

Yasushi Ishihama

List of Publications by Year in descending order

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167
papers

21,723
citations

22153

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10158

140
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171
docs citations

171
times ranked

32332
citing authors

#	ARTICLE	IF	CITATIONS
1	Ubiquitination at the lysine 27 residue of the Parkin ubiquitin-like domain is suggestive of a new mechanism of Parkin activation. <i>Human Molecular Genetics</i> , 2022, 31, 2623-2638.	2.9	1
2	One-Step Isolation of Protein C-Terminal Peptides from V8 Protease-Digested Proteins by Metal Oxide-Based Ligand-Exchange Chromatography. <i>Analytical Chemistry</i> , 2022, 94, 944-951.	6.5	7
3	Cyclin Jâ€CDK complexes limit innate immune responses by reducing proinflammatory changes in macrophage metabolism. <i>Science Signaling</i> , 2022, 15, eabm5011.	3.6	4
4	Quantitative nascent proteome profiling by dual-pulse labelling with <i>propargyl-puromycin</i> and stable isotope-labelled amino acids. <i>Journal of Biochemistry</i> , 2021, 169, 227-236.	1.7	12
5	The <i>Escherichia coli</i> S2P intramembrane protease RseP regulates ferric citrate uptake by cleaving the sigma factor regulator FecR. <i>Journal of Biological Chemistry</i> , 2021, 296, 100673.	3.4	14
6	Asia-Oceania HUPO: Past, Present, and Future. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100048.	3.8	1
7	Identification of Endogenous Kinase Substrates by Proximity Labeling Combined with Kinase Perturbation and Phosphorylation Motifs. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100119.	3.8	19
8	Peak Identification and Quantification by Proteomic Mass Spectrogram Decomposition. <i>Journal of Proteome Research</i> , 2021, 20, 2291-2298.	3.7	0
9	Maintenance of Neural Stem-Progenitor Cells by the Lysosomal Biosynthesis Regulators TFEB and TFE3 in the Embryonic Mouse Telencephalon. <i>Stem Cells</i> , 2021, 39, 929-944.	3.2	14
10	Exploring the landscape of ectodomain shedding by quantitative protein terminomics. <i>IScience</i> , 2021, 24, 102259.	4.1	12
11	Sequence-Specific Model for Predicting Peptide Collision Cross Section Values in Proteomic Ion Mobility Spectrometry. <i>Journal of Proteome Research</i> , 2021, 20, 3600-3610.	3.7	12
12	Acylated peptide enrichment utilizing lysine deacylases for lysine acylomics. <i>Biochemical and Biophysical Research Communications</i> , 2021, 563, 60-65.	2.1	2
13	Combinatorial analysis of translation dynamics reveals eIF2 dependence of translation initiation at near-cognate codons. <i>Nucleic Acids Research</i> , 2021, 49, 7298-7317.	14.5	22
14	Nanoscale Solid-Phase Isobaric Labeling for Multiplexed Quantitative Phosphoproteomics. <i>Journal of Proteome Research</i> , 2021, 20, 4193-4202.	3.7	7
15	Phosphatidylserine-deficient small extracellular vesicle is a major somatic cell-derived sEV subpopulation in blood. <i>IScience</i> , 2021, 24, 102839.	4.1	24
16	A protocol for analyzing the protein terminome of human cancer cell line culture supernatants. <i>STAR Protocols</i> , 2021, 2, 100682.	1.2	4
17	GlycoPOST realizes FAIR principles for glycomics mass spectrometry data. <i>Nucleic Acids Research</i> , 2021, 49, D1523-D1528.	14.5	78
18	IRAK1-dependent Regnase-1-14-3-3 complex formation controls Regnase-1-mediated mRNA decay. <i>ELife</i> , 2021, 10, .	6.0	12

