

Shabaz Mohammed

List of Publications by Citations

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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	Multiplex peptide stable isotope dimethyl labeling for quantitative proteomics. <i>Nature Protocols</i> , 2009 , 4, 484-94	18.8	1072
179	Lgr5 homologues associate with Wnt receptors and mediate R-spondin signalling. <i>Nature</i> , 2011 , 476, 293-7	50.4	903
178	The CRAPome: a contaminant repository for affinity purification-mass spectrometry data. <i>Nature Methods</i> , 2013 , 10, 730-6	21.6	894
177	Quantitative phosphoproteomics applied to the yeast pheromone signaling pathway. <i>Molecular and Cellular Proteomics</i> , 2005 , 4, 310-27	7.6	665
176	Wnt signaling through inhibition of β -catenin degradation in an intact Axin1 complex. <i>Cell</i> , 2012 , 149, 1245-56	56.2	619
175	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
174	Quantitative phosphoproteomics of early elicitor signaling in Arabidopsis. <i>Molecular and Cellular Proteomics</i> , 2007 , 6, 1198-214	7.6	528
173	The Lgr5 intestinal stem cell signature: robust expression of proposed quiescent T4Tcell markers. <i>EMBO Journal</i> , 2012 , 31, 3079-91	13	523
172	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
171	Phosphopeptide fragmentation and analysis by mass spectrometry. <i>Journal of Mass Spectrometry</i> , 2009 , 44, 861-78	2.2	290
170	Toward a comprehensive characterization of a human cancer cell phosphoproteome. <i>Journal of Proteome Research</i> , 2013 , 12, 260-71	5.6	276
169	Robust phosphoproteome enrichment using monodisperse microsphere-based immobilized titanium (IV) ion affinity chromatography. <i>Nature Protocols</i> , 2013 , 8, 461-80	18.8	270
168	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
167	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
166	A systematic approach to modeling, capturing, and disseminating proteomics experimental data. <i>Nature Biotechnology</i> , 2003 , 21, 247-54	44.5	220
165	Hydrophilic interaction liquid chromatography (HILIC) in proteomics. <i>Analytical and Bioanalytical Chemistry</i> , 2008 , 391, 151-9	4.4	206
164	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

163	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
162	An optimized protocol for metabolome analysis in yeast using direct infusion electrospray mass spectrometry. <i>Phytochemistry</i> , 2003 , 62, 929-37	4	192
161	Posttranslational mutagenesis: A chemical strategy for exploring protein side-chain diversity. <i>Science</i> , 2016 , 354,	33.3	182
160	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
159	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
158	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}	5.6	164
157	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	17.6	152
156	Nuclear PtdIns5P as a transducer of stress signaling: an in vivo role for PIP4Kbeta. <i>Molecular Cell</i> , 2006 , 23, 685-95	17.6	147
155	Cross-talk between phosphorylation and lysine acetylation in a genome-reduced bacterium. <i>Molecular Systems Biology</i> , 2012 , 8, 571	12.2	144
154	A large synthetic peptide and phosphopeptide reference library for mass spectrometry-based proteomics. <i>Nature Biotechnology</i> , 2013 , 31, 557-64	44.5	132
153	The kinase TNIK is an essential activator of Wnt target genes. <i>EMBO Journal</i> , 2009 , 28, 3329-40	13	130
152	Unambiguous phosphosite localization using electron-transfer/higher-energy collision dissociation (ETHcD). <i>Journal of Proteome Research</i> , 2013 , 12, 1520-5	5.6	125
151	Recent advances in peptide separation by multidimensional liquid chromatography for proteome analysis. <i>Journal of Proteomics</i> , 2012 , 75, 3791-813	3.9	124
150	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}	7.8	117
149	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
148	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, 790-8	5.8	108
147	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, 935-43	5.6	106
146	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

