Inmaculada Jorge

List of Publications by Year
in descending order

52 papers	2,795 citations	159585 30 h-index	182427 51 g-index
53 all docs	53 docs citations	53 times ranked	4712 citing authors

#	Article	IF	Citations
1	The Intracellular Interactome of Tetraspanin-enriched Microdomains Reveals Their Function as Sorting Machineries toward Exosomes. Journal of Biological Chemistry, 2013, 288, 11649-11661.	3.4	377
2	Priming of dendritic cells by DNA-containing extracellular vesicles from activated T cells through antigen-driven contacts. Nature Communications, 2018, 9, 2658.	12.8	242
3	General Statistical Framework for Quantitative Proteomics by Stable Isotope Labeling. Journal of Proteome Research, 2014, 13, 1234-1247.	3.7	165
4	Connexin43 in cardiomyocyte mitochondria contributes to mitochondrial potassium uptake. Cardiovascular Research, 2009, 83, 747-756.	3.8	124
5	The Holm Oak leaf proteome: Analytical and biological variability in the protein expression level assessed by 2-DE and protein identification tandem mass spectrometryde novosequencing and sequence similarity searching. Proteomics, 2005, 5, 222-234.	2.2	116
6	Variation in the holm oak leaf proteome at different plant developmental stages, between provenances and in response to drought stress. Proteomics, 2006, 6, S207-S214.	2.2	110
7	Changes in the protein profile of Quercus ilex leaves in response to drought stress and recovery. Journal of Plant Physiology, 2009, 166, 233-245.	3.5	101
8	CD69 controls the uptake of L-tryptophan through LAT1-CD98 and AhR-dependent secretion of IL-22 in psoriasis. Nature Immunology, 2016, 17, 985-996.	14.5	98
9	A Novel Systems-Biology Algorithm for the Analysis of Coordinated Protein Responses Using Quantitative Proteomics. Molecular and Cellular Proteomics, 2016, 15, 1740-1760.	3.8	86
10	Statistical Model to Analyze Quantitative Proteomics Data Obtained by 18O/16O Labeling and Linear Ion Trap Mass Spectrometry. Molecular and Cellular Proteomics, 2009, 8, 1130-1149.	3.8	76
11	ISG15 governs mitochondrial function in macrophages following vaccinia virus infection. PLoS Pathogens, 2017, 13, e1006651.	4.7	75
12	Two-dimensional electrophoresis protein profile of the phytopathogenic fungus Botrytis cinerea. Proteomics, 2006, 6, S88-S96.	2.2	70
13	Proteomic analysis of phytopathogenic fungus Botrytis cinerea as a potential tool for identifying pathogenicity factors, therapeutic targets and for basic research. Archives of Microbiology, 2007, 187, 207-215.	2.2	70
14	High-sensitivity analysis of specific peptides in complex samples by selected MS/MS ion monitoring and linear ion trap mass spectrometry: Application to biological studies. Journal of Mass Spectrometry, 2007, 42, 1391-1403.	1.6	68
15	Flow Cytometry Has a Significant Impact on the Cellular Metabolome. Journal of Proteome Research, 2019, 18, 169-181.	3.7	66
16	SanXoT: a modular and versatile package for the quantitative analysis of high-throughput proteomics experiments. Bioinformatics, 2019, 35, 1594-1596.	4.1	59
17	The immunomodulatory activity of extracellular vesicles derived from endometrial mesenchymal stem cells on CD4+ T cells is partially mediated by TGFbeta. Journal of Tissue Engineering and Regenerative Medicine, 2018, 12, 2088-2098.	2.7	58
18	Aurora A drives early signalling and vesicle dynamics during T-cell activation. Nature Communications, 2016, 7, 11389.	12.8	53

