List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Uncovering viral RNA–host cell interactions on a proteome-wide scale. Trends in Biochemical Sciences, 2022, 47, 23-38.	7.5	20
2	RNA-binding protein Mub1 and the nuclear RNA exosome act to fine-tune environmental stress response. Life Science Alliance, 2022, 5, e202101111.	2.8	1
3	Reductive site-selective atypical <i>C</i> , <i>Z</i> -type/N2-C2 cleavage allows C-terminal protein amidation. Science Advances, 2022, 8, eabl8675.	10.3	1
4	Broadâ€range metalloprotease profiling in plants uncovers immunity provided by defenceâ€related metalloenzyme. New Phytologist, 2022, 235, 1287-1301.	7.3	3
5	Global analysis of RNA-binding protein dynamics by comparative and enhanced RNA interactome capture. Nature Protocols, 2021, 16, 27-60.	12.0	31
6	NeissLock provides an inducible protein anhydride for covalent targeting of endogenous proteins. Nature Communications, 2021, 12, 717.	12.8	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.	9.7	108
8	LanCLs add glutathione to dehydroamino acids generated at phosphorylated sites in the proteome. Cell, 2021, 184, 2680-2695.e26.	28.9	34
9	Structural characterization of KKT4, an unconventional microtubule-binding kinetochore protein. Structure, 2021, 29, 1014-1028.e8.	3.3	9
10	Colicin-Mediated Transport of DNA through the Iron Transporter FepA. MBio, 2021, 12, e0178721.	4.1	7
11	Post-translational insertion of boron in proteins to probe and modulate function. Nature Chemical Biology, 2021, 17, 1245-1261.	8.0	15
12	Proteomics as a tool for live attenuated influenza vaccine characterisation. Vaccine, 2020, 38, 868-877.	3.8	6
13	Quantitative MSâ€Based Proteomics: Comparing the MCFâ€7 Cellular Response to Hypoxia and a 2â€Oxoglutarate Analogue. ChemBioChem, 2020, 21, 1647-1655.	2.6	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.	2.0	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.	13.8	31
16	Light-driven post-translational installation of reactive protein side chains. Nature, 2020, 585, 530-537.	27.8	100
17	Discovering the RNA-Binding Proteome of Plant Leaves with an Improved RNA Interactome Capture Method. Biomolecules, 2020, 10, 661.	4.0	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.	5.5	6

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19	A receptor for the complement regulator factor H increases transmission of trypanosomes to tsetse flies. Nature Communications, 2020, 11, 1326.	12.8	23
20	Threonine Phosphorylation of IκBζ Mediates Inhibition of Selective Proinflammatory TargetÂGenes. Journal of Investigative Dermatology, 2020, 140, 1805-1814.e6.	0.7	4
21	Comparative Poly(A)+ RNA Interactome Capture of RNA Surveillance Mutants. Methods in Molecular Biology, 2020, 2062, 255-276.	0.9	6
22	The role of the Xist 5' m6A region and RBM15 in X chromosome inactivation. Wellcome Open Research, 2020, 5, 31.	1.8	37
23	Ordered dephosphorylation initiated by the selective proteolysis of cyclin B drives mitotic exit. ELife, 2020, 9, .	6.0	22
24	Polyamines Control eIF5A Hypusination, TFEB Translation, and Autophagy to Reverse B Cell Senescence. Molecular Cell, 2019, 76, 110-125.e9.	9.7	205
25	Triazine Probes Target Ascorbate Peroxidases in Plants. Plant Physiology, 2019, 180, 1848-1859.	4.8	5
26	System-wide Profiling of RNA-Binding Proteins Uncovers Key Regulators of Virus Infection. Molecular Cell, 2019, 74, 196-211.e11.	9.7	137
27	Synthetic post-translational modification of histones. Current Opinion in Chemical Biology, 2018, 45, 35-47.	6.1	53
28	Doxorubicin-induced DNA Damage Causes Extensive Ubiquitination of Ribosomal Proteins Associated with a Decrease in Protein Translation*. Molecular and Cellular Proteomics, 2018, 17, 2297-2308.	3.8	28