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19	Peptide probes containing a non-hydrolyzable phosphotyrosine-mimetic residue for enrichment of protein tyrosine phosphatases. <i>Proteomics</i> , 2021, , 2100144.	2.2	1
20	Discovery of anti-inflammatory physiological peptides that promote tissue repair by reinforcing epithelial barrier formation. <i>Science Advances</i> , 2021, 7, eabj6895.	10.3	3
21	The ProteomeXchange consortium in 2020: enabling "big data" approaches in proteomics. <i>Nucleic Acids Research</i> , 2020, 48, D1145-D1152.	14.5	491
22	Mass Spectrometry-Compatible Subcellular Fractionation for Proteomics. <i>Journal of Proteome Research</i> , 2020, 19, 75-84.	3.7	20
23	Blood concentrations of small extracellular vesicles are determined by a balance between abundant secretion and rapid clearance. <i>Journal of Extracellular Vesicles</i> , 2020, 9, 1696517.	12.2	92
24	Phosphoproteomics and Bioinformatics Analyses Reveal Key Roles of GSK-3 and AKAP4 in Mouse Sperm Capacitation. <i>International Journal of Molecular Sciences</i> , 2020, 21, 7283.	4.1	4
25	Extending the Separation Space with Trapped Ion Mobility Spectrometry Improves the Accuracy of Isobaric Tag-Based Quantitation in Proteomic LC/MS/MS. <i>Analytical Chemistry</i> , 2020, 92, 8037-8040.	6.5	36
26	EDEM2 stably disulfide-bonded to TXNDC11 catalyzes the first mannose trimming step in mammalian glycoprotein ERAD. <i>ELife</i> , 2020, 9, .	6.0	31
27	Antipsychotic olanzapine-induced misfolding of proinsulin in the endoplasmic reticulum accounts for atypical development of diabetes. <i>ELife</i> , 2020, 9, .	6.0	14
28	Large-scale Discovery of Substrates of the Human Kinome. <i>Scientific Reports</i> , 2019, 9, 10503.	3.3	79
29	Algal Protein Kinase, Triacylglycerol Accumulation Regulator 1, Modulates Cell Viability and Gametogenesis in Carbon/Nitrogen-Imbalanced Conditions. <i>Plant and Cell Physiology</i> , 2019, 60, 916-930.	3.1	15
30	Removal of Interference MS/MS Spectra for Accurate Quantification in Isobaric Tag-Based Proteomics. <i>Journal of Proteome Research</i> , 2019, 18, 2535-2544.	3.7	15
31	Comparative proteomics of <i>Helicobacter pylori</i> strains reveals geographical features rather than genomic variations. <i>Genes To Cells</i> , 2019, 24, 139-150.	1.2	6
32	The jPOST environment: an integrated proteomics data repository and database. <i>Nucleic Acids Research</i> , 2019, 47, D1218-D1224.	14.5	94
33	Phosphoproteomic profiling reveals ABA-responsive phosphosignaling pathways in <i>Physcomitrella patens</i> . <i>Plant Journal</i> , 2018, 94, 699-708.	5.7	48
34	Peptide Retention in Hydrophilic Strong Anion Exchange Chromatography Is Driven by Charged and Aromatic Residues. <i>Analytical Chemistry</i> , 2018, 90, 4635-4640.	6.5	13
35	Progress in a selective method for the determination of the acetaldehyde-derived DNA adducts by using HILIC-ESI-MS/MS. <i>Talanta</i> , 2018, 177, 12-17.	5.5	19
36	"Biomolecular Mass Spectrometry". <i>Analytical Sciences</i> , 2018, 34, 989-989.	1.6	0