145	Straightforward ladder sequencing of peptides using a Lys-N metalloendopeptidase. <i>Nature Methods</i> , 2008 , 5, 405-7	21.6	103
144	Benchmarking stable isotope labeling based quantitative proteomics. <i>Journal of Proteomics</i> , 2013 , 88, 14-26	3.9	100
143	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
142	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
141	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
140	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
139	Optimal Synthetic Glycosylation of a Therapeutic Antibody. <i>Angewandte Chemie - International Edition</i> , 2016 , 55, 2361-7	16.4	92
138	Targeted analysis of protein termini. <i>Journal of Proteome Research</i> , 2007 , 6, 4634-45	5.6	85
137	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
136	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
135	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
134	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
133	The tyrosine phosphatase Shp2 interacts with NPM-ALK and regulates anaplastic lymphoma cell growth and migration. <i>Cancer Research</i> , 2007 , 67, 4278-86	10.1	75
132	The leukemia-associated Mllt10/AF10-Dot1l are Tcf4/Ectenin coactivators essential for intestinal homeostasis. <i>PLoS Biology</i> , 2010 , 8, e1000539	9.7	70
131	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
130	Selective Metal-Site-Guided Arylation of Proteins. <i>Journal of the American Chemical Society</i> , 2016 , 138, 8678-81	16.4	68
129	Coupled activation and degradation of eEF2K regulates protein synthesis in response to genotoxic stress. <i>Science Signaling</i> , 2012 , 5, ra40	8.8	68
128	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

127	Toward an Optimized Workflow for Middle-Down Proteomics. <i>Analytical Chemistry</i> , 2017 , 89, 3318-3325	7.8	67
126	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
125	Protease bias in absolute protein quantitation. <i>Nature Methods</i> , 2012 , 9, 524-5	21.6	67
124	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
123	p130Cas mediates the transforming properties of the anaplastic lymphoma kinase. <i>Blood</i> , 2005 , 106, 3907-16	2.2	66
122	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
121	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
120	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
119	Perturbation of the yeast N-acetyltransferase NatB induces elevation of protein phosphorylation levels. <i>BMC Genomics</i> , 2010 , 11, 685	4.5	61
118	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
117	Genetic and proteomic evidences support the localization of yeast enolase in the cell surface. <i>Proteomics</i> , 2006 , 6 Suppl 1, S107-18	4.8	59
116	Applications of stable isotope dimethyl labeling in quantitative proteomics. <i>Analytical and Bioanalytical Chemistry</i> , 2012 , 404, 991-1009	4.4	57
115	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, 973-82	5.6	53
114	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, 1127-34	2.2	53
113	Probing genuine strong interactions and post-translational modifications in the heterogeneous yeast exosome protein complex. <i>Molecular and Cellular Proteomics</i> , 2006 , 5, 1581-92	7.6	51
112	Highly sensitive proteome analysis of FACS-sorted adult colon stem cells. <i>Journal of Proteome Research</i> , 2011 , 10, 3814-9	5.6	50
111	Comparative phosphoproteomics of zebrafish Fyn/Yes morpholino knockdown embryos. <i>Molecular and Cellular Proteomics</i> , 2008 , 7, 2176-87	7.6	50
110	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

109	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
108	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
107	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, 1578-86	7.2	48
106	Quantitative Map of Proteome Dynamics during Neuronal Differentiation. <i>Cell Reports</i> , 2017 , 18, 1527-1542	7.2	47
105	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
104	Ultra acidic strong cation exchange enabling the efficient enrichment of basic phosphopeptides. <i>Analytical Chemistry</i> , 2012 , 84, 1804-8	7.8	45
103	Peptide orientation affects selectivity in ion-exchange chromatography. <i>Analytical Chemistry</i> , 2010 , 82, 5253-9	7.8	45
102	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
101	Cleavage specificities of the brother and sister proteases Lys-C and Lys-N. <i>Chemical Communications</i> , 2010 , 46, 8827-9	5.8	44
100	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
99	Generation of a synthetic GlcNAcylated nucleosome reveals regulation of stability by H2A-Thr101 GlcNAcylation. <i>Nature Communications</i> , 2015 , 6, 7978	17.4	40
98	Synthetic phosphorylation of p38 recapitulates protein kinase activity. <i>Journal of the American Chemical Society</i> , 2014 , 136, 1698-701	16.4	40
97	Atorvastatin modulates the profile of proteins released by human atherosclerotic plaques. <i>European Journal of Pharmacology</i> , 2007 , 562, 119-29	5.3	40
96	Light-driven post-translational installation of reactive protein side chains. <i>Nature</i> , 2020 , 585, 530-537	50.4	40
95	Ligand binding to a G protein-coupled receptor captured in a mass spectrometer. <i>Science Advances</i> , 2017 , 3, e1701016	14.3	39
94	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
93	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, 1367-78	5.6	39
92	Synthetic post-translational modification of histones. <i>Current Opinion in Chemical Biology</i> , 2018 , 45, 35-43	7.7	37