29	YcfDRM is a thermophilic oxygen-dependent ribosomal protein uL16 oxygenase. Extremophiles, 2018, 22, 553-562.	2.3	6
30	Protein Syndesmos is a novel RNA-binding protein that regulates primary cilia formation. Nucleic Acids Research, 2018, 46, 12067-12086.	14.5	20
31	Elongation/Termination Factor Exchange Mediated by PP1 Phosphatase Orchestrates Transcription Termination. Cell Reports, 2018, 25, 259-269.e5.	6.4	58
32	Genetic Incorporation of Olefin Cross-Metathesis Reaction Tags for Protein Modification. Journal of the American Chemical Society, 2018, 140, 14599-14603.	13.7	38
33	Personalized Proteome Profiles of Healthy and Tumor Human Colon Organoids Reveal Both Individual Diversity and Basic Features of Colorectal Cancer. Cell Reports, 2017, 18, 263-274.	6.4	126
34	Acetylation and phosphorylation control both local and global stability of the chloroplast F1 ATP synthase. Scientific Reports, 2017, 7, 44068.	3.3	18
35	Toward an Optimized Workflow for Middle-Down Proteomics. Analytical Chemistry, 2017, 89, 3318-3325.	6.5	91
36	Quantitative Map of Proteome Dynamics during Neuronal Differentiation. Cell Reports, 2017, 18, 1527-1542.	6.4	79

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37	Ligand binding to a G protein–coupled receptor captured in a mass spectrometer. Science Advances, 2017, 3, e1701016.	10.3	52
38	Monitoring the Disassembly of Virus-like Particles by ¹⁹ F-NMR. Journal of the American Chemical Society, 2017, 139, 5277-5280.	13.7	23
39	Exploitation of an iron transporter for bacterial protein antibiotic import. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 12051-12056.	7.1	76
40	hnRNPK Recruits PCGF3/5-PRC1 to the Xist RNA B-Repeat to Establish Polycomb-Mediated Chromosomal Silencing. Molecular Cell, 2017, 68, 955-969.e10.	9.7	255
41	Nuclear phosphorylated Dicer processes double-stranded RNA in response to DNA damage. Journal of Cell Biology, 2017, 216, 2373-2389.	5.2	73
42	Combining Deep Sequencing, Proteomics, Phosphoproteomics, and Functional Screens To Discover Novel Regulators of Sphingolipid Homeostasis. Journal of Proteome Research, 2017, 16, 571-582.	3.7	11
43	Interdomain conformational flexibility underpins the activity of UGCT, the eukaryotic glycoprotein secretion checkpoint. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 8544-8549.	7.1	48
44	Synthetic Nucleosomes Reveal that GlcNAcylation Modulates Direct Interaction with the FACT Complex. Angewandte Chemie, 2016, 128, 9064-9068.	2.0	4
45	Synthetic Nucleosomes Reveal that GlcNAcylation Modulates Direct Interaction with the FACT Complex. Angewandte Chemie - International Edition, 2016, 55, 8918-8922.	13.8	32
46	Optimal Synthetic Glycosylation of a Therapeutic Antibody. Angewandte Chemie - International Edition, 2016, 55, 2361-2367.	13.8	122
47	Dimer interface of bovine cytochrome <i>c</i> oxidase is influenced by local posttranslational modifications and lipid binding. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 8230-8235.	7.1	40
48	The anti-sigma factor RsrA responds to oxidative stress by reburying its hydrophobic core. Nature Communications, 2016, 7, 12194.	12.8	26
49	Posttranslational mutagenesis: A chemical strategy for exploring protein side-chain diversity. Science, 2016, 354, .	12.6	247
50	A PP2A-B55 recognition signal controls substrate dephosphorylation kinetics during mitotic exit. Journal of Cell Biology, 2016, 214, 539-554.	5.2	164
51	On the Statistical Significance of Compressed Ratios in Isobaric Labeling: A Cross-Platform Comparison. Journal of Proteome Research, 2016, 15, 3029-3038.	3.7	13