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37	Two <i>Ckl1</i> transcripts regulated by m6A methylation code for two antagonistic kinases in the control of the circadian clock. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 5980-5985.	7.1	79
38	Necrostatin-7 suppresses RANK-NFATc1 signaling and attenuates macrophage to osteoclast differentiation. <i>Biochemical and Biophysical Research Communications</i> , 2018, 503, 544-549.	2.1	6
39	Selective HDAC3 Inhibition Induces Apoptosis in B Cell Lymphoma through Protein Acetylation. <i>Blood</i> , 2018, 132, 1583-1583.	1.4	0
40	jPOSTrepo: an international standard data repository for proteomes. <i>Nucleic Acids Research</i> , 2017, 45, D1107-D1111.	14.5	451
41	Secretome analysis to elucidate metalloprotease-dependent ectodomain shedding of glycoproteins during neuronal differentiation. <i>Genes To Cells</i> , 2017, 22, 237-244.	1.2	9
42	Identifications of Putative PKA Substrates with Quantitative Phosphoproteomics and Primary-Sequence-Based Scoring. <i>Journal of Proteome Research</i> , 2017, 16, 1825-1830.	3.7	26
43	An Optimized Chromatographic Strategy for Multiplexing In Parallel Reaction Monitoring Mass Spectrometry: Insights from Quantitation of Activated Kinases. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 265-277.	3.8	42
44	Metabolic shift induced by systemic activation of T cells in PD-1-deficient mice perturbs brain monoamines and emotional behavior. <i>Nature Immunology</i> , 2017, 18, 1342-1352.	14.5	83
45	Phospholipid flippase ATP11C is endocytosed and downregulated following Ca ²⁺ -mediated protein kinase C activation. <i>Nature Communications</i> , 2017, 8, 1423.	12.8	44
46	Comprehensive identification of translation start sites by tetracycline-inhibited ribosome profiling. <i>DNA Research</i> , 2016, 23, 193-201.	3.4	83
47	Identification of Mitosis-Specific Phosphorylation in Mitotic Chromosome-Associated Proteins. <i>Journal of Proteome Research</i> , 2016, 15, 3331-3341.	3.7	17
48	MEKK1-dependent phosphorylation of calponin-3 tunes cell contractility. <i>Journal of Cell Science</i> , 2016, 129, 3574-3582.	2.0	12
49	A conditional proteomics approach to identify proteins involved in zinc homeostasis. <i>Nature Methods</i> , 2016, 13, 931-937.	19.0	45
50	Improved Proteome and Phosphoproteome Analysis on a Cation Exchanger by a Combined Acid and Salt Gradient. <i>Analytical Chemistry</i> , 2016, 88, 7899-7903.	6.5	67
51	Large-scale profiling of protein kinases for cellular signaling studies by mass spectrometry and other techniques. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2016, 130, 264-272.	2.8	10
52	Membrane-Spanning Sequences in Endoplasmic Reticulum Proteins Promote Phospholipid Flip-Flop. <i>Biophysical Journal</i> , 2016, 110, 2689-2697.	0.5	23
53	Uncovering Phosphorylation-Based Specificities through Functional Interaction Networks. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 236-245.	3.8	68
54	Flagellin FliC Phosphorylation Affects Type 2 Protease Secretion and Biofilm Dispersal in <i>Pseudomonas aeruginosa</i> PAO1. <i>PLoS ONE</i> , 2016, 11, e0164155.	2.5	17

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55	LATS1 and LATS2 Phosphorylate CDC26 to Modulate Assembly of the Tetratricopeptide Repeat Subcomplex of APC/C. <i>PLoS ONE</i> , 2015, 10, e0118662.	2.5	12
56	Temporal Phosphoproteome Dynamics Induced by an ATP Synthase Inhibitor Citreoviridin*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 3284-3298.	3.8	23
57	PCK1 Regulates Integrin-Dependent Spindle Orientation via Protein Kinase A Regulatory Subunit KAPO and Myosin X. <i>Molecular and Cellular Biology</i> , 2015, 35, 1197-1208.	2.3	24
58	Systematic profiling of the bacterial phosphoproteome reveals bacterium-specific features of phosphorylation. <i>Science Signaling</i> , 2015, 8, rs10.	3.6	49
59	Extended Coverage of Singly and Multiply Phosphorylated Peptides from a Single Titanium Dioxide Microcolumn. <i>Analytical Chemistry</i> , 2015, 87, 10213-10221.	6.5	33
60	Phosphoproteomics Identifies CK2 as a Negative Regulator of Beige Adipocyte Thermogenesis and Energy Expenditure. <i>Cell Metabolism</i> , 2015, 22, 997-1008.	16.2	74
61	Phosphorylation of Mitochondrial Polyubiquitin by PINK1 Promotes Parkin Mitochondrial Tethering. <i>PLoS Genetics</i> , 2014, 10, e1004861.	3.5	140
62	Pregnenolone Functions in Centriole Cohesion during Mitosis. <i>Chemistry and Biology</i> , 2014, 21, 1707-1721.	6.0	12
63	Discovery of Colorectal Cancer Biomarker Candidates by Membrane Proteomic Analysis and Subsequent Verification using Selected Reaction Monitoring (SRM) and Tissue Microarray (TMA) Analysis. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1471-1484.	3.8	65
64	Inhibition of endocytic vesicle fusion by Plk1-mediated phosphorylation of vimentin during mitosis. <i>Cell Cycle</i> , 2014, 13, 126-137.	2.6	16
65	Application of partially fluorinated carboxylic acids as ion-pairing reagents in LC/ESI-MS. <i>Talanta</i> , 2014, 127, 219-224.	5.5	14
66	Estrogen Response element-GFP (ERE-GFP) introduced MCF-7 cells demonstrated the coexistence of multiple estrogen-deprivation resistant mechanisms. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2014, 139, 61-72.	2.5	20
67	Hydrophilic Interaction Chromatography Using a Meter-Scale Monolithic Silica Capillary Column for Proteomics LC-MS. <i>Analytical Chemistry</i> , 2014, 86, 3817-3824.	6.5	54
68	Phosphoproteome Analysis of Formalin-Fixed and Paraffin-Embedded Tissue Sections Mounted on Microscope Slides. <i>Journal of Proteome Research</i> , 2014, 13, 915-924.	3.7	45
69	p38-Mediated phosphorylation of Eps15 endocytic adaptor protein. <i>FEBS Letters</i> , 2014, 588, 131-137.	2.8	14
70	Large-Scale Identification of Phosphorylation Sites for Profiling Protein Kinase Selectivity. <i>Journal of Proteome Research</i> , 2014, 13, 3410-3419.	3.7	52
71	Facile and Effective Pretreatment Using Stop and Go Extraction Tips for LC-MS/MS Analysis of Trace Amounts of DNA Adducts. <i>Analytical Sciences</i> , 2014, 30, 519-522.	1.6	8
72	Rapid and Deep Profiling of Human Induced Pluripotent Stem Cell Proteome by One-shot NanoLC-MS/MS Analysis with Meter-scale Monolithic Silica Columns. <i>Journal of Proteome Research</i> , 2013, 12, 214-221.	3.7	55

