

Salvador Martínez de Bartolomé©

List of Publications by Year in descending order

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42
papers

3,888
citations

361045

20
h-index

276539

41
g-index

49
all docs

49
docs citations

49
times ranked

9421
citing authors

#	ARTICLE	IF	CITATIONS
1	Cancer Conformational Landscape Shapes Tumorigenesis. <i>Journal of Proteome Research</i> , 2022, 21, 1017-1028.	1.8	7
2	Temporal Quantitative Profiling of Newly Synthesized Proteins during A β Accumulation. <i>Journal of Proteome Research</i> , 2021, 20, 763-775.	1.8	9
3	Altered network and rescue of human neurons derived from individuals with early-onset genetic epilepsy. <i>Molecular Psychiatry</i> , 2021, 26, 7047-7068.	4.1	38
4	Protein Footprinting via Covalent Protein Painting Reveals Structural Changes of the Proteome in Alzheimer's Disease. <i>Journal of Proteome Research</i> , 2021, 20, 2762-2771.	1.8	34
5	DeGlyPHER: An Ultrasensitive Method for the Analysis of Viral Spike <i>N</i> -Glycoforms. <i>Analytical Chemistry</i> , 2021, 93, 13651-13657.	3.2	7
6	Interactome analysis illustrates diverse gene regulatory processes associated with LIN28A in human iPS cell-derived neural progenitor cells. <i>IScience</i> , 2021, 24, 103321.	1.9	2
7	Improving Proteomics Data Reproducibility with a Dual-Search Strategy. <i>Analytical Chemistry</i> , 2020, 92, 1697-1701.	3.2	8
8	Quantitative analysis of global protein stability rates in tissues. <i>Scientific Reports</i> , 2020, 10, 15983.	1.6	13
9	Impact of the Identification Strategy on the Reproducibility of the DDA and DIA Results. <i>Journal of Proteome Research</i> , 2020, 19, 3153-3161.	1.8	61
10	Comparison of CRISPR Genomic Tagging for Affinity Purification and Endogenous Immunoprecipitation Coupled with Quantitative Mass Spectrometry To Identify the Dynamic AMPK \pm 2 Interactome. <i>Journal of Proteome Research</i> , 2019, 18, 3703-3714.	1.8	6
11	Proteomics INTEGRator (PINT): An Online Tool To Store, Query, and Visualize Large Proteomics Experiment Results. <i>Journal of Proteome Research</i> , 2019, 18, 2999-3008.	1.8	0
12	Identification of new transmembrane proteins concentrated at the nuclear envelope using organellar proteomics of mesenchymal cells. <i>Nucleus</i> , 2019, 10, 126-143.	0.6	43
13	Understanding molecular mechanisms of disease through spatial proteomics. <i>Current Opinion in Chemical Biology</i> , 2019, 48, 19-25.	2.8	20
14	Increased proteomic complexity in <i>Drosophila</i> hybrids during development. <i>Science Advances</i> , 2018, 4, eaao3424.	4.7	12
15	PACOM: A Versatile Tool for Integrating, Filtering, Visualizing, and Comparing Multiple Large Mass Spectrometry Proteomics Data Sets. <i>Journal of Proteome Research</i> , 2018, 17, 1547-1558.	1.8	7
16	Structural Analysis of Hippocampal Kinase Signal Transduction. <i>ACS Chemical Neuroscience</i> , 2018, 9, 3072-3085.	1.7	6
17	Deducing the presence of proteins and proteoforms in quantitative proteomics. <i>Nature Communications</i> , 2018, 9, 2320.	5.8	23
18	Validation of In Vivo Protein Surface Accessibility Method. <i>FASEB Journal</i> , 2018, 32, 802.12.	0.2	0