52	Selective Metal-Site-Guided Arylation of Proteins. Journal of the American Chemical Society, 2016, 138, 8678-8681.	13.7	92
53	Sampling From the Proteome to the Human Leukocyte Antigen-DR (HLA-DR) Ligandome Proceeds Via High Specificity. Molecular and Cellular Proteomics, 2016, 15, 1412-1423.	3.8	80
54	Nicotinamide Cofactors Suppress Active-Site Labeling of Aldehyde Dehydrogenases. ACS Chemical Biology, 2016, 11, 1578-1586.	3.4	6

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55	elF2 interactions with initiator tRNA and elF2B are regulated by post-translational modifications and conformational dynamics. Cell Discovery, 2015, 1, 15020.	6.7	29
56	Signal Transduction Reaction Monitoring Deciphers Site-Specific PI3K-mTOR/MAPK Pathway Dynamics in Oncogene-Induced Senescence. Journal of Proteome Research, 2015, 14, 2906-2914.	3.7	33
57	Rapid Analyses of Proteomes and Interactomes Using an Integrated Solid-Phase Extraction–Liquid Chromatography–MS/MS System. Journal of Proteome Research, 2015, 14, 977-985.	3.7	6
58	Datasets from an interaction proteomics screen for substrates of the SCF βTrCP ubiquitin ligase. Data in Brief, 2015, 4, 229-234.	1.0	0
59	De novo sequencing of two novel peptides homologous to calcitonin-like peptides, from skin secretion of the Chinese Frog, Odorrana schmackeri. EuPA Open Proteomics, 2015, 8, 157-166.	2.5	3
60	Generation of a synthetic GlcNAcylated nucleosome reveals regulation of stability by H2A-Thr101 GlcNAcylation. Nature Communications, 2015, 6, 7978.	12.8	51
61	A systems-wide screen identifies substrates of the SCF ^{βTrCP} ubiquitin ligase. Science Signaling, 2014, 7, rs8.	3.6	49
62	USP17- and SCF ^{βTrCP} -Regulated Degradation of DEC1 Controls the DNA Damage Response. Molecular and Cellular Biology, 2014, 34, 4177-4185.	2.3	30
63	Proteasome-dependent Degradation of Transcription Factor Activating Enhancer-binding Protein 4 (TFAP4) Controls Mitotic Division. Journal of Biological Chemistry, 2014, 289, 7730-7737.	3.4	25
64	Characterization and usage of the EASY-spray technology as part of an online 2D SCX-RP ultra-high pressure system. Analyst, The, 2014, 139, 6520-6528.	3.5	18
65	Proteome Adaptation of <i>Saccharomyces cerevisiae</i> to Severe Calorie Restriction in Retentostat Cultures. Journal of Proteome Research, 2014, 13, 3542-3553.	3.7	17
66	Synthetic Phosphorylation of p38α Recapitulates Protein Kinase Activity. Journal of the American Chemical Society, 2014, 136, 1698-1701.	13.7	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. Analytical Chemistry, 2014, 86, 8312-8320.	6.5	43
68	Phosphoproteomics. Analytical Chemistry, 2014, 86, 1313-1313.	6.5	9
69	The CRAPome: a contaminant repository for affinity purification–mass spectrometry data. Nature Methods, 2013, 10, 730-736.	19.0	1,353
70	Profiling of Diet-Induced Neuropeptide Changes in Rat Brain by Quantitative Mass Spectrometry. Analytical Chemistry, 2013, 85, 4594-4604.	6.5	24
71	Toward a Comprehensive Characterization of a Human Cancer Cell Phosphoproteome. Journal of Proteome Research, 2013, 12, 260-271.	3.7	363
72	Control of Epithelial Cell Migration and Invasion by the IKKÎ ² - and CK1α-Mediated Degradation of RAPGEF2. Developmental Cell, 2013, 27, 574-585.	7.0	30

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73	Quantitative and Qualitative Proteome Characteristics Extracted from In-Depth Integrated Genomics and Proteomics Analysis. Cell Reports, 2013, 5, 1469-1478.	6.4	113
74	Benchmarking stable isotope labeling based quantitative proteomics. Journal of Proteomics, 2013, 88, 14-26.	2.4	112
75	Unambiguous Phosphosite Localization using Electron-Transfer/Higher-Energy Collision Dissociation (EThcD). Journal of Proteome Research, 2013, 12, 1520-1525.	3.7	145