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19	Murine embryos exposed to human endometrial MSCs-derived extracellular vesicles exhibit higher VEGF/PDGF AA release, increased blastomere count and hatching rates. PLoS ONE, 2018, 13, e0196080.	2.5	49
20	Targeting L-type amino acid transporter 1 in innate and adaptive T cells efficiently controls skin inflammation. Journal of Allergy and Clinical Immunology, 2020, 145, 199-214.e11.	2.9	47
21	Extracellular vesicles derived from endometrial human mesenchymal stem cells enhance embryo yield and quality in an aged murine modelâ€. Biology of Reproduction, 2019, 100, 1180-1192.	2.7	44
22	Beneficial effects of omega-3 fatty acids in the proteome of high-density lipoprotein proteome. Lipids in Health and Disease, 2012, 11, 116.	3.0	41
23	ApoA-I/HDL-C levels are inversely associated with abdominal aortic aneurysm progression. Thrombosis and Haemostasis, 2015, 113, 1335-1346.	3.4	41
24	APOA1 oxidation is associated to dysfunctional high-density lipoproteins in human abdominal aortic aneurysm. EBioMedicine, 2019, 43, 43-53.	6.1	40
25	HDAC6 controls innate immune and autophagy responses to TLR-mediated signalling by the intracellular bacteria Listeria monocytogenes. PLoS Pathogens, 2017, 13, e1006799.	4.7	38
26	Unraveling the Molecular Signature of Extracellular Vesicles From Endometrial-Derived Mesenchymal Stem Cells: Potential Modulatory Effects and Therapeutic Applications. Frontiers in Bioengineering and Biotechnology, 2019, 7, 431.	4.1	38
27	Proteomic footprint of myocardial ischemia/reperfusion injury: Longitudinal study of the at-risk and remote regions in the pig model. Scientific Reports, 2017, 7, 12343.	3.3	37
28	A Single In-Vial Dual Extraction Strategy for the Simultaneous Lipidomics and Proteomics Analysis of HDL and LDL Fractions. Journal of Proteome Research, 2016, 15, 1762-1775.	3.7	35
29	The apparent variability of silkworm (Bombyx mori) silk and its relationship with degumming. European Polymer Journal, 2016, 78, 129-140.	5.4	33
30	Complement C5 Protein as a Marker of Subclinical Atherosclerosis. Journal of the American College of Cardiology, 2020, 75, 1926-1941.	2.8	32
31	The human HDL proteome displays high inter-individual variability and is altered dynamically in response to angioplasty-induced atheroma plaque rupture. Journal of Proteomics, 2014, 106, 61-73.	2.4	30
32	Quantitative HDL Proteomics Identifies Peroxiredoxin-6 as a Biomarker of Human Abdominal Aortic Aneurysm. Scientific Reports, 2016, 6, 38477.	3.3	29
33	Multiplexed Quantitative Proteomic Analysis of HEK293 Provides Insights into Molecular Changes Associated with the Cell Density Effect, Transient Transfection, and Virus-Like Particle Production. Journal of Proteome Research, 2020, 19, 1085-1099.	3.7	23
34	Quantitative proteomics by 2â€ÐE, $^{16}O/^{18}O$ labelling and linear ion trap mass spectrometry analysis of lymph nodes from piglets inoculated by porcine circovirus type 2. Proteomics, 2011, 11, 3452-3469.	2.2	22
35	Extracellular xylanases from two pathogenic races of Fusarium oxysporum f. sp. ciceris: enzyme production in culture and purification and characterization of a major isoform as an alkaline endo-Î²-(1,4)-xylanase of low molecular weight. Antonie Van Leeuwenhoek, 2005, 88, 48-59.	1.7	20
36	Proteomics, Holm Oak (Quercus ilex L.) and Other Recalcitrant and Orphan Forest Tree Species: How do They See Each Other?. International Journal of Molecular Sciences, 2019, 20, 692.	4.1	20

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37	Mesenchymal stem cell–coated sutures enhance collagen depositions in sutured tissues. Wound Repair and Regeneration, 2014, 22, 256-264.	3.0	19
38	Interferon-stimulated gene 15 pathway is a novel mediator of endothelial dysfunction and aneurysms development in angiotensin II infused mice through increased oxidative stress. Cardiovascular Research, 2022, 118, 3250-3268.	3.8	18
39	Unexpected behavior of irradiated spider silk links conformational freedom to mechanical performance. Soft Matter, 2015, 11, 4868-4878.	2.7	17
40	Cell wall degrading enzymes in fusarium wilt of chickpea: correlation between pectinase and xylanase activities and disease development in plants infected with two pathogenic races of Fusarium oxysporum f. sp. ciceris. Canadian Journal of Botany, 2006, 84, 1395-1404.	1.1	15
41	CIBER-CLAP (CIBERCV Cardioprotection Large Animal Platform): A multicenter preclinical network for testing reproducibility in cardiovascular interventions. Scientific Reports, 2019, 9, 20290.	3.3	15
42	Molecular Characterization of the Coproduced Extracellular Vesicles in HEK293 during Virus-Like Particle Production. Journal of Proteome Research, 2020, 19, 4516-4532.	3.7	15
43	Improved integrative analysis of the thiol redox proteome using filter-aided sample preparation. Journal of Proteomics, 2020, 214, 103624.	2.4	14
44	The Immunomodulatory Signature of Extracellular Vesicles From Cardiosphere-Derived Cells: A Proteomic and miRNA Profiling. Frontiers in Cell and Developmental Biology, 2020, 8, 321.	3.7	11
45	Identification of common cardiometabolic alterations and deregulated pathways in mouse and pig models of aging. Aging Cell, 2020, 19, e13203.	6.7	10
46	Preparation and characterization of *Nephila clavipes* tubuliform silk gut. Soft Matter, 2019, 15, 2960-2970.	2.7	9
47	Quantitative Proteomics Analysis of High-Density Lipoproteins by Stable 18O-Isotope Labeling. Methods in Molecular Biology, 2013, 1000, 139-156.	0.9	6
48	^{18}O proteomics reveal increased human apolipoprotein CIII in Hispanic HIV-1 + women with HAART that use cocaine. Proteomics - Clinical Applications, 2016, 10, 144-155.	1.6	4
49	Identification of hepatic protein-protein interaction targets for betaine homocysteine S-methyltransferase. PLoS ONE, 2018, 13, e0199472.	2.5	4
50	Protein Identification and Quantification by Mass Spectrometry-Based Analysis: Applications in Plant-Pathogen Interactions Studies. Current Proteomics, 2010, 7, 234-243.	0.3	3
51	A Proteomics Signature of Mild Hypospadias: A Pilot Study. Frontiers in Pediatrics, 2020, 8, 586287.	1.9	2
52	The Application of Proteomic Techniques in the Study of HDL Particle Characterization and Biomarker Discovery. , 2017, , 231-255.		0