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73	In-depth Membrane Proteomic Study of Breast Cancer Tissues for the Generation of a Chromosome-based Protein List. <i>Journal of Proteome Research</i> , 2013, 12, 208-213.	3.7	20
74	Control of phospholipid flip-flop by transmembrane peptides. <i>Chemical Physics</i> , 2013, 419, 78-83.	1.9	26
75	Effects of Lipid Membrane Curvature on Lipid Packing State Evaluated by Isothermal Titration Calorimetry. <i>Langmuir</i> , 2013, 29, 857-860.	3.5	13
76	Integrated View of the Human Chromosome X-centric Proteome Project. <i>Journal of Proteome Research</i> , 2013, 12, 58-61.	3.7	4
77	Global microRNA elevation by inducible Exportin 5 regulates cell cycle entry. <i>Rna</i> , 2013, 19, 490-497.	3.5	56
78	Atg38 is required for autophagy-specific phosphatidylinositol 3-kinase complex integrity. <i>Journal of Cell Biology</i> , 2013, 203, 299-313.	5.2	97
79	Genetics and Phosphoproteomics Reveal a Protein Phosphorylation Network in the Abscisic Acid Signaling Pathway in <i>Arabidopsis thaliana</i> . <i>Science Signaling</i> , 2013, 6, rs8.	3.6	355
80	Temporal Profiling of Lapatinib-suppressed Phosphorylation Signals in EGFR/HER2 Pathways. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1741-1757.	3.8	55
81	Characterization of kinase inhibitors using different phosphorylation states of colony stimulating factor-1 receptor tyrosine kinase. <i>Journal of Biochemistry</i> , 2012, 151, 47-55.	1.7	17
82	A Putative Polypeptide N-Acetylgalactosaminyltransferase/Williams-Beuren Syndrome Chromosome Region 17 (WBSCR17) Regulates Lamellipodium Formation and Macropinocytosis. <i>Journal of Biological Chemistry</i> , 2012, 287, 32222-32235.	3.4	20
83	Shotguns in the Front Line: Phosphoproteomics in Plants. <i>Plant and Cell Physiology</i> , 2012, 53, 118-124.	3.1	55
84	Analytical strategies for shotgun phosphoproteomics: Status and prospects. <i>Seminars in Cell and Developmental Biology</i> , 2012, 23, 836-842.	5.0	20
85	Transcriptional Regulation by Pol II(G) Involving Mediator and Competitive Interactions of Gdown1 and TFIIF with Pol II. <i>Molecular Cell</i> , 2012, 45, 51-63.	9.7	68
86	Ectopic expression of Hmgn2 antagonizes mouse erythroid differentiation in vitro. <i>Cell Biology International</i> , 2012, 36, 195-202.	3.0	2
87	Phosphoproteomic Analysis of <i>Rhodospseudomonas palustris</i> Reveals the Role of Pyruvate Phosphate Dikinase Phosphorylation in Lipid Production. <i>Journal of Proteome Research</i> , 2012, 11, 5362-5375.	3.7	37
88	The Rice Proteogenomics Database OryzaPG-DB: Development, Expansion, and New Features. <i>Frontiers in Plant Science</i> , 2012, 3, 65.	3.6	17
89	Close proximity of phosphorylation sites to ligand in the phosphoproteome of the extreme thermophile <i>Thermoplasma volcanophilum</i> . <i>Proteomics</i> , 2012, 12, 1414-1430.	2.2	23
90	LATS1/WARTS phosphorylates MYPT1 to counteract PLK1 and regulate mammalian mitotic progression. <i>Journal of Cell Biology</i> , 2012, 197, 625-641.	5.2	51