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19	Amyloid Accumulation Drives Proteome-wide Alterations in Mouse Models of Alzheimer's Disease-like Pathology. <i>Cell Reports</i> , 2017, 21, 2614-2627.	2.9	56
20	The mzIdentML Data Standard Version 1.2, Supporting Advances in Proteome Informatics. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1275-1285.	2.5	55
21	Global quantitative analysis of phosphorylation underlying phencyclidine signaling and sensorimotor gating in the prefrontal cortex. <i>Molecular Psychiatry</i> , 2016, 21, 205-215.	4.1	13
22	From Raw Data to Biological Discoveries: A Computational Analysis Pipeline for Mass Spectrometry-Based Proteomics. <i>Journal of the American Society for Mass Spectrometry</i> , 2015, 26, 1820-1826.	1.2	17
23	Multicenter experiment for quality control of peptide-centric LC-MS/MS analysis: A longitudinal performance assessment with nLC coupled to orbitrap MS analyzers. <i>Journal of Proteomics</i> , 2015, 127, 264-274.	1.2	14
24	Quantitative Proteomics of Human Fibroblasts with I1061T Mutation in Niemann-Pick C1 (NPC1) Protein Provides Insights into the Disease Pathogenesis*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 1734-1749.	2.5	41
25	Pulsed Azidohomoalanine Labeling in Mammals (PALM) Detects Changes in Liver-Specific LKB1 Knockout Mice. <i>Journal of Proteome Research</i> , 2015, 14, 4815-4822.	1.8	69
26	CFTR interactome remodelling promotes rescue of cystic fibrosis. <i>Nature</i> , 2015, 528, 510-516.	13.7	225
27	A standardized framing for reporting protein identifications in mzIdentML 1.2. <i>Proteomics</i> , 2014, 14, 2389-2399.	1.3	23
28	ProteomeXchange provides globally coordinated proteomics data submission and dissemination. <i>Nature Biotechnology</i> , 2014, 32, 223-226.	9.4	2,505
29	Surfing Transcriptomic Landscapes. A Step beyond the Annotation of Chromosome 16 Proteome. <i>Journal of Proteome Research</i> , 2014, 13, 158-172.	1.8	26
30	The Minimal Information About a Proteomics Experiment (MIAPE) from the Proteomics Standards Initiative. <i>Methods in Molecular Biology</i> , 2014, 1072, 765-780.	0.4	31
31	Spanish Human Proteome Project: Dissection of Chromosome 16. <i>Journal of Proteome Research</i> , 2013, 12, 112-122.	1.8	17
32	Guidelines for reporting quantitative mass spectrometry based experiments in proteomics. <i>Journal of Proteomics</i> , 2013, 95, 84-88.	1.2	46
33	Tools (Viewer, Library and Validator) that Facilitate Use of the Peptide and Protein Identification Standard Format, Termed mzIdentML. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3026-3035.	2.5	32
34	A DIGE study on the effects of salbutamol on the rat muscle proteome - an exemplar of best practice for data sharing in proteomics. <i>BMC Research Notes</i> , 2011, 4, 86.	0.6	6
35	The ProteoRed MIAPE web toolkit: A User-friendly Framework to Connect and Share Proteomics Standards. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.008334.	2.5	23
36	Relevance of proteomics standards for the ProteoRed Spanish organization. <i>Journal of Proteomics</i> , 2010, 73, 1061-1066.	1.2	11

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37	Semi-automatic tool to describe, store and compare proteomics experiments based on MIAPE compliant reports. <i>Proteomics</i> , 2010, 10, 1256-1260.	1.3	16
38	The Gel Electrophoresis Markup Language (GelML) from the Proteomics Standards Initiative. <i>Proteomics</i> , 2010, 10, 3073-3081.	1.3	19
39	Guidelines for reporting the use of gel image informatics in proteomics. <i>Nature Biotechnology</i> , 2010, 28, 655-656.	9.4	22
40	Properties of Average Score Distributions of SEQUEST. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 1135-1145.	2.5	142
41	Quantitative proteomics using 16O/18O labeling and linear ion trap mass spectrometry. <i>Proteomics</i> , 2006, 6, S4-S11.	1.3	57
42	Statistical Model for Large-Scale Peptide Identification in Databases from Tandem Mass Spectra Using SEQUEST. <i>Analytical Chemistry</i> , 2004, 76, 6853-6860.	3.2	101