91	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
90	Effect of chemical modifications on peptide fragmentation behavior upon electron transfer induced dissociation. <i>Analytical Chemistry</i> , 2009 , 81, 7814-22	7.8	37
89	A role for PtdIns(4,5)P2 and PIP5Kalpha in regulating stress-induced apoptosis. <i>Current Biology</i> , 2006 , 16, 1850-6	6.3	37
88	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
87	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
86	Characterization of biases in phosphopeptide enrichment by Ti(4+)-immobilized metal affinity chromatography and TiO2 using a massive synthetic library and human cell digests. <i>Analytical Chemistry</i> , 2014 , 86, 8312-20	7.8	35
85	A systems-wide screen identifies substrates of the SCF ^{TrCP} ubiquitin ligase. <i>Science Signaling</i> , 2014 , 7, rs8	8.8	35
84	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
83	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
82	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
81	β-Syntrophin is a Cdk5 substrate that restrains the motility of insulin secretory granules. <i>PLoS ONE</i> , 2010 , 5, e12929	3.7	32
80	Elongation/Termination Factor Exchange Mediated by PP1 Phosphatase Orchestrates Transcription Termination. <i>Cell Reports</i> , 2018 , 25, 259-269.e5	10.6	32
79	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
78	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
77	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
76	ZIC-CHILIC as a fractionation method for sensitive and powerful shotgun proteomics. <i>Nature Protocols</i> , 2012 , 7, 2041-55	18.8	29
75	MAP3K1 functionally interacts with Axin1 in the canonical Wnt signalling pathway. <i>Biological Chemistry</i> , 2010 , 391, 171-180	4.5	29
74	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

73	Guanidination chemistry for qualitative and quantitative proteomics. <i>Rapid Communications in Mass Spectrometry</i> , 2006 , 20, 3245-56	2.2	29
72	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
71	RockerBox: analysis and filtering of massive proteomics search results. <i>Journal of Proteome Research</i> , 2011 , 10, 1420-4	5.6	28
70	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
69	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
68	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
67	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
66	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
65	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
64	Discovering the RNA-Binding Proteome of Plant Leaves with an Improved RNA Interactome Capture Method. <i>Biomolecules</i> , 2020 , 10,	5.9	22
63	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
62	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
61	Profiling of diet-induced neuropeptide changes in rat brain by quantitative mass spectrometry. <i>Analytical Chemistry</i> , 2013 , 85, 4594-604	7.8	21
60	Deconvolution of overlapping isotopic clusters improves quantification of stable isotope-labeled peptides. <i>Journal of Proteomics</i> , 2011 , 74, 2204-9	3.9	19
59	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
58	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
57	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
56	A novel tandem quadrupole mass spectrometer allowing gaseous collisional activation and surface induced dissociation. <i>Journal of Mass Spectrometry</i> , 2001 , 36, 1260-8	2.2	18

55	The role of the Xist 5Tm6A region and RBM15 in X chromosome inactivation. <i>Wellcome Open Research</i> , 2020 , 5, 31	4.8	18
54	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
53	The anti-sigma factor RsrA responds to oxidative stress by reburying its hydrophobic core. <i>Nature Communications</i> , 2016 , 7, 12194	17.4	16
52	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
51	Acetylation and phosphorylation control both local and global stability of the chloroplast F ATP synthase. <i>Scientific Reports</i> , 2017 , 7, 44068	4.9	14
50	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
49	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
48	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
47	HGF signaling regulates Claudin-3 dynamics through its C-terminal tyrosine residues. <i>Tissue Barriers</i> , 2013 , 1, e27425	4.3	14
46	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
45	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
44	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
43	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
42	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
41	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
40	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
39	Comparative phosphoproteomic analysis of checkpoint recovery identifies new regulators of the DNA damage response. <i>Science Signaling</i> , 2013 , 6, rs9	8.8	11
38	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