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91	Human proteome analysis by using reversed phase monolithic silica capillary columns with enhanced sensitivity. <i>Journal of Chromatography A</i> , 2012, 1228, 292-297.	3.7	60
92	Estimation and optimization of the peak capacity of one-dimensional gradient high performance liquid chromatography using a long monolithic silica capillary column. <i>Journal of Chromatography A</i> , 2012, 1228, 283-291.	3.7	47
93	Short-chain fatty acid receptor GPR41-mediated activation of sympathetic neurons involves synapsin 2b phosphorylation. <i>FEBS Letters</i> , 2012, 586, 1547-1554.	2.8	83
94	Mass spectrum sequential subtraction speeds up searching large peptide <sc>MS</sc>/<sc>MS</sc> spectra datasets against large nucleotide databases for proteogenomics. <i>Genes To Cells</i> , 2012, 17, 633-644.	1.2	26
95	Microscale Phosphoproteome Analysis of 10 ⁶ Cells from Human Cancer Cell Lines. <i>Analytical Chemistry</i> , 2011, 83, 7698-7703.	6.5	68
96	Functional Preconcentration Tip of Total Volume Injection for ESI/MS Analysis of DNA Adducts. <i>Analytical Sciences</i> , 2011, 27, 217.	1.6	10
97	Use of stable isotope labeling by amino acids in cell culture as a spike-in standard in quantitative proteomics. <i>Nature Protocols</i> , 2011, 6, 147-157.	12.0	265
98	Integrative Features of the Yeast Phosphoproteome and Protein-Protein Interaction Map. <i>PLoS Computational Biology</i> , 2011, 7, e1001064.	3.2	60
99	Detection of Rap1A as a yessotoxin binding protein from blood cell membranes. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2010, 20, 6443-6446.	2.2	11
100	Chemical dephosphorylation for identification of multiply phosphorylated peptides and phosphorylation site determination. <i>Rapid Communications in Mass Spectrometry</i> , 2010, 24, 2277-2282.	1.5	14
101	A systematic survey of in vivo obligate chaperonin-dependent substrates. <i>EMBO Journal</i> , 2010, 29, 1552-1564.	7.8	156
102	One-Dimensional Capillary Liquid Chromatographic Separation Coupled with Tandem Mass Spectrometry Unveils the <i>Escherichia coli</i> Proteome on a Microarray Scale. <i>Analytical Chemistry</i> , 2010, 82, 2616-2620.	6.5	131
103	Large-Scale Comparative Phosphoproteomics Identifies Conserved Phosphorylation Sites in Plants. <i>Plant Physiology</i> , 2010, 153, 1161-1174.	4.8	361
104	Quantitative proteome and phosphoproteome analyses of cultured cells based on SILAC labeling without requirement of serum dialysis. <i>Molecular BioSystems</i> , 2010, 6, 594.	2.9	27
105	In Silico Analysis of Phosphoproteome Data Suggests a Rich-get-richer Process of Phosphosite Accumulation over Evolution. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 1061-1071.	3.8	31
106	Identification of DNA-dependent Protein Kinase as a Cofactor for the Forkhead Transcription Factor FoxA2. <i>Journal of Biological Chemistry</i> , 2009, 284, 19915-19926.	3.4	8
107	Unbiased Quantitation of <i>Escherichia coli</i> Membrane Proteome Using Phase Transfer Surfactants. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 2770-2777.	3.8	136
108	Ser/Thr/Tyr phosphoproteome analysis of pathogenic and non-pathogenic <i>Pseudomonas</i> species. <i>Proteomics</i> , 2009, 9, 2764-2775.	2.2	107

