

An Staes

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1805350/publications.pdf>

Version: 2024-02-01

59
papers

4,283
citations

136885

32
h-index

143943

57
g-index

66
all docs

66
docs citations

66
times ranked

6015
citing authors

#	ARTICLE	IF	CITATIONS
1	Exploring proteomes and analyzing protein processing by mass spectrometric identification of sorted N-terminal peptides. <i>Nature Biotechnology</i> , 2003, 21, 566-569.	9.4	573
2	Chromatographic Isolation of Methionine-containing Peptides for Gel-free Proteome Analysis. <i>Molecular and Cellular Proteomics</i> , 2002, 1, 896-903.	2.5	219
3	Caspase-specific and nonspecific in vivo protein processing during Fas-induced apoptosis. <i>Nature Methods</i> , 2005, 2, 771-777.	9.0	208
4	Damage on plants activates Ca ²⁺ -dependent metacaspases for release of immunomodulatory peptides. <i>Science</i> , 2019, 363, .	6.0	170
5	Selecting protein N-terminal peptides by combined fractional diagonal chromatography. <i>Nature Protocols</i> , 2011, 6, 1130-1141.	5.5	164
6	Impairment of Angiogenesis by Fatty Acid Synthase Inhibition Involves mTOR Malonylation. <i>Cell Metabolism</i> , 2018, 28, 866-880.e15.	7.2	154
7	Identification and Functional Characterization of N-Terminally Acetylated Proteins in <i>Drosophila melanogaster</i> . <i>PLoS Biology</i> , 2009, 7, e1000236.	2.6	149
8	Improved recovery of proteome-informative, protein N-terminal peptides by combined fractional diagonal chromatography (COFRADIC). <i>Proteomics</i> , 2008, 8, 1362-1370.	1.3	144
9	Citrullinated Glucose-Regulated Protein 78 Is an Autoantigen in Type 1 Diabetes. <i>Diabetes</i> , 2015, 64, 573-586.	0.3	136
10	The human platelet proteome mapped by peptide-centric proteomics: A functional protein profile. <i>Proteomics</i> , 2005, 5, 3193-3204.	1.3	126
11	Global Differential Non-Gel Proteomics by Quantitative and Stable Labeling of Tryptic Peptides with Oxygen-18. <i>Journal of Proteome Research</i> , 2004, 3, 786-791.	1.8	125
12	Analysis of the β -secretase interactome and validation of its association with tetraspanin-enriched microdomains. <i>Nature Cell Biology</i> , 2009, 11, 1340-1346.	4.6	121
13	Matrix metalloproteinase 13 modulates intestinal epithelial barrier integrity in inflammatory diseases by activating TNF. <i>EMBO Molecular Medicine</i> , 2013, 5, 1000-1016.	3.3	114
14	Large-Scale Identification of N-Terminal Peptides in the Halophilic Archaea <i>Halobacterium salinarum</i> and <i>Natronomonas pharaonis</i> . <i>Journal of Proteome Research</i> , 2007, 6, 2195-2204.	1.8	109
15	The <i>Arabidopsis</i> METACASPASE9 Degradome. <i>Plant Cell</i> , 2013, 25, 2831-2847.	3.1	109
16	Complementary positional proteomics for screening substrates of endo- and exoproteases. <i>Nature Methods</i> , 2010, 7, 512-515.	9.0	106
17	Reversible labeling of cysteine-containing peptides allows their specific chromatographic isolation for non-gel proteome studies. <i>Proteomics</i> , 2004, 4, 897-908.	1.3	93
18	Cells Lacking β -Actin are Genetically Reprogrammed and Maintain Conditional Migratory Capacity*. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 255-271.	2.5	93

#	ARTICLE	IF	CITATIONS
19	cIAP1/2 Are Direct E3 Ligases Conjugating Diverse Types of Ubiquitin Chains to Receptor Interacting Proteins Kinases 1 to 4 (RIP1â€“4). PLoS ONE, 2011, 6, e22356.	1.1	91
20	Disruption of endocytosis through chemical inhibition of clathrin heavy chain function. Nature Chemical Biology, 2019, 15, 641-649.	3.9	86
21	<scp>GRIM REAPER</scp> peptide binds to receptor kinase <scp>PRK</scp> 5 to trigger cell death in <i>Arabidopsis</i>. EMBO Journal, 2015, 34, 55-66.	3.5	83
22	Quality control in mass spectrometryâ€“based proteomics. Mass Spectrometry Reviews, 2018, 37, 697-711.	2.8	82
23	CEP5 and XIP1/CEPR1 regulate lateral root initiation in Arabidopsis. Journal of Experimental Botany, 2016, 67, 4889-4899.	2.4	81
24	ms_lim, a simple yet powerful open source laboratory information management system for MSâ€“driven proteomics. Proteomics, 2010, 10, 1261-1264.	1.3	73
25	Global phosphoproteome analysis on human HepG2 hepatocytes using reversed-phase diagonal LC. Proteomics, 2005, 5, 3589-3599.	1.3	65
26	De novo design of a biologically active amyloid. Science, 2016, 354, .	6.0	63
27	A review of COFRADIC techniques targeting protein N-terminal acetylation. BMC Proceedings, 2009, 3, S6.	1.8	56
28	moFF: a robust and automated approach to extract peptide ion intensities. Nature Methods, 2016, 13, 964-966.	9.0	56
29	Chromatographic retention time prediction for posttranslationally modified peptides. Proteomics, 2012, 12, 1151-1159.	1.3	49
30	Protein aggregation as an antibiotic design strategy. Molecular Microbiology, 2016, 99, 849-865.	1.2	44
31	qcML: An Exchange Format for Quality Control Metrics from Mass Spectrometry Experiments. Molecular and Cellular Proteomics, 2014, 13, 1905-1913.	2.5	42
32	Improved tandem mass spectrometric characterization of 3-nitrotyrosine sites in peptides. Rapid Communications in Mass Spectrometry, 2006, 20, 2885-2893.	0.7	41
33	A catalogue of putative HIV-1 protease host cell substrates. Biological Chemistry, 2012, 393, 915-931.	1.2	32
34	A New Functional, Chemical Proteomics Technology To Identify Purine Nucleotide Binding Sites in Complex Proteomes. Journal of Proteome Research, 2006, 5, 3438-3445.	1.8	31
35	Four Stage Liquid Chromatographic Selection of Methionyl Peptides for Peptide-Centric Proteome Analysis: A The Proteome of Human Multipotent Adult Progenitor Cells. Journal of Proteome Research, 2006, 5, 1415-1428.	1.8	29
36	The Response of the Root Proteome to the Synthetic Strigolactone GR24 in Arabidopsis. Molecular and Cellular Proteomics, 2016, 15, 2744-2755.	2.5	28

