEBS Letters</i> , 2008 , 582, 2838-42	3.8	23
39	Highly robust, automated, and sensitive online TiO ₂ -based phosphoproteomics applied to study endogenous phosphorylation in <i>Drosophila melanogaster</i> . <i>Journal of Proteome Research</i> , 2008 , 7, 687-97	5.6	164
38	Regulation of retromer recruitment to endosomes by sequential action of Rab5 and Rab7. <i>Journal of Cell Biology</i> , 2008 , 183, 513-26	7.3	328

37	Online automated in vivo zebrafish phosphoproteomics: from large-scale analysis down to a single embryo. <i>Journal of Proteome Research</i> , 2008 , 7, 1555-64	5.6	68
36	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, 3584-92	7.8	35
35	Highly efficient depletion strategy for the two most abundant erythrocyte soluble proteins improves proteome coverage dramatically. <i>Journal of Proteome Research</i> , 2008 , 7, 3060-3	5.6	65
34	Chip-Based Enrichment and NanoLC-MS/MS Analysis of Phosphopeptides from Whole Lysates. <i>Journal of Proteome Research</i> , 2008 , 7, 1565-71	5.6	61
33	Comparative phosphoproteomics of zebrafish Fyn/Yes morpholino knockdown embryos. <i>Molecular and Cellular Proteomics</i> , 2008 , 7, 2176-87	7.6	50
32	Activation of FoxM1 during G2 requires cyclin A/Cdk-dependent relief of autorepression by the FoxM1 N-terminal domain. <i>Molecular and Cellular Biology</i> , 2008 , 28, 3076-87	4.8	116
31	Automated online sequential isotope labeling for protein quantitation applied to proteasome tissue-specific diversity. <i>Molecular and Cellular Proteomics</i> , 2008 , 7, 1755-62	7.6	63
30	Hydrophilic interaction liquid chromatography (HILIC) in proteomics. <i>Analytical and Bioanalytical Chemistry</i> , 2008 , 391, 151-9	4.4	206
29	Triplex protein quantification based on stable isotope labeling by peptide dimethylation applied to cell and tissue lysates. <i>Proteomics</i> , 2008 , 8, 4624-32	4.8	174
28	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	2.1	13
27	Targeted analysis of protein termini. <i>Journal of Proteome Research</i> , 2007 , 6, 4634-45	5.6	85
26	Atorvastatin modulates the profile of proteins released by human atherosclerotic plaques. <i>European Journal of Pharmacology</i> , 2007 , 562, 119-29	5.3	40
25	Evaluation and optimization of ZIC-HILIC-RP as an alternative MudPIT strategy. <i>Journal of Proteome Research</i> , 2007 , 6, 937-46	5.6	169
24	Quantitative phosphoproteomics of early elicitor signaling in Arabidopsis. <i>Molecular and Cellular Proteomics</i> , 2007 , 6, 1198-214	7.6	528
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4	Proteome-wide Profiling of RNA-Binding Protein Responses to flg22 Reveals Novel Components of Plant Immunity		1
3	Structural characterisation of KKT4, an unconventional microtubule-binding kinetochore protein		1
2	Global analysis of protein-RNA interactions in SARS-CoV-2 infected cells reveals key regulators of infection		6

1 System-wide analyses of the fission yeast poly(A)⁺ RNA interactome reveal insights into organisation and function of RNA-protein complexes

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