

Pedro Navarro

List of Publications by Year in descending order

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Version: 2024-02-01

23
papers

5,851
citations

361413

20
h-index

642732

23
g-index

26
all docs

26
docs citations

26
times ranked

7741
citing authors

#	ARTICLE	IF	CITATIONS
1	Standardization and harmonization of distributed multi-center proteotype analysis supporting precision medicine studies. <i>Nature Communications</i> , 2020, 11, 5248.	12.8	49
2	A multicenter study benchmarks software tools for label-free proteome quantification. <i>Nature Biotechnology</i> , 2016, 34, 1130-1136.	17.5	321
3	TRIC: an automated alignment strategy for reproducible protein quantification in targeted proteomics. <i>Nature Methods</i> , 2016, 13, 777-783.	19.0	173
4	Label-free quantification in ion mobility-enhanced data-independent acquisition proteomics. <i>Nature Protocols</i> , 2016, 11, 795-812.	12.0	258
5	In-depth evaluation of software tools for data-independent acquisition based label-free quantification. <i>Proteomics</i> , 2015, 15, 3140-3151.	2.2	66
6	Building high-quality assay libraries for targeted analysis of SWATH MS data. <i>Nature Protocols</i> , 2015, 10, 426-441.	12.0	319
7	Reproducible and Consistent Quantification of the <i>Saccharomyces cerevisiae</i> Proteome by SWATH-mass spectrometry*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 739-749.	3.8	158
8	An open-source computational and data resource to analyze digital maps of immunopeptidomes. <i>ELife</i> , 2015, 4, .	6.0	107
9	The Tegument Protein pp65 of Human Cytomegalovirus Acts as an Optional Scaffold Protein That Optimizes Protein Uploading into Viral Particles. <i>Journal of Virology</i> , 2014, 88, 9633-9646.	3.4	27
10	Conserved Peptide Fragmentation as a Benchmarking Tool for Mass Spectrometers and a Discriminating Feature for Targeted Proteomics. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2056-2071.	3.8	96
11	General Statistical Framework for Quantitative Proteomics by Stable Isotope Labeling. <i>Journal of Proteome Research</i> , 2014, 13, 1234-1247.	3.7	165
12	OpenSWATH enables automated, targeted analysis of data-independent acquisition MS data. <i>Nature Biotechnology</i> , 2014, 32, 219-223.	17.5	692
13	Drift time-specific collision energies enable deep-coverage data-independent acquisition proteomics. <i>Nature Methods</i> , 2014, 11, 167-170.	19.0	411
14	Quantitative measurements of N-linked glycoproteins in human plasma by SWATH-MS. <i>Proteomics</i> , 2013, 13, 1247-1256.	2.2	190
15	Alzheimer's Disease Amyloid Peptides Interact with DNA, As Proved by Surface Plasmon Resonance. <i>Current Alzheimer Research</i> , 2012, 9, 924-934.	1.4	14
16	Targeted Data Extraction of the MS/MS Spectra Generated by Data-independent Acquisition: A New Concept for Consistent and Accurate Proteome Analysis. <i>Molecular and Cellular Proteomics</i> , 2012, 11, O111.016717.	3.8	2,285
17	Quantitative in-depth analysis of the dynamic secretome of activated Jurkat T-cells. <i>Journal of Proteomics</i> , 2011, 75, 561-571.	2.4	16
18	Quantitative proteomics by 2D, ¹⁶ O/ ¹⁸ O labelling and linear ion trap mass spectrometry analysis of lymph nodes from piglets inoculated by porcine circovirus type 2. <i>Proteomics</i> , 2011, 11, 3452-3469.	2.2	22

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19	A Robust Method for Quantitative High-throughput Analysis of Proteomes by 18O Labeling. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.003335.	3.8	95
20	Statistical Model to Analyze Quantitative Proteomics Data Obtained by 18O/16O Labeling and Linear Ion Trap Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 1130-1149.	3.8	76
21	A Refined Method To Calculate False Discovery Rates for Peptide Identification Using Decoy Databases. <i>Journal of Proteome Research</i> , 2009, 8, 1792-1796.	3.7	161
22	Properties of Average Score Distributions of SEQUEST. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 1135-1145.	3.8	142
23	A DNA and histone immobilization method to study DNA-histone interactions by surface plasmon resonance. <i>Analytical Biochemistry</i> , 2006, 352, 151-153.	2.4	7