#	ARTICLE	IF	CITATIONS
37	SCX charge state selective separation of tryptic peptides combined with 2D-RP-HPLC allows for detailed proteome mapping. <i>Journal of Proteomics</i> , 2013, 91, 164-171.	1.2	27
38	Salmonella Typhi, Paratyphi A, Enteritidis and Typhimurium core proteomes reveal differentially expressed proteins linked to the cell surface and pathogenicity. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007416.	1.3	27
39	Simple Peptide Quantification Approach for MS-Based Proteomics Quality Control. <i>ACS Omega</i> , 2020, 5, 6754-6762.	1.6	26
40	Assessing a novel microfluidic interface for shotgun proteome analyses. <i>Journal of Separation Science</i> , 2007, 30, 1468-1476.	1.3	25
41	A New Approach for Mapping Sialylated N-Glycosites in Serum Proteomes. <i>Journal of Proteome Research</i> , 2007, 6, 4304-4312.	1.8	21
42	Combining quantitative proteomics data processing workflows for greater sensitivity. <i>Nature Methods</i> , 2011, 8, 481-483.	9.0	18
43	The Arabidopsis Iron-Sulfur Protein GRXS17 is a Target of the Ubiquitin E3 Ligases RGLC3 and RGLC4. <i>Plant and Cell Physiology</i> , 2016, 57, 1801-1813.	1.5	16
44	Study of Protein Expression in Peri-Infarct Tissue after Cerebral Ischemia. <i>Scientific Reports</i> , 2015, 5, 12030.	1.6	15
45	An extra dimension in protein tagging by quantifying universal proteotypic peptides using targeted proteomics. <i>Scientific Reports</i> , 2016, 6, 27220.	1.6	15
46	Use of Hybrid Data-Dependent and -Independent Acquisition Spectral Libraries Empowers Dual-Proteome Profiling. <i>Journal of Proteome Research</i> , 2021, 20, 1165-1177.	1.8	15
47	Multiple isoforms of the tumor suppressor myopodin are simultaneously transcribed in cancer cells. <i>Biochemical and Biophysical Research Communications</i> , 2008, 370, 269-273.	1.0	13
48	The Tandem PDZ Protein Syntenin Interacts with the Aminoacyl tRNA Synthetase Complex in a Lysyl-tRNA Synthetase-Dependent Manner. <i>Journal of Proteome Research</i> , 2008, 7, 4962-4973.	1.8	13
49	Asn ³ , a Reliable, Robust, and Universal Lock Mass for Improved Accuracy in LC-MS and LC-MS/MS. <i>Analytical Chemistry</i> , 2013, 85, 11054-11060.	3.2	13
50	Update on the moFF Algorithm for Label-Free Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2019, 18, 728-731.	1.8	13
51	Proteomic and metabolomic responses to connexin43 silencing in primary hepatocyte cultures. <i>Archives of Toxicology</i> , 2013, 87, 883-894.	1.9	12
52	Expanding the Interactome of TES by Exploiting TES Modules with Different Subcellular Localizations. <i>Journal of Proteome Research</i> , 2017, 16, 2054-2071.	1.8	12
53	Protease Substrate Profiling by N-Terminal COFRADIC. <i>Methods in Molecular Biology</i> , 2017, 1574, 51-76.	0.4	11
54	Limited Evidence for Protein Products of Noncoding Transcripts in the HEK293T Cellular Cytosol. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100264.	2.5	11

#	ARTICLE	IF	CITATIONS
55	Evolutionarily conserved and species-specific glycoproteins in the N-glycoproteomes of diverse insect species. <i>Insect Biochemistry and Molecular Biology</i> , 2018, 100, 22-29.	1.2	10
56	N-glycosylation Site Analysis Reveals Sex-related Differences in Protein N-glycosylation in the Rice Brown Planthopper (<i>Nilaparvata lugens</i>). <i>Molecular and Cellular Proteomics</i> , 2020, 19, 529-539.	2.5	10
57	Open-Source, Platform-Independent Library and Online Scripting Environment for Accessing Thermo Scientific RAW Files. <i>Journal of Proteome Research</i> , 2015, 14, 4940-4943.	1.8	3
58	Using moFF to Extract Peptide Ion Intensities from LC-MS experiments. <i>Protocol Exchange</i> , 0, , .	0.3	2
59	A Strong Cation Exchange Chromatography Protocol for Examining N-Terminal Proteoforms. <i>Methods in Molecular Biology</i> , 2022, 2477, 293-309.	0.4	0