

# An Staes

## List of Publications by Year in descending order

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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	A Strong Cation Exchange Chromatography Protocol for Examining N-Terminal Proteoforms. <i>Methods in Molecular Biology</i> , 2022, 2477, 293-309.	0.4	0
2	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
3	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
4	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
5	Simple Peptide Quantification Approach for MS-Based Proteomics Quality Control. <i>ACS Omega</i> , 2020, 5, 6754-6762.	1.6	26
6	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
7	Disruption of endocytosis through chemical inhibition of clathrin heavy chain function. <i>Nature Chemical Biology</i> , 2019, 15, 641-649.	3.9	86
8	Damage on plants activates Ca <sup>2+</sup> -dependent metacaspases for release of immunomodulatory peptides. <i>Science</i> , 2019, 363, .	6.0	170
9	Update on the moFF Algorithm for Label-Free Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2019, 18, 728-731.	1.8	13
10	Quality control in mass spectrometry-based proteomics. <i>Mass Spectrometry Reviews</i> , 2018, 37, 697-711.	2.8	82
11	Impairment of Angiogenesis by Fatty Acid Synthase Inhibition Involves mTOR Malonylation. <i>Cell Metabolism</i> , 2018, 28, 866-880.e15.	7.2	154
12	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
13	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
14	Protease Substrate Profiling by N-Terminal COFRADIC. <i>Methods in Molecular Biology</i> , 2017, 1574, 51-76.	0.4	11
15	Protein aggregation as an antibiotic design strategy. <i>Molecular Microbiology</i> , 2016, 99, 849-865.	1.2	44
16	moFF: a robust and automated approach to extract peptide ion intensities. <i>Nature Methods</i> , 2016, 13, 964-966.	9.0	56
17	The Arabidopsis Iron-Sulfur Protein GRXS17 is a Target of the Ubiquitin E3 Ligases RGLG3 and RGLG4. <i>Plant and Cell Physiology</i> , 2016, 57, 1801-1813.	1.5	16
18	CEP5 and XIP1/CEPR1 regulate lateral root initiation in Arabidopsis. <i>Journal of Experimental Botany</i> , 2016, 67, 4889-4899.	2.4	81

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19	The Response of the Root Proteome to the Synthetic Strigolactone GR24 in Arabidopsis. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2744-2755.	2.5	28
20	De novo design of a biologically active amyloid. <i>Science</i> , 2016, 354, .	6.0	63
21	An extra dimension in protein tagging by quantifying universal proteotypic peptides using targeted proteomics. <i>Scientific Reports</i> , 2016, 6, 27220.	1.6	15
22	Study of Protein Expression in Peri-Infarct Tissue after Cerebral Ischemia. <i>Scientific Reports</i> , 2015, 5, 12030.	1.6	15
23	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
24	<sc>GRIM REAPER</sc> peptide binds to receptor kinase <sc>PRK</sc> 5 to trigger cell death in <i>Arabidopsis</i>. <i>EMBO Journal</i> , 2015, 34, 55-66.	3.5	83
25	Citrullinated Glucose-Regulated Protein 78 Is an Autoantigen in Type 1 Diabetes. <i>Diabetes</i> , 2015, 64, 573-586.	0.3	136
26	qcML: An Exchange Format for Quality Control Metrics from Mass Spectrometry Experiments. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1905-1913.	2.5	42
27	Proteomic and metabolomic responses to connexin43 silencing in primary hepatocyte cultures. <i>Archives of Toxicology</i> , 2013, 87, 883-894.	1.9	12
28	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
29	Asn<sup>3</sup>, 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
30	The <i>Arabidopsis</i> METACASPASE9 Degradome. <i>Plant Cell</i> , 2013, 25, 2831-2847.	3.1	109
31	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
32	Cells Lacking Î²-Actin are Genetically Reprogrammed and Maintain Conditional Migratory Capacity*. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 255-271.	2.5	93
33	A catalogue of putative HIV-1 protease host cell substrates. <i>Biological Chemistry</i> , 2012, 393, 915-931.	1.2	32
34	Chromatographic retention time prediction for posttranslationally modified peptides. <i>Proteomics</i> , 2012, 12, 1151-1159.	1.3	49
35	Selecting protein N-terminal peptides by combined fractional diagonal chromatography. <i>Nature Protocols</i> , 2011, 6, 1130-1141.	5.5	164
36	Combining quantitative proteomics data processing workflows for greater sensitivity. <i>Nature Methods</i> , 2011, 8, 481-483.	9.0	18

