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List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/12107625/publications.pdf

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30	1,398	19	29
papers	citations	h-index	g-index
31	31	31	2619
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	Robust, reproducible and quantitative analysis of thousands of proteomes by micro-flow LC–MS/MS. Nature Communications, 2020, 11, 157.	12.8	218
2	An enzyme assisted RP-RPLC approach for in-depth analysis of human liver phosphoproteome. Journal of Proteomics, 2014, 96, 253-262.	2.4	209
3	Ultra-deep tyrosine phosphoproteomics enabled by a phosphotyrosine superbinder. Nature Chemical Biology, 2016, 12, 959-966.	8.0	141
4	A large-scale protein phosphorylation analysis reveals novel phosphorylation motifs and phosphoregulatory networks in Arabidopsis. Journal of Proteomics, 2013, 78, 486-498.	2.4	103
5	Global Screening of CK2 Kinase Substrates by an Integrated Phosphoproteomics Workflow. Scientific Reports, 2013, 3, 3460.	3.3	89
6	A Comprehensive Differential Proteomic Study of Nitrate Deprivation in <i>Arabidopsis</i> Reveals Complex Regulatory Networks of Plant Nitrogen Responses. Journal of Proteome Research, 2012, 11, 2301-2315.	3.7	71
7	S100A4+ Macrophages Are Necessary for Pulmonary Fibrosis by Activating Lung Fibroblasts. Frontiers in Immunology, 2018, 9, 1776.	4.8	65
8	S100A4 enhances protumor macrophage polarization by control of PPAR- \hat{l}^3 -dependent induction of fatty acid oxidation., 2021, 9, e002548.		62
9	Improve the Coverage for the Analysis of Phosphoproteome of HeLa Cells by a Tandem Digestion Approach. Journal of Proteome Research, 2012, 11, 2828-2837.	3.7	47
10	Salinity-Induced Palmella Formation Mechanism in Halotolerant Algae Dunaliella salina Revealed by Quantitative Proteomics and Phosphoproteomics. Frontiers in Plant Science, 2017, 8, 810.	3.6	41
11	Robust Microflow LC-MS/MS for Proteome Analysis: 38†000 Runs and Counting. Analytical Chemistry, 2021, 93, 3686-3690.	6.5	36
12	MiR-143 inhibits endometrial cancer cell proliferation and metastasis by targeting <i>MAPK1</i> Oncotarget, 2017, 8, 84384-84395.	1.8	32
13	HIFâ€1α is necessary for activation and tumourâ€promotion effect of cancerâ€associated fibroblasts in lung cancer. Journal of Cellular and Molecular Medicine, 2021, 25, 5457-5469.	3.6	30
14	Sensitive, Robust, and Cost-Effective Approach for Tyrosine Phosphoproteome Analysis. Analytical Chemistry, 2017, 89, 9307-9314.	6.5	27
15	Determination of CK2 Specificity and Substrates by Proteome-Derived Peptide Libraries. Journal of Proteome Research, 2013, 12, 3813-3821.	3.7	26
16	Large-Scale Quantification of Single Amino-Acid Variations by a Variation-Associated Database Search Strategy. Journal of Proteome Research, 2014, 13, 241-248.	3.7	26
17	Recurrent GNAQ mutation encoding T96S in natural killer/T cell lymphoma. Nature Communications, 2019, 10, 4209.	12.8	25
18	Identification of 7 000–9 000 Proteins from Cell Lines and Tissues by Single-Shot Microflow LC–MS/MS. Analytical Chemistry, 2021, 93, 8687-8692.	6.5	25

#	Article	IF	CITATION
19	Depletion of Acidic Phosphopeptides by SAX To Improve the Coverage for the Detection of Basophilic Kinase Substrates. Journal of Proteome Research, 2012, 11, 4673-4681.	3.7	23
20	Integration of Cell Lysis, Protein Extraction, and Digestion into One Step for Ultrafast Sample Preparation for Phosphoproteome Analysis. Analytical Chemistry, 2014, 86, 6786-6791.	6.5	20
21	SH2 Superbinder Modified Monolithic Capillary Column for the Sensitive Analysis of Protein Tyrosine Phosphorylation. Journal of Proteome Research, 2018, 17, 243-251.	3.7	13
22	<i>In Situ</i> Sample Processing Approach (iSPA) for Comprehensive Quantitative Phosphoproteome Analysis. Journal of Proteome Research, 2014, 13, 3896-3904.	3.7	12
23	Identification of phosphopeptides with unknown cleavage specificity by a de novo sequencing assisted database search strategy. Proteomics, 2014, 14, 2410-2416.	2.2	12
24	Selective Enrichment of Cysteine-Containing Phosphopeptides for Subphosphoproteome Analysis. Journal of Proteome Research, 2015, 14, 5341-5347.	3.7	12
25	Low SCRIB expression in fibroblasts promotes invasion of lung cancer cells. Life Sciences, 2020, 256, 117955.	4.3	10
26	A bead-based cleavage method for large-scale identification of protease substrates. Scientific Reports, 2016, 6, 22645.	3.3	9
27	High specific phosphopeptides enrichment by titanium silicalite with post-treatment of desilication. Analytical Methods, 2013, 5, 2939.	2.7	5
28	Identifying tumor promoting genomic alterations in tumor-associated fibroblasts via retrovirus-insertional mutagenesis. Oncotarget, 2017, 8, 97231-97245.	1.8	4
29	The proteomic analysis improved by cleavage kinetics-based fractionation of tryptic peptides. Proteomics, 2015, 15, 3613-3616.	2.2	3
30	Ampholine immobilized polymer microspheres for increasing coverage of human urinary proteome. Talanta, 2020, 215, 120931.	5.5	2