76	Robust phosphoproteome enrichment using monodisperse microsphere–based immobilized titanium (IV) ion affinity chromatography. Nature Protocols, 2013, 8, 461-480.	12.0	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. Journal of Proteome Research, 2013, 12, 2214-2224.	3.7	45
78	Quantitative global phosphoproteomics of human umbilical vein endothelial cells after activation of the Rap signaling pathway. Molecular BioSystems, 2013, 9, 732.	2.9	8
79	A large synthetic peptide and phosphopeptide reference library for mass spectrometry–based proteomics. Nature Biotechnology, 2013, 31, 557-564.	17.5	164
80	Characterization of Electron Transfer Dissociation in the Orbitrap Velos HCD Cell. Journal of the American Society for Mass Spectrometry, 2013, 24, 1663-1670.	2.8	5
81	HGF signaling regulates Claudin-3 dynamics through its C-terminal tyrosine residues. Tissue Barriers, 2013, 1, e27425.	3.2	17
82	Comparative Phosphoproteomic Analysis of Checkpoint Recovery Identifies New Regulators of the DNA Damage Response. Science Signaling, 2013, 6, rs9.	3.6	18
83	Collaboration of AMPK and PKC to induce phosphorylation of Ser413 on PIP5K1B resulting in decreased kinase activity and reduced PtdIns(4,5) <i>P</i> 2 synthesis in response to oxidative stress and energy restriction. Biochemical Journal, 2013, 455, 347-358.	3.7	10
84	Quantitative Phosphoproteomics after Auxin-stimulated Lateral Root Induction Identifies an SNX1 Protein Phosphorylation Site Required for Growth. Molecular and Cellular Proteomics, 2013, 12, 1158-1169.	3.8	95
85	Enhancing the Identification of Phosphopeptides from Putative Basophilic Kinase Substrates Using Ti (IV) Based IMAC Enrichment. Molecular and Cellular Proteomics, 2013, 12, 2673.	3.8	6
86	Coupled Activation and Degradation of eEF2K Regulates Protein Synthesis in Response to Genotoxic Stress. Science Signaling, 2012, 5, ra40.	3.6	76
87	Database independent proteomics analysis of the ostrich and human proteome. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 407-412.	7.1	13
88	Crossâ€ŧalk between phosphorylation and lysine acetylation in a genomeâ€reduced bacterium. Molecular Systems Biology, 2012, 8, 571.	7.2	169
89	Toward Full Peptide Sequence Coverage by Dual Fragmentation Combining Electron-Transfer and Higher-Energy Collision Dissociation Tandem Mass Spectrometry. Analytical Chemistry, 2012, 84, 9668-9673.	6.5	246
90	Fully automated isotopic dimethyl labeling and phosphopeptide enrichment using a microfluidic HPLC phosphochip. Analytical and Bioanalytical Chemistry, 2012, 404, 2507-2512.	3.7	17

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91	Ultra Acidic Strong Cation Exchange Enabling the Efficient Enrichment of Basic Phosphopeptides. Analytical Chemistry, 2012, 84, 1804-1808.	6.5	45
92	The Lgr5 intestinal stem cell signature: robust expression of proposed quiescent â€~+4' cell markers. EMBO Journal, 2012, 31, 3079-3091.	7.8	634
93	In-house construction of a UHPLC system enabling the identification of over 4000 protein groups in a single analysis. Analyst, The, 2012, 137, 3541.	3.5	43
94	Recent advances in peptide separation by multidimensional liquid chromatography for proteome analysis. Journal of Proteomics, 2012, 75, 3791-3813.	2.4	141
95	Wnt Signaling through Inhibition of β-Catenin Degradation in an Intact Axin1 Complex. Cell, 2012, 149, 1245-1256.	28.9	747
96	ZIC-cHILIC as a fractionation method for sensitive and powerful shotgun proteomics. Nature Protocols, 2012, 7, 2041-2055.	12.0	31
97	Tumour suppressor RNF43 is a stem-cell E3 ligase that induces endocytosis of Wnt receptors. Nature, 2012, 488, 665-669.	27.8	791