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37	cIAP1/2 Are Direct E3 Ligases Conjugating Diverse Types of Ubiquitin Chains to Receptor Interacting Proteins Kinases 1 to 4 (RIP1-4). PLoS ONE, 2011, 6, e22356.	1.1	91
38	ms_lims, a simple yet powerful open source laboratory information management system for MS-driven proteomics. Proteomics, 2010, 10, 1261-1264.	1.3	73
39	Complementary positional proteomics for screening substrates of endo- and exoproteases. Nature Methods, 2010, 7, 512-515.	9.0	106
40	Identification and Functional Characterization of N-Terminally Acetylated Proteins in Drosophila melanogaster. PLoS Biology, 2009, 7, e1000236.	2.6	149
41	A review of COFRADIC techniques targeting protein N-terminal acetylation. BMC Proceedings, 2009, 3, S6.	1.8	56
42	Analysis of the $\beta$ -secretase interactome and validation of its association with tetraspanin-enriched microdomains. Nature Cell Biology, 2009, 11, 1340-1346.	4.6	121
43	Improved recovery of proteome-informative, protein N-terminal peptides by combined fractional diagonal chromatography (COFRADIC). Proteomics, 2008, 8, 1362-1370.	1.3	144
44	Multiple isoforms of the tumor suppressor myopodin are simultaneously transcribed in cancer cells. Biochemical and Biophysical Research Communications, 2008, 370, 269-273.	1.0	13
45	The Tandem PDZ Protein Syntenin Interacts with the Aminoacyl tRNA Synthetase Complex in a Lysyl-tRNA Synthetase-Dependent Manner. Journal of Proteome Research, 2008, 7, 4962-4973.	1.8	13
46	Large-Scale Identification of N-Terminal Peptides in the Halophilic Archaea Halobacterium salinarum and Natronomonas pharaonis. Journal of Proteome Research, 2007, 6, 2195-2204.	1.8	109
47	A New Approach for Mapping Sialylated N-Glycosites in Serum Proteomes. Journal of Proteome Research, 2007, 6, 4304-4312.	1.8	21
48	Assessing a novel microfluidic interface for shotgun proteome analyses. Journal of Separation Science, 2007, 30, 1468-1476.	1.3	25
49	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
50	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
51	Improved tandem mass spectrometric characterization of 3-nitrotyrosine sites in peptides. Rapid Communications in Mass Spectrometry, 2006, 20, 2885-2893.	0.7	41
52	Caspase-specific and nonspecific in vivo protein processing during Fas-induced apoptosis. Nature Methods, 2005, 2, 771-777.	9.0	208
53	The human platelet proteome mapped by peptide-centric proteomics: A functional protein profile. Proteomics, 2005, 5, 3193-3204.	1.3	126
54	Global phosphoproteome analysis on human HepG2 hepatocytes using reversed-phase diagonal LC. Proteomics, 2005, 5, 3589-3599.	1.3	65

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55	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
56	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
57	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
58	Chromatographic Isolation of Methionine-containing Peptides for Gel-free Proteome Analysis. <i>Molecular and Cellular Proteomics</i> , 2002, 1, 896-903.	2.5	219
59	Using moFF to Extract Peptide Ion Intensities from LC-MS experiments. <i>Protocol Exchange</i> , 0, , .	0.3	2