

Inmaculada Jorge

List of Publications by Year in descending order

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Version: 2024-02-01

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	Interferon-stimulated gene 15 pathway is a novel mediator of endothelial dysfunction and aneurysms development in angiotensin II infused mice through increased oxidative stress. <i>Cardiovascular Research</i> , 2022, 118, 3250-3268.	3.8	18
2	Targeting L-type amino acid transporter 1 in innate and adaptive T cells efficiently controls skin inflammation. <i>Journal of Allergy and Clinical Immunology</i> , 2020, 145, 199-214.e11.	2.9	47
3	Improved integrative analysis of the thiol redox proteome using filter-aided sample preparation. <i>Journal of Proteomics</i> , 2020, 214, 103624.	2.4	14
4	Identification of common cardiometabolic alterations and deregulated pathways in mouse and pig models of aging. <i>Aging Cell</i> , 2020, 19, e13203.	6.7	10
5	Molecular Characterization of the Coproduced Extracellular Vesicles in HEK293 during Virus-Like Particle Production. <i>Journal of Proteome Research</i> , 2020, 19, 4516-4532.	3.7	15
6	A Proteomics Signature of Mild Hypospadias: A Pilot Study. <i>Frontiers in Pediatrics</i> , 2020, 8, 586287.	1.9	2
7	The Immunomodulatory Signature of Extracellular Vesicles From Cardiosphere-Derived Cells: A Proteomic and miRNA Profiling. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 321.	3.7	11
8	Multiplexed Quantitative Proteomic Analysis of HEK293 Provides Insights into Molecular Changes Associated with the Cell Density Effect, Transient Transfection, and Virus-Like Particle Production. <i>Journal of Proteome Research</i> , 2020, 19, 1085-1099.	3.7	23
9	Complement C5 Protein as a Marker of Subclinical Atherosclerosis. <i>Journal of the American College of Cardiology</i> , 2020, 75, 1926-1941.	2.8	32
10	Flow Cytometry Has a Significant Impact on the Cellular Metabolome. <i>Journal of Proteome Research</i> , 2019, 18, 169-181.	3.7	66
11	APOA1 oxidation is associated to dysfunctional high-density lipoproteins in human abdominal aortic aneurysm. <i>EBioMedicine</i> , 2019, 43, 43-53.	6.1	40
12	Preparation and characterization of <i>Nephila clavipes</i> tubuliform silk gut. <i>Soft Matter</i> , 2019, 15, 2960-2970.	2.7	9
13	Proteomics, Holm Oak (<i>Quercus ilex</i> L.) and Other Recalcitrant and Orphan Forest Tree Species: How do They See Each Other?. <i>International Journal of Molecular Sciences</i> , 2019, 20, 692.	4.1	20
14	CIBER-CLAP (CIBERCV Cardioprotection Large Animal Platform): A multicenter preclinical network for testing reproducibility in cardiovascular interventions. <i>Scientific Reports</i> , 2019, 9, 20290.	3.3	15
15	Unraveling the Molecular Signature of Extracellular Vesicles From Endometrial-Derived Mesenchymal Stem Cells: Potential Modulatory Effects and Therapeutic Applications. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019, 7, 431.	4.1	38
16	Extracellular vesicles derived from endometrial human mesenchymal stem cells enhance embryo yield and quality in an aged murine model. <i>Biology of Reproduction</i> , 2019, 100, 1180-1192.	2.7	44
17	SanXoT: a modular and versatile package for the quantitative analysis of high-throughput proteomics experiments. <i>Bioinformatics</i> , 2019, 35, 1594-1596.	4.1	59
18	The immunomodulatory activity of extracellular vesicles derived from endometrial mesenchymal stem cells on CD4+ T cells is partially mediated by TGFbeta. <i>Journal of Tissue Engineering and Regenerative Medicine</i> , 2018, 12, 2088-2098.	2.7	58