98	Applications of stable isotope dimethyl labeling in quantitative proteomics. Analytical and Bioanalytical Chemistry, 2012, 404, 991-1009.	3.7	61
99	Protease bias in absolute protein quantitation. Nature Methods, 2012, 9, 524-525.	19.0	80
100	Abstract 983: Wnt pathway activation involves inhibition of \hat{I}^2 -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. Molecular and Cellular Proteomics, 2011, 10, M110.006452.	3.8	81
102	RockerBox: Analysis and Filtering of Massive Proteomics Search Results. Journal of Proteome Research, 2011, 10, 1420-1424.	3.7	28
103	Exploring New Proteome Space: Combining Lys-N Proteolytic Digestion and Strong Cation Exchange (SCX) Separation in Peptide-Centric MS-Driven Proteomics. Methods in Molecular Biology, 2011, 753, 157-167.	0.9	5
104	Improved Peptide Identification by Targeted Fragmentation Using CID, HCD and ETD on an LTQ-Orbitrap Velos. Journal of Proteome Research, 2011, 10, 2377-2388.	3.7	277
105	Lgr5 homologues associate with Wnt receptors and mediate R-spondin signalling. Nature, 2011, 476, 293-297.	27.8	1,096
106	Zwitterionic Hydrophilic Interaction Liquid Chromatography (ZIC-HILIC and ZIC-cHILIC) Provide High Resolution Separation and Increase Sensitivity in Proteome Analysis. Analytical Chemistry, 2011, 83, 3440-3447.	6.5	128
107	Highly Sensitive Proteome Analysis of FACS-Sorted Adult Colon Stem Cells. Journal of Proteome Research, 2011, 10, 3814-3819.	3.7	60
108	Deconvolution of overlapping isotopic clusters improves quantification of stable isotope–labeled peptides. Journal of Proteomics, 2011, 74, 2204-2209.	2.4	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. Analytical Chemistry, 2011, 83, 8352-8356.	6.5	28
110	Improving Depth in Phosphoproteomics by Using a Strong Cation Exchange-Weak Anion Exchange-Reversed Phase Multidimensional Separation Approach. Analytical Chemistry, 2011, 83, 7137-7143.	6.5	49
111	Improving SRM Assay Development: A Global Comparison between Triple Quadrupole, Ion Trap, and Higher Energy CID Peptide Fragmentation Spectra. Journal of Proteome Research, 2011, 10, 4334-4341.	3.7	90
112	Strong cation exchange (SCX) based analytical methods for the targeted analysis of protein post-translational modifications. Current Opinion in Biotechnology, 2011, 22, 9-16.	6.6	79
113	In-depth Quantitative Cardiac Proteomics Combining Electron Transfer Dissociation and the Metalloendopeptidase Lys-N with the SILAC Mouse. Molecular and Cellular Proteomics, 2011, 10, O111.008474.	3.8	26
114	Protein Phosphatase 2A (B55α) Prevents Premature Activation of Forkhead Transcription Factor FoxM1 by Antagonizing Cyclin A/Cyclin-dependent Kinase-mediated Phosphorylation. Journal of Biological Chemistry, 2011, 286, 33029-33036.	3.4	31
115	Protein phosphatase 2A (B55α) prevents premature activation of forkhead transcription factor FoxM1 by antagonizing cyclin A/cyclin-dependent kinase-mediated phosphorylation Journal of Biological Chemistry, 2011, 286, 39674.	3.4	1
116	Comparative Assessment of Site Assignments in CID and Electron Transfer Dissociation Spectra of Phosphopeptides Discloses Limited Relocation of Phosphate Groups. Molecular and Cellular Proteomics, 2010, 9, 2140-2148.	3.8	42
117	Identification of Salt-Tolerant Sinorhizobium sp. Strain BL3 Membrane Proteins Based on Proteomics. Microbes and Environments, 2010, 25, 275-280.	1.6	2
118	Perturbation of the yeast N-acetyltransferase NatB induces elevation of protein phosphorylation levels. BMC Genomics, 2010, 11, 685.	2.8	77
119	Dimethyl isotope labeling assisted de novo peptide sequencing. Journal of the American Society for Mass Spectrometry, 2010, 21, 1957-1965.	2.8	25
