Salvador MartÃ-nez de BartolomÃ©

List of Publications by Year
in descending order

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42
papers

3,888
citations

361413
20
h-index

276875
41
g-index

49
all docs

49
docs citations

49
times ranked

9421
citing authors

#	Article	IF	Citations
1	Cancer Conformational Landscape Shapes Tumorigenesis. Journal of Proteome Research, 2022, 21, 1017-1028.	3.7	7
2	Temporal Quantitative Profiling of Newly Synthesized Proteins during AÎ² Accumulation. Journal of Proteome Research, 2021, 20, 763-775.	3.7	9
3	Altered network and rescue of human neurons derived from individuals with early-onset genetic epilepsy. Molecular Psychiatry, 2021, 26, 7047-7068.	7.9	38
4	Protein Footprinting via Covalent Protein Painting Reveals Structural Changes of the Proteome in Alzheimerâ€™s Disease. Journal of Proteome Research, 2021, 20, 2762-2771.	3.7	34
5	DeGlyPHER: An Ultrasensitive Method for the Analysis of Viral Spike <i>N</i>-Glycoforms. Analytical Chemistry, 2021, 93, 13651-13657.	6.5	7
6	Interactome analysis illustrates diverse gene regulatory processes associated with LIN28A in human iPS cell-derived neural progenitor cells. IScience, 2021, 24, 103321.	4.1	2
7	Improving Proteomics Data Reproducibility with a Dual-Search Strategy. Analytical Chemistry, 2020, 92, 1697-1701.	6.5	8
8	Quantitative analysis of global protein stability rates in tissues. Scientific Reports, 2020, 10, 15983.	3.3	13
9	Impact of the Identification Strategy on the Reproducibility of the DDA and DIA Results. Journal of Proteome Research, 2020, 19, 3153-3161.	3.7	61
10	Comparison of CRISPR Genomic Tagging for Affinity Purification and Endogenous Immunoprecipitation Coupled with Quantitative Mass Spectrometry To Identify the Dynamic AMPKÎ±2 Interactome. Journal of Proteome Research, 2019, 18, 3703-3714.	3.7	6
11	Proteomics INTegrator (PINT): An Online Tool To Store, Query, and Visualize Large Proteomics Experiment Results. Journal of Proteome Research, 2019, 18, 2999-3008.	3.7	0
12	Identification of new transmembrane proteins concentrated at the nuclear envelope using organellar proteomics of mesenchymal cells. Nucleus, 2019, 10, 126-143.	2.2	43
13	Understanding molecular mechanisms of disease through spatial proteomics. Current Opinion in Chemical Biology, 2019, 48, 19-25.	6.1	20
14	Increased proteomic complexity in <i>Drosophila</i> hybrids during development. Science Advances, 2018, 4, eaao3424.	10.3	12
15	PACOM: A Versatile Tool for Integrating, Filtering, Visualizing, and Comparing Multiple Large Mass Spectrometry Proteomics Data Sets. Journal of Proteome Research, 2018, 17, 1547-1558.	3.7	7
16	Structural Analysis of Hippocampal Kinase Signal Transduction. ACS Chemical Neuroscience, 2018, 9, 3072-3085.	3.5	6
17	Deducing the presence of proteins and proteoforms in quantitative proteomics. Nature Communications, 2018, 9, 2320.	12.8	23
18	Validation of In Vivo Protein Surface Accessibility Method. FASEB Journal, 2018, 32, 802.12.	0.5	0

