

Juan Casado-Vela

List of Publications by Year in descending order

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Version: 2024-02-01

47
papers

1,724
citations

279798

23
h-index

276875

41
g-index

50
all docs

50
docs citations

50
times ranked

3146
citing authors

#	ARTICLE	IF	CITATIONS
1	The Role of Propranolol as a Repurposed Drug in Rare Vascular Diseases. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4217.	4.1	7
2	A Novel Splicing Mutation in the ACVRL1/ALK1 Gene as a Cause of HHT2. <i>Journal of Clinical Medicine</i> , 2022, 11, 3053.	2.4	3
3	Endoglin Protein Interactome Profiling Identifies TRIM21 and Galectin-3 as New Binding Partners. <i>Cells</i> , 2019, 8, 1082.	4.1	21
4	Nanotechnology in the Fabrication of Protein Microarrays. <i>Methods in Molecular Biology</i> , 2016, 1368, 197-208.	0.9	4
5	Activating transcription factor 6 derepression mediates neuroprotection in Huntington disease. <i>Journal of Clinical Investigation</i> , 2016, 126, 627-638.	8.2	56
6	NAPPA as a Real New Method for Protein Microarray Generation. <i>Microarrays (Basel, Switzerland)</i> , 2015, 4, 214-227.	1.4	24
7	Differential protein expression in compatible and incompatible pollen-pistil interactions in almond [<i>Prunus dulcis</i> (Miller) D. A. Webb] by 2D-DIGE and HPLC-MS/MS. <i>Journal of Horticultural Science and Biotechnology</i> , 2015, 90, 71-77.	1.9	8
8	High-throughput phage-display screening in array format. <i>Enzyme and Microbial Technology</i> , 2015, 79-80, 34-41.	3.2	1
9	High-throughput proteomic characterization of plasma rich in growth factors (PRGF-Endoret)-derived fibrin clot interactome. <i>Journal of Tissue Engineering and Regenerative Medicine</i> , 2015, 9, E1-E12.	2.7	66
10	Evaluation of homo- and hetero-functionally activated glass surfaces for optimized antibody arrays. <i>Analytical Biochemistry</i> , 2014, 450, 37-45.	2.4	24
11	Differential Plant Proteome Analysis by Isobaric Tags for Relative and Absolute Quantitation (iTRAQ). <i>Methods in Molecular Biology</i> , 2014, 1072, 155-169.	0.9	17
12	Nanovesicles Are Secreted during Pollen Germination and Pollen Tube Growth: A Possible Role in Fertilization. <i>Molecular Plant</i> , 2014, 7, 573-577.	8.3	63
13	Screening of Protein-Protein and Protein-DNA Interactions Using Microarrays. <i>Advances in Protein Chemistry and Structural Biology</i> , 2014, 95, 231-281.	2.3	6
14	Suspension-Cultured Plant Cells as a Tool to Analyze the Extracellular Proteome. <i>Methods in Molecular Biology</i> , 2014, 1072, 407-433.	0.9	0
15	Protein chimerism: Novel source of protein diversity in humans adds complexity to bottom-up proteomics. <i>Proteomics</i> , 2013, 13, 5-11.	2.2	10
16	Protein-Protein Interactions: Gene Acronym Redundancies and Current Limitations Precluding Automated Data Integration. <i>Proteomes</i> , 2013, 1, 3-24.	3.5	1
17	Protein Arrays: Recent Achievements and their Application to Study the Human Proteome. <i>Current Proteomics</i> , 2013, 10, 83-97.	0.3	9
18	Uromodulin and Antitrypsin Urinary Peptide Analysis to Differentiate Glomerular Kidney Diseases. <i>Kidney and Blood Pressure Research</i> , 2012, 35, 314-325.	2.0	22