120	<i>LysNDeNovo</i> : An algorithm enabling <i>de novo</i> sequencing of Lysâ€N generated peptides fragmented by electron transfer dissociation. Proteomics, 2010, 10, 1196-1201.	2.2	8
121	β2-Syntrophin Is a Cdk5 Substrate That Restrains the Motility of Insulin Secretory Granules. PLoS ONE, 2010, 5, e12929.	2.5	40
122	Profiling of N-Acetylated Protein Termini Provides In-depth Insights into the N-terminal Nature of the Proteome. Molecular and Cellular Proteomics, 2010, 9, 928-939.	3.8	113
123	MAP3K1 functionally interacts with Axin1 in the canonical Wnt signalling pathway. Biological Chemistry, 2010, 391, 171-180.	2.5	33
124	The Generating Function of CID, ETD, and CID/ETD Pairs of Tandem Mass Spectra: Applications to Database Search. Molecular and Cellular Proteomics, 2010, 9, 2840-2852.	3.8	226
125	The Leukemia-Associated Mllt10/Af10-Dot1l Are Tcf4/β-Catenin Coactivators Essential for Intestinal Homeostasis. PLoS Biology, 2010, 8, e1000539.	5.6	78
126	Exploring the Human Leukocyte Phosphoproteome Using a Microfluidic Reversed-Phaseâ^'TiO ₂ â''Reversed-Phase High-Performance Liquid Chromatography Phosphochip Coupled to a Quadrupole Time-of-Flight Mass Spectrometer. Analytical Chemistry, 2010, 82, 824-832.	6.5	74

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127	Peptide Orientation Affects Selectivity in Ion-Exchange Chromatography. Analytical Chemistry, 2010, 82, 5253-5259.	6.5	49
128	Evaluation of Metalloendopeptidase Lys-N Protease Performance under Different Sample Handling Conditions. Journal of Proteome Research, 2010, 9, 4282-4288.	3.7	36
129	Recovery from a DNAâ€damageâ€induced G2 arrest requires Cdkâ€dependent activation of FoxM1. EMBO Reports, 2010, 11, 452-458.	4.5	50
130	Cleavage specificities of the brother and sister proteases Lys-C and Lys-N. Chemical Communications, 2010, 46, 8827.	4.1	55
131	Phosphorylation of Not4p Functions Parallel to BUR2 to Regulate Resistance to Cellular Stresses in Saccharomyces cerevisiae. PLoS ONE, 2010, 5, e9864.	2.5	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. Molecular and Cellular Proteomics, 2009, 8, 1016-1028.	3.8	39
133	Strong Cation Exchange-based Fractionation of Lys-N-generated Peptides Facilitates the Targeted Analysis of Post-translational Modifications. Molecular and Cellular Proteomics, 2009, 8, 190-200.	3.8	69
134	Phosphopeptide fragmentation and analysis by mass spectrometry. Journal of Mass Spectrometry, 2009, 44, 861-878.	1.6	349
135	A threeâ€way proteomics strategy allows differential analysis of yeast mitochondrial membrane protein complexes under anaerobic and aerobic conditions. Proteomics, 2009, 9, 4787-4798.	2.2	39
136	The kinase TNIK is an essential activator of Wnt target genes. EMBO Journal, 2009, 28, 3329-3340.	7.8	169
137	Multiplex peptide stable isotope dimethyl labeling for quantitative proteomics. Nature Protocols, 2009, 4, 484-494.	12.0	1,247
138	Effect of Chemical Modifications on Peptide Fragmentation Behavior upon Electron Transfer Induced Dissociation. Analytical Chemistry, 2009, 81, 7814-7822.	6.5	38
139	Improved Identification of Endogenous Peptides from Murine Nervous Tissue by Multiplexed Peptide Extraction Methods and Multiplexed Mass Spectrometric Analysis. Journal of Proteome Research, 2009, 8, 870-876.	3.7	25
140	Straightforward and de Novo Peptide Sequencing by MALDI-MS/MS Using a Lys-N Metalloendopeptidase. Molecular and Cellular Proteomics, 2009, 8, 650-660.	3.8	42
141	Lys-N and Trypsin Cover Complementary Parts of the Phosphoproteome in a Refined SCX-Based Approach. Analytical Chemistry, 2009, 81, 4493-4501.	6.5	251
142	Assessing biological variation and protein processing in primary human leukocytes by automated multiplex stable isotope labeling coupled to 2 dimensional peptide separation. Molecular BioSystems, 2009, 5, 992.	2.9	10