#	ARTICLE	IF	CITATIONS
19	Amyloid Accumulation Drives Proteome-wide Alterations in Mouse Models of Alzheimerâ€™s Disease-like Pathology. Cell Reports, 2017, 21, 2614-2627.	6.4	56
20	The mzIdentML Data Standard Version 1.2, Supporting Advances in Proteome Informatics. Molecular and Cellular Proteomics, 2017, 16, 1275-1285.	3.8	55
21	Global quantitative analysis of phosphorylation underlying phencyclidine signaling and sensorimotor gating in the prefrontal cortex. Molecular Psychiatry, 2016, 21, 205-215.	7.9	13
22	From Raw Data to Biological Discoveries: A Computational Analysis Pipeline for Mass Spectrometry-Based Proteomics. Journal of the American Society for Mass Spectrometry, 2015, 26, 1820-1826.	2.8	17
23	Multicenter experiment for quality control of peptide-centric LCâ€“MS/MS analysis â€” A longitudinal performance assessment with nLC coupled to orbitrap MS analyzers. Journal of Proteomics, 2015, 127, 264-274.	2.4	14
24	Quantitative Proteomics of Human Fibroblasts with I1061T Mutation in Niemannâ€“Pick C1 (NPC1) Protein Provides Insights into the Disease Pathogenesis*. Molecular and Cellular Proteomics, 2015, 14, 1734-1749.	3.8	41
25	Pulsed Azidohomoalanine Labeling in Mammals (PALM) Detects Changes in Liver-Specific LKB1 Knockout Mice. Journal of Proteome Research, 2015, 14, 4815-4822.	3.7	69
26	âˆ†F508 CFTR interactome remodelling promotes rescue of cystic fibrosis. Nature, 2015, 528, 510-516.	27.8	225
27	A standardized framing for reporting protein identifications in mzIdentML 1.2. Proteomics, 2014, 14, 2389-2399.	2.2	23
28	ProteomeXchange provides globally coordinated proteomics data submission and dissemination. Nature Biotechnology, 2014, 32, 223-226.	17.5	2,505
29	Surfing Transcriptomic Landscapes. A Step beyond the Annotation of Chromosome 16 Proteome. Journal of Proteome Research, 2014, 13, 158-172.	3.7	26
30	The Minimal Information About a Proteomics Experiment (MIAPE) from the Proteomics Standards Initiative. Methods in Molecular Biology, 2014, 1072, 765-780.	0.9	31
31	Spanish Human Proteome Project: Dissection of Chromosome 16. Journal of Proteome Research, 2013, 12, 112-122.	3.7	17
32	Guidelines for reporting quantitative mass spectrometry based experiments in proteomics. Journal of Proteomics, 2013, 95, 84-88.	2.4	46
33	Tools (Viewer, Library and Validator) that Facilitate Use of the Peptide and Protein Identification Standard Format, Termed mzIdentML. Molecular and Cellular Proteomics, 2013, 12, 3026-3035.	3.8	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. BMC Research Notes, 2011, 4, 86.	1.4	6
35	The ProteoRed MIAPE web toolkit: A User-friendly Framework to Connect and Share Proteomics Standards. Molecular and Cellular Proteomics, 2011, 10, M111.008334.	3.8	23
36	Relevance of proteomics standards for the ProteoRed Spanish organization. Journal of Proteomics, 2010, 73, 1061-1066.	2.4	11

#	Article	IF	Citations
37	Semiâ€automatic tool to describe, store and compare proteomics experiments based on MIAPE compliant reports. Proteomics, 2010, 10, 1256-1260.	2.2	16
38	The Gel Electrophoresis Markup Language (GelML) from the Proteomics Standards Initiative. Proteomics, 2010, 10, 3073-3081.	2.2	19
39	Guidelines for reporting the use of gel image informatics in proteomics. Nature Biotechnology, 2010, 28, 655-656.	17.5	22
40	Properties of Average Score Distributions of SEQUEST. Molecular and Cellular Proteomics, 2008, 7, 1135-1145.	3.8	142
41	Quantitative proteomics using 16O/18O labeling and linear ion trap mass spectrometry. Proteomics, 2006, 6, S4-S11.	2.2	57
42	Statistical Model for Large-Scale Peptide Identification in Databases from Tandem Mass Spectra Using SEQUEST. Analytical Chemistry, 2004, 76, 6853-6860.	6.5	101