

Salvador Martinez de Bartolom

List of Publications by Citations

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44
papers

2,989
citations

16
h-index

49
g-index

49
ext. papers

3,589
ext. citations

9.1
avg, IF

4.34
L-index

#	Paper	IF	Citations
44	ProteomeXchange provides globally coordinated proteomics data submission and dissemination. <i>Nature Biotechnology</i> , 2014 , 32, 223-6	44.5	2053
43	B508 CFTR interactome remodelling promotes rescue of cystic fibrosis. <i>Nature</i> , 2015 , 528, 510-6	50.4	163
42	Properties of average score distributions of SEQUEST: the probability ratio method. <i>Molecular and Cellular Proteomics</i> , 2008 , 7, 1135-45	7.6	96
41	Statistical model for large-scale peptide identification in databases from tandem mass spectra using SEQUEST. <i>Analytical Chemistry</i> , 2004 , 76, 6853-60	7.8	95
40	Quantitative proteomics using 16O/18O labeling and linear ion trap mass spectrometry. <i>Proteomics</i> , 2006 , 6 Suppl 1, S4-11	4.8	52
39	Pulsed Azidohomoalanine Labeling in Mammals (PALM) Detects Changes in Liver-Specific LKB1 Knockout Mice. <i>Journal of Proteome Research</i> , 2015 , 14, 4815-22	5.6	48
38	Guidelines for reporting quantitative mass spectrometry based experiments in proteomics. <i>Journal of Proteomics</i> , 2013 , 95, 84-8	3.9	37
37	The mzIdentML Data Standard Version 1.2, Supporting Advances in Proteome Informatics. <i>Molecular and Cellular Proteomics</i> , 2017 , 16, 1275-1285	7.6	37
36	Amyloid Accumulation Drives Proteome-wide Alterations in Mouse Models of Alzheimer's Disease-like Pathology. <i>Cell Reports</i> , 2017 , 21, 2614-2627	10.6	35
35	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, 1734-49	7.6	33
34	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, 3026-35	7.6	28
33	Surfing transcriptomic landscapes. A step beyond the annotation of chromosome 16 proteome. <i>Journal of Proteome Research</i> , 2014 , 13, 158-72	5.6	24
32	The Minimal Information about a Proteomics Experiment (MIAPE) from the Proteomics Standards Initiative. <i>Methods in Molecular Biology</i> , 2014 , 1072, 765-80	1.4	23
31	Guidelines for reporting the use of gel image informatics in proteomics. <i>Nature Biotechnology</i> , 2010 , 28, 655-6	44.5	21
30	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	7.6	19
29	Spanish human proteome project: dissection of chromosome 16. <i>Journal of Proteome Research</i> , 2013 , 12, 112-22	5.6	17
28	A standardized framing for reporting protein identifications in mzIdentML 1.2. <i>Proteomics</i> , 2014 , 14, 2389-99	4.8	16

27	The gel electrophoresis markup language (GelML) from the Proteomics Standards Initiative. <i>Proteomics</i> , 2010 , 10, 3073-81	4.8	16
26	Impact of the Identification Strategy on the Reproducibility of the DDA and DIA Results. <i>Journal of Proteome Research</i> , 2020 , 19, 3153-3161	5.6	14
25	Identification of new transmembrane proteins concentrated at the nuclear envelope using organellar proteomics of mesenchymal cells. <i>Nucleus</i> , 2019 , 10, 126-143	3.9	13
24	Deducing the presence of proteins and proteoforms in quantitative proteomics. <i>Nature Communications</i> , 2018 , 9, 2320	17.4	13
23	Semi-automatic tool to describe, store and compare proteomics experiments based on MIAPE compliant reports. <i>Proteomics</i> , 2010 , 10, 1256-60	4.8	13
22	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, 264-74	3.9	12
21	Global quantitative analysis of phosphorylation underlying phencyclidine signaling and sensorimotor gating in the prefrontal cortex. <i>Molecular Psychiatry</i> , 2016 , 21, 205-15	15.1	11
20	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, 1820-6	3.5	11
19	Altered network and rescue of human neurons derived from individuals with early-onset genetic epilepsy. <i>Molecular Psychiatry</i> , 2021 ,	15.1	11
18	Understanding molecular mechanisms of disease through spatial proteomics. <i>Current Opinion in Chemical Biology</i> , 2019 , 48, 19-25	9.7	11
17	Relevance of proteomics standards for the ProteoRed Spanish organization. <i>Journal of Proteomics</i> , 2010 , 73, 1061-6	3.9	10
16	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	5.6	9
15	Increased proteomic complexity in hybrids during development. <i>Science Advances</i> , 2018 , 4, eaao3424	14.3	8
14	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	5.6	6
13	Quantitative analysis of global protein stability rates in tissues. <i>Scientific Reports</i> , 2020 , 10, 15983	4.9	5
12	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	2.3	4
11	Comparison of CRISPR Genomic Tagging for Affinity Purification and Endogenous Immunoprecipitation Coupled with Quantitative Mass Spectrometry To Identify the Dynamic AMPK Interactome. <i>Journal of Proteome Research</i> , 2019 , 18, 3703-3714	5.6	3
10	Improving Proteomics Data Reproducibility with a Dual-Search Strategy. <i>Analytical Chemistry</i> , 2020 , 92, 1697-1701	7.8	3

9	Temporal Quantitative Profiling of Newly Synthesized Proteins during A β Accumulation. <i>Journal of Proteome Research</i> , 2021 , 20, 763-775	5.6	3
8	Structural Analysis of Hippocampal Kinase Signal Transduction. <i>ACS Chemical Neuroscience</i> , 2018 , 9, 3072-3085	5.7	2
7	Covalent Protein Painting Reveals Structural Changes in the Proteome in Alzheimer Disease		2
6	DeGlyPHER: An Ultrasensitive Method for the Analysis of Viral Spike -Glycoforms. <i>Analytical Chemistry</i> , 2021 , 93, 13651-13657	7.8	2
5	A Temporal Quantitative Profiling of Newly Synthesized Proteins during A β Accumulation		1
4	Cancer Conformational Landscape Shape Tumorigenesis.. <i>Journal of Proteome Research</i> , 2022 ,	5.6	1
3	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	5.6	
2	Interactome analysis illustrates diverse gene regulatory processes associated with LIN28A in human iPS cell-derived neural progenitor cells. <i>IScience</i> , 2021 , 24, 103321	6.1	
1	Validation of In Vivo Protein Surface Accessibility Method. <i>FASEB Journal</i> , 2018 , 32, 802.12	0.9	