143	Hydrophilic interaction liquid chromatography (HILIC) in proteomics. Analytical and Bioanalytical Chemistry, 2008, 391, 151-159.	3.7	234
144	Triplex protein quantification based on stable isotope labeling by peptide dimethylation applied to cell and tissue lysates. Proteomics, 2008, 8, 4624-4632.	2.2	192

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145	Straightforward ladder sequencing of peptides using a Lys-N metalloendopeptidase. Nature Methods, 2008, 5, 405-407.	19.0	116
146	A unique residue in rab3c determines the interaction with novel binding protein Zwintâ€1. FEBS Letters, 2008, 582, 2838-2842.	2.8	26
147	Highly Robust, Automated, and Sensitive Online TiO ₂ -Based Phosphoproteomics Applied To Study Endogenous Phosphorylation in <i>Drosophila melanogaster</i> . Journal of Proteome Research, 2008, 7, 687-697.	3.7	165
148	Regulation of retromer recruitment to endosomes by sequential action of Rab5 and Rab7. Journal of Cell Biology, 2008, 183, 513-526.	5.2	395
149	Online Automated <i>in Vivo</i> Zebrafish Phosphoproteomics: From Large-Scale Analysis Down to a Single Embryo. Journal of Proteome Research, 2008, 7, 1555-1564.	3.7	73
150	Multiplexed Proteomics Mapping of Yeast RNA Polymerase II and III Allows Near-Complete Sequence Coverage and Reveals Several Novel Phosphorylation Sites. Analytical Chemistry, 2008, 80, 3584-3592.	6.5	40
151	Highly Efficient Depletion Strategy for the Two Most Abundant Erythrocyte Soluble Proteins Improves Proteome Coverage Dramatically. Journal of Proteome Research, 2008, 7, 3060-3063.	3.7	74
152	Chip-Based Enrichment and NanoLCâ^'MS/MS Analysis of Phosphopeptides from Whole Lysates. Journal of Proteome Research, 2008, 7, 1565-1571.	3.7	63
153	Comparative Phosphoproteomics of Zebrafish Fyn/Yes Morpholino Knockdown Embryos. Molecular and Cellular Proteomics, 2008, 7, 2176-2187.	3.8	53
154	Activation of FoxM1 during G ₂ Requires Cyclin A/Cdk-Dependent Relief of Autorepression by the FoxM1 N-Terminal Domain. Molecular and Cellular Biology, 2008, 28, 3076-3087.	2.3	131
155	Automated Online Sequential Isotope Labeling for Protein Quantitation Applied to Proteasome Tissue-specific Diversity. Molecular and Cellular Proteomics, 2008, 7, 1755-1762.	3.8	66
156	Targeted SCX Based Peptide Fractionation for Optimal Sequencing by Collision Induced, and Electron Transfer Dissociation. Journal of Proteomics and Bioinformatics, 2008, 01, 379-388.	0.4	14
157	Characterization of HSP27 Phosphorylation Sites in Human Atherosclerotic Plaque Secretome. , 2007, 357, 151-164.		9
158	Quantitative Phosphoproteomics of Early Elicitor Signaling in Arabidopsis. Molecular and Cellular Proteomics, 2007, 6, 1198-1214.	3.8	614
159	The Tyrosine Phosphatase Shp2 Interacts with NPM-ALK and Regulates Anaplastic Lymphoma Cell Growth and Migration. Cancer Research, 2007, 67, 4278-4286.	0.9	86
160	Targeted Analysis of Protein Termini. Journal of Proteome Research, 2007, 6, 4634-4645.	3.7	93
161	Atorvastatin modulates the profile of proteins released by human atherosclerotic plaques. European Journal of Pharmacology, 2007, 562, 119-129.	3.5	48
162	Evaluation and Optimization of ZIC-HILIC-RP as an Alternative MudPIT Strategy. Journal of Proteome Research, 2007, 6, 937-946.	3.7	182

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163	Quantitative Proteomics Identifies Gemin5, A Scaffolding Protein Involved in Ribonucleoprotein Assembly, as a Novel Partner for Eukaryotic Initiation Factor 4E. Journal of Proteome Research, 2006, 5, 1367-1378.	3.7	44
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