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109	Chemical Cleavage-Assisted Tryptic Digestion for Membrane Proteome Analysis. <i>Journal of Proteome Research</i> , 2009, 8, 3169-3175.	3.7	29
110	Type 2C protein phosphatases directly regulate abscisic acid-activated protein kinases in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 17588-17593.	7.1	980
111	Informatics for peptide retention properties in proteomic LC-MS. <i>Proteomics</i> , 2008, 8, 787-798.	2.2	33
112	On-line selective enrichment and ion-pair reaction for structural determination of sulfated glycopeptides by capillary electrophoresis-mass spectrometry. <i>Journal of Chromatography A</i> , 2008, 1194, 237-242.	3.7	18
113	Successive and Selective Release of Phosphorylated Peptides Captured by Hydroxy Acid-Modified Metal Oxide Chromatography. <i>Journal of Proteome Research</i> , 2008, 7, 4585-4593.	3.7	110
114	Phase Transfer Surfactant-Aided Trypsin Digestion for Membrane Proteome Analysis. <i>Journal of Proteome Research</i> , 2008, 7, 731-740.	3.7	536
115	High-Efficiency Liquid Chromatographic Separation Utilizing Long Monolithic Silica Capillary Columns. <i>Analytical Chemistry</i> , 2008, 80, 8741-8750.	6.5	132
116	Large-scale phosphorylation mapping reveals the extent of tyrosine phosphorylation in <i>Arabidopsis</i> . <i>Molecular Systems Biology</i> , 2008, 4, 193.	7.2	347
117	Automated Phosphoproteome Analysis for Cultured Cancer Cells by Two-Dimensional NanoLC-MS Using a Calcined Titania/C18 Biphasic Column. <i>Analytical Sciences</i> , 2008, 24, 161-166.	1.6	114
118	Development of Solid Phase Extraction Mini-Columns for Proteome Analysis. <i>Bunseki Kagaku</i> , 2008, 57, 1011-1018.	0.2	1
119	LGI1 and LGI4 bind to ADAM22, ADAM23 and ADAM11. <i>International Journal of Biological Sciences</i> , 2008, 4, 387-396.	6.4	101
120	Polymer Entrapment in Polymerized Silicate for Preparing Highly Stable Capillary Coatings for CE and CE-MS. <i>Analytical Chemistry</i> , 2007, 79, 7838-7844.	6.5	24
121	Enhancement of the Efficiency of Phosphoproteomic Identification by Removing Phosphates after Phosphopeptide Enrichment. <i>Journal of Proteome Research</i> , 2007, 6, 1139-1144.	3.7	70
122	Phosphopeptide Enrichment by Aliphatic Hydroxy Acid-modified Metal Oxide Chromatography for Nano-LC-MS/MS in Proteomics Applications. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 1103-1109.	3.8	397
123	Simple on-line sample preconcentration technique for peptides based on dynamic pH junction in capillary electrophoresis-mass spectrometry. <i>Journal of Chromatography A</i> , 2007, 1148, 250-255.	3.7	59
124	Splicing factor SF3b as a target of the antitumor natural product pladienolide. <i>Nature Chemical Biology</i> , 2007, 3, 570-575.	8.0	554
125	Protocol for micro-purification, enrichment, pre-fractionation and storage of peptides for proteomics using StageTips. <i>Nature Protocols</i> , 2007, 2, 1896-1906.	12.0	3,693
126	Modular Stop and Go Extraction Tips with Stacked Disks for Parallel and Multidimensional Peptide Fractionation in Proteomics. <i>Journal of Proteome Research</i> , 2006, 5, 988-994.	3.7	294