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19	Priming of dendritic cells by DNA-containing extracellular vesicles from activated T cells through antigen-driven contacts. <i>Nature Communications</i> , 2018, 9, 2658.	12.8	242
20	Murine embryos exposed to human endometrial MSCs-derived extracellular vesicles exhibit higher VEGF/PDGF AA release, increased blastomere count and hatching rates. <i>PLoS ONE</i> , 2018, 13, e0196080.	2.5	49
21	Identification of hepatic protein-protein interaction targets for betaine homocysteine S-methyltransferase. <i>PLoS ONE</i> , 2018, 13, e0199472.	2.5	4
22	Proteomic footprint of myocardial ischemia/reperfusion injury: Longitudinal study of the at-risk and remote regions in the pig model. <i>Scientific Reports</i> , 2017, 7, 12343.	3.3	37
23	HDAC6 controls innate immune and autophagy responses to TLR-mediated signalling by the intracellular bacteria <i>Listeria monocytogenes</i> . <i>PLoS Pathogens</i> , 2017, 13, e1006799.	4.7	38
24	The Application of Proteomic Techniques in the Study of HDL Particle Characterization and Biomarker Discovery. , 2017, , 231-255.		0
25	ISG15 governs mitochondrial function in macrophages following vaccinia virus infection. <i>PLoS Pathogens</i> , 2017, 13, e1006651.	4.7	75
26	CD69 controls the uptake of L-tryptophan through LAT1-CD98 and AhR-dependent secretion of IL-22 in psoriasis. <i>Nature Immunology</i> , 2016, 17, 985-996.	14.5	98
27	Quantitative HDL Proteomics Identifies Peroxiredoxin-6 as a Biomarker of Human Abdominal Aortic Aneurysm. <i>Scientific Reports</i> , 2016, 6, 38477.	3.3	29
28	Aurora A drives early signalling and vesicle dynamics during T-cell activation. <i>Nature Communications</i> , 2016, 7, 11389.	12.8	53
29	The apparent variability of silkworm (<i>Bombyx mori</i>) silk and its relationship with degumming. <i>European Polymer Journal</i> , 2016, 78, 129-140.	5.4	33
30	A Single In-Vial Dual Extraction Strategy for the Simultaneous Lipidomics and Proteomics Analysis of HDL and LDL Fractions. <i>Journal of Proteome Research</i> , 2016, 15, 1762-1775.	3.7	35
31	¹⁸ O proteomics reveal increased human apolipoprotein CIII in Hispanic HIV ⁺ women with HAART that use cocaine. <i>Proteomics - Clinical Applications</i> , 2016, 10, 144-155.	1.6	4
32	A Novel Systems-Biology Algorithm for the Analysis of Coordinated Protein Responses Using Quantitative Proteomics. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1740-1760.	3.8	86
33	ApoA-I/HDL-C levels are inversely associated with abdominal aortic aneurysm progression. <i>Thrombosis and Haemostasis</i> , 2015, 113, 1335-1346.	3.4	41
34	Unexpected behavior of irradiated spider silk links conformational freedom to mechanical performance. <i>Soft Matter</i> , 2015, 11, 4868-4878.	2.7	17
35	Mesenchymal stem cell-coated sutures enhance collagen depositions in sutured tissues. <i>Wound Repair and Regeneration</i> , 2014, 22, 256-264.	3.0	19
36	The human HDL proteome displays high inter-individual variability and is altered dynamically in response to angioplasty-induced atheroma plaque rupture. <i>Journal of Proteomics</i> , 2014, 106, 61-73.	2.4	30

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37	General Statistical Framework for Quantitative Proteomics by Stable Isotope Labeling. <i>Journal of Proteome Research</i> , 2014, 13, 1234-1247.	3.7	165
38	Quantitative Proteomics Analysis of High-Density Lipoproteins by Stable ¹⁸ O-Isotope Labeling. <i>Methods in Molecular Biology</i> , 2013, 1000, 139-156.	0.9	6
39	The Intracellular Interactome of Tetraspanin-enriched Microdomains Reveals Their Function as Sorting Machineries toward Exosomes. <i>Journal of Biological Chemistry</i> , 2013, 288, 11649-11661.	3.4	377
40	Beneficial effects of omega-3 fatty acids in the proteome of high-density lipoprotein proteome. <i>Lipids in Health and Disease</i> , 2012, 11, 116.	3.0	41
41	Quantitative proteomics by ² DE, ¹⁶ O/ ¹⁸ O labelling and linear ion trap mass spectrometry analysis of lymph nodes from piglets inoculated by porcine circovirus type 2. <i>Proteomics</i> , 2011, 11, 3452-3469.	2.2	22
42	Protein Identification and Quantification by Mass Spectrometry-Based Analysis: Applications in Plant-Pathogen Interactions Studies. <i>Current Proteomics</i> , 2010, 7, 234-243.	0.3	3
43	Statistical Model to Analyze Quantitative Proteomics Data Obtained by ¹⁸ O/ ¹⁶ O Labeling and Linear Ion Trap Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 1130-1149.	3.8	76
44	Connexin43 in cardiomyocyte mitochondria contributes to mitochondrial potassium uptake. <i>Cardiovascular Research</i> , 2009, 83, 747-756.	3.8	124
45	Changes in the protein profile of <i>Quercus ilex</i> leaves in response to drought stress and recovery. <i>Journal of Plant Physiology</i> , 2009, 166, 233-245.	3.5	101
46	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. <i>Journal of Mass Spectrometry</i> , 2007, 42, 1391-1403.	1.6	68
47	Proteomic analysis of phytopathogenic fungus <i>Botrytis cinerea</i> as a potential tool for identifying pathogenicity factors, therapeutic targets and for basic research. <i>Archives of Microbiology</i> , 2007, 187, 207-215.	2.2	70
48	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 <i>Fusarium oxysporum</i> f. sp. <i>ciceris</i> . <i>Canadian Journal of Botany</i> , 2006, 84, 1395-1404.	1.1	15
49	Variation in the holm oak leaf proteome at different plant developmental stages, between provenances and in response to drought stress. <i>Proteomics</i> , 2006, 6, S207-S214.	2.2	110
50	Two-dimensional electrophoresis protein profile of the phytopathogenic fungus <i>Botrytis cinerea</i> . <i>Proteomics</i> , 2006, 6, S88-S96.	2.2	70
51	Extracellular xylanases from two pathogenic races of <i>Fusarium oxysporum</i> f. sp. <i>ciceris</i> : enzyme production in culture and purification and characterization of a major isoform as an alkaline endo- β -(1,4)-xylanase of low molecular weight. <i>Antonie Van Leeuwenhoek</i> , 2005, 88, 48-59.	1.7	20
52	The Holm Oak leaf proteome: Analytical and biological variability in the protein expression level assessed by 2-DE and protein identification tandem mass spectrometry de novo sequencing and sequence similarity searching. <i>Proteomics</i> , 2005, 5, 222-234.	2.2	116