37	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
36	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
35	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
34	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
33	Characterization of HSP27 phosphorylation sites in human atherosclerotic plaque secretome. <i>Methods in Molecular Biology</i> , 2007 , 357, 151-63	1.4	8
32	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
31	Ordered dephosphorylation initiated by the selective proteolysis of cyclin B drives mitotic exit. <i>ELife</i> , 2020 , 9,	8.9	7
30	Nicotinamide Cofactors Suppress Active-Site Labeling of Aldehyde Dehydrogenases. <i>ACS Chemical Biology</i> , 2016 , 11, 1578-86	4.9	6
29	Global analysis of protein-RNA interactions in SARS-CoV-2 infected cells reveals key regulators of infection		6
28	Proteomics as a tool for live attenuated influenza vaccine characterisation. <i>Vaccine</i> , 2020 , 38, 868-877	4.1	6
27	LanCLs add glutathione to dehydroamino acids generated at phosphorylated sites in the proteome. <i>Cell</i> , 2021 , 184, 2680-2695.e26	56.2	6
26	YcfD is a thermophilic oxygen-dependent ribosomal protein uL16 oxygenase. <i>Extremophiles</i> , 2018 , 22, 553-562	3	5
25	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
24	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
23	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
22	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, 157-67 [†]	1.4	4
21	Post-translational insertion of boron in proteins to probe and modulate function. <i>Nature Chemical Biology</i> , 2021 , 17, 1245-1261	11.7	4
20	Synthetic Nucleosomes Reveal that GlcNAcylation Modulates Direct Interaction with the FACT Complex. <i>Angewandte Chemie</i> , 2016 , 128, 9064-9068	3.6	4

19	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
18	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
17	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
16	Quantitative Proteomics for Differential Protein Expression Profiling 2019 , 1-27		2
15	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
14	NeissLock provides an inducible protein anhydride for covalent targeting of endogenous proteins. <i>Nature Communications</i> , 2021 , 12, 717	17.4	2
13	Structural characterization of KKT4, an unconventional microtubule-binding kinetochore protein. <i>Structure</i> , 2021 , 29, 1014-1028.e8	5.2	2
12	Triazine Probes Target Ascorbate Peroxidases in Plants. <i>Plant Physiology</i> , 2019 , 180, 1848-1859	6.6	1
11	Threonine Phosphorylation of IBIMediates Inhibition of Selective Proinflammatory Target Genes. <i>Journal of Investigative Dermatology</i> , 2020 , 140, 1805-1814.e6	4.3	1
10	Comparative Poly(A)+ RNA Interactome Capture of RNA Surveillance Mutants. <i>Methods in Molecular Biology</i> , 2020 , 2062, 255-276	1.4	1
9	Proteome-wide Profiling of RNA-Binding Protein Responses to flg22 Reveals Novel Components of Plant Immunity		1
8	Structural characterisation of KKT4, an unconventional microtubule-binding kinetochore protein		1
7	System-wide analyses of the fission yeast poly(A)+ RNA interactome reveal insights into organisation and function of RNA-protein complexes		1
6	Colicin-Mediated Transport of DNA through the Iron Transporter FepA. <i>MBio</i> , 2021 , 12, e0178721	7.8	1
5	Uncovering viral RNA-host cell interactions on a proteome-wide scale. <i>Trends in Biochemical Sciences</i> , 2021 ,	10.3	1
4	Reductive site-selective atypical γ -type/N2-C2 cleavage allows C-terminal protein amidation.. <i>Science Advances</i> , 2022 , 8, eabl8675	14.3	0
3	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	
2	Modulación mediante tratamiento con atorvastatina y/o amlodipino del perfil de proteínas liberadas por placas ateroscleróticas humanas. <i>Clínica E Investigación En Arteriosclerosis</i> , 2006 , 18, 167-175	1.4	

- 1 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 3.6