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127	Multiplexed Two-Dimensional Liquid Chromatography for MALDI and Nanoelectrospray Ionization Mass Spectrometry in Proteomics. <i>Journal of Proteome Research</i> , 2006, 5, 1803-1807.	3.7	34
128	Simplified gradient generator for micro- and nano-liquid chromatography. <i>Journal of Chromatography A</i> , 2006, 1123, 47-52.	3.7	14
129	A Protein Associated with Toll-Like Receptor 4 (PRAT4A) Regulates Cell Surface Expression of TLR4. <i>Journal of Immunology</i> , 2006, 177, 1772-1779.	0.8	101
130	Proteomic LC-MS systems using nanoscale liquid chromatography with tandem mass spectrometry. <i>Journal of Chromatography A</i> , 2005, 1067, 73-83.	3.7	156
131	Quantitative mouse brain proteomics using culture-derived isotope tags as internal standards. <i>Nature Biotechnology</i> , 2005, 23, 617-621.	17.5	216
132	Specificity of Immobilized Metal Affinity-Based IMAC/C18 Tip Enrichment of Phosphopeptides for Protein Phosphorylation Analysis. <i>Analytical Chemistry</i> , 2005, 77, 5144-5154.	6.5	195
133	Exponentially Modified Protein Abundance Index (emPAI) for Estimation of Absolute Protein Amount in Proteomics by the Number of Sequenced Peptides per Protein. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 1265-1272.	3.8	1,817
134	Proteome-wide Analysis of Chaperonin-Dependent Protein Folding in <i>Escherichia coli</i> . <i>Cell</i> , 2005, 122, 209-220.	28.9	590
135	Efficient in-gel digestion procedure using 5-cyclohexyl-1-pentyl- α -D-maltoside as an additive for gel-based membrane proteomics. <i>Rapid Communications in Mass Spectrometry</i> , 2004, 18, 2388-2394.	1.5	60
136	Stop and Go Extraction Tips for Matrix-Assisted Laser Desorption/Ionization, Nanoelectrospray, and LC/MS Sample Pretreatment in Proteomics. <i>Analytical Chemistry</i> , 2003, 75, 663-670.	6.5	2,337
137	Drug-plasma protein binding assay by electrokinetic chromatography-frontal analysis. <i>Electrophoresis</i> , 2002, 23, 951-955.	2.4	29
138	A Rapid Method for pKa Determination of Drugs Using Pressure-Assisted Capillary Electrophoresis with Photodiode Array Detection in Drug Discovery. <i>Journal of Pharmaceutical Sciences</i> , 2002, 91, 933-942.	3.3	105
139	Highly robust stainless steel tips as microelectrospray emitters. <i>Rapid Communications in Mass Spectrometry</i> , 2002, 16, 913-918.	1.5	34
140	Analysis of the <i>Plasmodium falciparum</i> proteome by high-accuracy mass spectrometry. <i>Nature</i> , 2002, 419, 537-542.	27.8	596
141	Microcolumns with self-assembled particle frits for proteomics. <i>Journal of Chromatography A</i> , 2002, 979, 233-239.	3.7	327
142	Methylcellulose-immobilized Reversed-phase Precolumn for Direct Analysis of Drugs in Plasma by HPLC. <i>Analytical Sciences</i> , 2001, 17, 1155-1159.	1.6	42
143	Development of an N-shaped cell for two-phase partitioning. <i>Bunseki Kagaku</i> , 2000, 49, 313-317.	0.2	1
144	Electrophoretic mobility-assisted identification of proteins by nanoelectrospray capillary electrophoresis/mass spectrometry under methanolic conditions. <i>Rapid Communications in Mass Spectrometry</i> , 2000, 14, 1167-1178.	1.5	10

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145	Surfactants Usable for Electrospray Ionization Mass Spectrometry. <i>Analytical Biochemistry</i> , 2000, 287, 45-54.	2.4	79
146	Enantiomeric separation by capillary electrophoresis with an electroosmotic flow-controlled capillary. <i>Journal of Chromatography A</i> , 2000, 875, 315-322.	3.7	18
147	A novel method for peptide block synthesis using unprotected peptides. <i>Tetrahedron Letters</i> , 1999, 40, 3415-3418.	1.4	7
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