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19	Data Analysis Strategies for Protein Microarrays. <i>Microarrays</i> (Basel, Switzerland), 2012, 1, 64-83.	1.4	34
20	Integrative analysis of the ubiquitin proteome isolated using Tandem Ubiquitin Binding Entities (TUBEs). <i>Journal of Proteomics</i> , 2012, 75, 2998-3014.	2.4	90
21	Human urine proteomics: building a list of human urine cancer biomarkers. <i>Expert Review of Proteomics</i> , 2011, 8, 347-360.	3.0	21
22	Changes to the proteome and targeted metabolites of xylem sap in <i>Brassica oleracea</i> in response to salt stress. <i>Plant, Cell and Environment</i> , 2011, 34, 821-836.	5.7	56
23	iTRAQ-based profiling of grape berry exocarp proteins during ripening using a parallel mass spectrometric method. <i>Molecular BioSystems</i> , 2011, 7, 749-765.	2.9	27
24	Approaches for the study of cancer: towards the integration of genomics, proteomics and metabolomics. <i>Clinical and Translational Oncology</i> , 2011, 13, 617-628.	2.4	31
25	Lights and shadows of proteomic technologies for the study of protein species including isoforms, splicing variants and protein post-translational modifications. <i>Proteomics</i> , 2011, 11, 590-603.	2.2	19
26	iTRAQ-based quantitative analysis of protein mixtures with large fold change and dynamic range. <i>Proteomics</i> , 2010, 10, 343-347.	2.2	67
27	Novel Snail1 Target Proteins in Human Colon Cancer Identified by Proteomic Analysis. <i>PLoS ONE</i> , 2010, 5, e10221.	2.5	29
28	A p120-catenin-CK1 complex regulates Wnt signaling. <i>Journal of Cell Science</i> , 2010, 123, 2621-2631.	2.0	67
29	Expression of serine proteases in egg-parasitic nematophagous fungi during barley root colonization. <i>Fungal Genetics and Biology</i> , 2010, 47, 342-351.	2.1	60
30	Analysis of Root Plasma Membrane Aquaporins from <i>Brassica oleracea</i> : Post-Translational Modifications, <i>de novo</i> Sequencing and Detection of Isoforms by High Resolution Mass Spectrometry. <i>Journal of Proteome Research</i> , 2010, 9, 3479-3494.	3.7	25
31	Cohesin organizes chromatin loops at DNA replication factories. <i>Genes and Development</i> , 2010, 24, 2812-2822.	5.9	195
32	Differential phosphorylation patterns between the Cyclin-A2/CDK2 complex and their monomers. <i>Protein Expression and Purification</i> , 2009, 66, 15-21.	1.3	9
33	Comprehensive Proteomic Analysis of Human Endometrial Fluid Aspirate. <i>Journal of Proteome Research</i> , 2009, 8, 4622-4632.	3.7	107
34	Proteomics of Multigenic Families from Species Underrepresented in Databases: The Case of Loquat (<i>Eriobotrya japonica</i> Lindl.) Polyphenol Oxidases. <i>Journal of Proteome Research</i> , 2008, 7, 4095-4106.	3.7	16
35	Effect of detergents, trypsin and unsaturated fatty acids on latent loquat fruit polyphenol oxidase: Basis for the enzyme's activity regulation. <i>Archives of Biochemistry and Biophysics</i> , 2007, 464, 295-305.	3.0	23
36	A combination of neutral loss and targeted product ion scanning with two enzymatic digestions facilitates the comprehensive mapping of phosphorylation sites. <i>Proteomics</i> , 2007, 7, 2522-2529.	2.2	22

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37	Effect of composted sewage sludge application to soil on sweet pepper crop (<i>Capsicum annuum</i> var.) Tj ETQq1 1 0,784314 rgBT /Overl 7.4	7.4	56
38	Modified Cyclodextrins Are Chemically Defined Glucan Inducers of Defense Responses in Grapevine Cell Cultures. <i>Journal of Agricultural and Food Chemistry</i> , 2006, 54, 65-71.	5.2	134
39	Isolation of a latent polyphenol oxidase from loquat fruit (<i>Eriobotrya japonica</i> Lindl.): Kinetic characterization and comparison with the active form. <i>Archives of Biochemistry and Biophysics</i> , 2006, 446, 175-185.	3.0	60
40	Proteomic analysis of tobacco mosaic virus-infected tomato (<i>Lycopersicon esculentum</i> M.) fruits and detection of viral coat protein. <i>Proteomics</i> , 2006, 6, S196-S206.	2.2	57
41	INFLUENCE OF DEVELOPMENTAL STAGE, CULTIVAR, AND HEXAPEPTIDE AND CYCLODEXTRIN INHIBITORS ON POLYPHENOL OXIDASE ACTIVITY FROM TOMATO FRUITS. <i>Journal of Food Biochemistry</i> , 2006, 30, 623-640.	2.9	10
42	Evaluation of composted sewage sludge as nutritional source for horticultural soils. <i>Waste Management</i> , 2006, 26, 946-952.	7.4	64
43	Release of Hypoacetylated and Trimethylated Histone H4 Is an Epigenetic Marker of Early Apoptosis. <i>Journal of Biological Chemistry</i> , 2006, 281, 13540-13547.	3.4	34
44	PURIFICATION AND KINETIC CHARACTERIZATION OF POLYPHENOL OXIDASE FROM TOMATO FRUITS (<i>LYCOPERSICON ESCULENTUM</i> CV. MUCHAMIEL). <i>Journal of Food Biochemistry</i> , 2005, 29, 381-401.	2.9	28
45	Proteomic approach to blossom-end rot in tomato fruits (<i>Lycopersicon esculentum</i> M.): Antioxidant enzymes and the pentose phosphate pathway. <i>Proteomics</i> , 2005, 5, 2488-2496.	2.2	33
46	Methodological Requirements for Lipidomics Research. , 0, , 30-53.		0
47	Biological Methods for Metabolic Research. , 0, , 54-76.		0