

# Salvador Martínez de Bartolomé©

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1241108/publications.pdf>

Version: 2024-02-01

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	ProteomeXchange provides globally coordinated proteomics data submission and dissemination. <i>Nature Biotechnology</i> , 2014, 32, 223-226.	17.5	2,505
2	â†F508 CFTR interactome remodelling promotes rescue of cystic fibrosis. <i>Nature</i> , 2015, 528, 510-516.	27.8	225
3	Properties of Average Score Distributions of SEQUEST. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 1135-1145.	3.8	142
4	Statistical Model for Large-Scale Peptide Identification in Databases from Tandem Mass Spectra Using SEQUEST. <i>Analytical Chemistry</i> , 2004, 76, 6853-6860.	6.5	101
5	Pulsed Azidohomoalanine Labeling in Mammals (PALM) Detects Changes in Liver-Specific LKB1 Knockout Mice. <i>Journal of Proteome Research</i> , 2015, 14, 4815-4822.	3.7	69
6	Impact of the Identification Strategy on the Reproducibility of the DDA and DIA Results. <i>Journal of Proteome Research</i> , 2020, 19, 3153-3161.	3.7	61
7	Quantitative proteomics using 16O/18O labeling and linear ion trap mass spectrometry. <i>Proteomics</i> , 2006, 6, S4-S11.	2.2	57
8	Amyloid Accumulation Drives Proteome-wide Alterations in Mouse Models of Alzheimerâ€™s Disease-like Pathology. <i>Cell Reports</i> , 2017, 21, 2614-2627.	6.4	56
9	The mzIdentML Data Standard Version 1.2, Supporting Advances in Proteome Informatics. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1275-1285.	3.8	55
10	Guidelines for reporting quantitative mass spectrometry based experiments in proteomics. <i>Journal of Proteomics</i> , 2013, 95, 84-88.	2.4	46
11	Identification of new transmembrane proteins concentrated at the nuclear envelope using organellar proteomics of mesenchymal cells. <i>Nucleus</i> , 2019, 10, 126-143.	2.2	43
12	Quantitative Proteomics of Human Fibroblasts with I1061T Mutation in Niemannâ€™Pick C1 (NPC1) Protein Provides Insights into the Disease Pathogenesis*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 1734-1749.	3.8	41
13	Altered network and rescue of human neurons derived from individuals with early-onset genetic epilepsy. <i>Molecular Psychiatry</i> , 2021, 26, 7047-7068.	7.9	38
14	Protein Footprinting via Covalent Protein Painting Reveals Structural Changes of the Proteome in Alzheimerâ€™s Disease. <i>Journal of Proteome Research</i> , 2021, 20, 2762-2771.	3.7	34
15	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.	3.8	32
16	The Minimal Information About a Proteomics Experiment (MIAPE) from the Proteomics Standards Initiative. <i>Methods in Molecular Biology</i> , 2014, 1072, 765-780.	0.9	31
17	Surfing Transcriptomic Landscapes. A Step beyond the Annotation of Chromosome 16 Proteome. <i>Journal of Proteome Research</i> , 2014, 13, 158-172.	3.7	26
18	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.	3.8	23

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19	A standardized framing for reporting protein identifications in mzIdentML 1.2. <i>Proteomics</i> , 2014, 14, 2389-2399.	2.2	23
20	Deducing the presence of proteins and proteoforms in quantitative proteomics. <i>Nature Communications</i> , 2018, 9, 2320.	12.8	23
21	Guidelines for reporting the use of gel image informatics in proteomics. <i>Nature Biotechnology</i> , 2010, 28, 655-656.	17.5	22
22	Understanding molecular mechanisms of disease through spatial proteomics. <i>Current Opinion in Chemical Biology</i> , 2019, 48, 19-25.	6.1	20
23	The Gel Electrophoresis Markup Language (GelML) from the Proteomics Standards Initiative. <i>Proteomics</i> , 2010, 10, 3073-3081.	2.2	19
24	Spanish Human Proteome Project: Dissection of Chromosome 16. <i>Journal of Proteome Research</i> , 2013, 12, 112-122.	3.7	17
25	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.	2.8	17
26	Semi-automatic tool to describe, store and compare proteomics experiments based on MIAPE compliant reports. <i>Proteomics</i> , 2010, 10, 1256-1260.	2.2	16
27	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.	2.4	14
28	Global quantitative analysis of phosphorylation underlying phenacyclidine signaling and sensorimotor gating in the prefrontal cortex. <i>Molecular Psychiatry</i> , 2016, 21, 205-215.	7.9	13
29	Quantitative analysis of global protein stability rates in tissues. <i>Scientific Reports</i> , 2020, 10, 15983.	3.3	13
30	Increased proteomic complexity in <i>Drosophila</i> hybrids during development. <i>Science Advances</i> , 2018, 4, eaao3424.	10.3	12
31	Relevance of proteomics standards for the ProteoRed Spanish organization. <i>Journal of Proteomics</i> , 2010, 73, 1061-1066.	2.4	11
32	Temporal Quantitative Profiling of Newly Synthesized Proteins during A $\beta$ Accumulation. <i>Journal of Proteome Research</i> , 2021, 20, 763-775.	3.7	9
33	Improving Proteomics Data Reproducibility with a Dual-Search Strategy. <i>Analytical Chemistry</i> , 2020, 92, 1697-1701.	6.5	8
34	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.	3.7	7
35	DeGlyPHER: An Ultrasensitive Method for the Analysis of Viral Spike N-Glycoforms. <i>Analytical Chemistry</i> , 2021, 93, 13651-13657.	6.5	7
36	Cancer Conformational Landscape Shapes Tumorigenesis. <i>Journal of Proteome Research</i> , 2022, 21, 1017-1028.	3.7	7

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37	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
38	Structural Analysis of Hippocampal Kinase Signal Transduction. ACS Chemical Neuroscience, 2018, 9, 3072-3085.	3.5	6
39	Comparison of CRISPR Genomic Tagging for Affinity Purification and Endogenous Immunoprecipitation Coupled with Quantitative Mass Spectrometry To Identify the Dynamic AMPK $\pm$ 2 Interactome. Journal of Proteome Research, 2019, 18, 3703-3714.	3.7	6
40	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
41	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
42	Validation of In Vivo Protein Surface Accessibility Method. FASEB Journal, 2018, 32, 802.12.	0.5	0