

## List of Publications by Year in descending order

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18  
papers

1,947  
citations

567281

15  
h-index

839539

18  
g-index

19  
all docs

19  
docs citations

19  
times ranked

3445  
citing authors

#	ARTICLE	IF	CITATIONS
1	Global Ion Suppression Limits the Potential of Mass Spectrometry Based Phosphoproteomics. <i>Journal of Proteome Research</i> , 2019, 18, 493-507.	3.7	12
2	Deuterium induces a distinctive <i>Escherichia coli</i> proteome that correlates with the reduction in growth rate. <i>Journal of Biological Chemistry</i> , 2019, 294, 2279-2292.	3.4	20
3	Quantitative proteomic and phosphoproteomic comparison of human colon cancer DLD-1 cells differing in ploidy and chromosome stability. <i>Molecular Biology of the Cell</i> , 2018, 29, 1031-1047.	2.1	41
4	Evaluation and Improvement of Quantification Accuracy in Isobaric Mass Tag-Based Protein Quantification Experiments. <i>Journal of Proteome Research</i> , 2016, 15, 2537-2547.	3.7	148
5	The quantitative and condition-dependent <i>Escherichia coli</i> proteome. <i>Nature Biotechnology</i> , 2016, 34, 104-110.	17.5	655
6	Assessment of current mass spectrometric workflows for the quantification of low abundant proteins and phosphorylation sites. <i>Data in Brief</i> , 2015, 5, 297-304.	1.0	7
7	Exploiting the multiplexing capabilities of tandem mass tags for high-throughput estimation of cellular protein abundances by mass spectrometry. <i>Methods</i> , 2015, 85, 100-107.	3.8	5
8	Comparison of Different Sample Preparation Protocols Reveals Lysis Buffer-Specific Extraction Biases in Gram-Negative Bacteria and Human Cells. <i>Journal of Proteome Research</i> , 2015, 14, 4472-4485.	3.7	62
9	Quantitative isoform-profiling of highly diversified recognition molecules. <i>ELife</i> , 2015, 4, e07794.	6.0	48
10	Evaluation of Data-Dependent and -Independent Mass Spectrometric Workflows for Sensitive Quantification of Proteins and Phosphorylation Sites. <i>Journal of Proteome Research</i> , 2014, 13, 5973-5988.	3.7	44
11	Targeted Combinatorial Alternative Splicing Generates Brain Region-Specific Repertoires of Neurexins. <i>Neuron</i> , 2014, 84, 386-398.	8.1	165
12	Systems-Level Overview of Host Protein Phosphorylation During <i>Shigella flexneri</i> Infection Revealed by Phosphoproteomics. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2952-2968.	3.8	50
13	Critical assessment of proteome-wide label-free absolute abundance estimation strategies. <i>Proteomics</i> , 2013, 13, 2567-2578.	2.2	190
14	Large-Scale Quantitative Assessment of Different In-Solution Protein Digestion Protocols Reveals Superior Cleavage Efficiency of Tandem Lys-C/Trypsin Proteolysis over Trypsin Digestion. <i>Journal of Proteome Research</i> , 2012, 11, 5145-5156.	3.7	298
15	QuickMod: A Tool for Open Modification Spectrum Library Searches. <i>Journal of Proteome Research</i> , 2011, 10, 2913-2921.	3.7	58
16	An improved method for the construction of decoy peptide MS/MS spectra suitable for the accurate estimation of false discovery rates. <i>Proteomics</i> , 2011, 11, 4085-4095.	2.2	25
17	Unrestricted identification of modified proteins using MS/MS. <i>Proteomics</i> , 2010, 10, 671-686.	2.2	86
18	A simple workflow to increase MS2 identification rate by subsequent spectral library search. <i>Proteomics</i> , 2009, 9, 1731-1736.	2.2	32