

Fernando De la Cuesta

List of Publications by Year in descending order

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Version: 2024-02-01

55
papers

1,546
citations

257101

24
h-index

315357

38
g-index

58
all docs

58
docs citations

58
times ranked

2517
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification of a urine metabolomic signature in patients with advanced-stage chronic kidney disease. <i>Kidney International</i> , 2014, 85, 103-111.	2.6	135
2	Diabetic nephropathy induces changes in the proteome of human urinary exosomes as revealed by label-free comparative analysis. <i>Journal of Proteomics</i> , 2014, 96, 92-102.	1.2	127
3	Metabolomic Profiling for Identification of Novel Potential Biomarkers in Cardiovascular Diseases. <i>Journal of Biomedicine and Biotechnology</i> , 2011, 2011, 1-9.	3.0	81
4	A Proteomic Focus on the Alterations Occurring at the Human Atherosclerotic Coronary Intima. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.003517.	2.5	71
5	Kidney tissue proteomics reveals regucalcin downregulation in response to diabetic nephropathy with reflection in urinary exosomes. <i>Translational Research</i> , 2015, 166, 474-484.e4.	2.2	62
6	Secretome analysis of atherosclerotic and non-atherosclerotic arteries reveals dynamic extracellular remodeling during pathogenesis. <i>Journal of Proteomics</i> , 2012, 75, 2960-2971.	1.2	56
7	Circulating Human Monocytes in the Acute Coronary Syndrome Express a Characteristic Proteomic Profile. <i>Journal of Proteome Research</i> , 2007, 6, 876-886.	1.8	52
8	Analysis of the Plasma Proteome Associated with Acute Coronary Syndrome: Does a Permanent Protein Signature Exist in the Plasma of ACS Patients?. <i>Journal of Proteome Research</i> , 2010, 9, 4420-4432.	1.8	52
9	Deregulation of smooth muscle cell cytoskeleton within the human atherosclerotic coronary media layer. <i>Journal of Proteomics</i> , 2013, 82, 155-165.	1.2	49
10	Transcriptional dynamics of pluripotent stem cell-derived endothelial cell differentiation revealed by single-cell RNA sequencing. <i>European Heart Journal</i> , 2020, 41, 1024-1036.	1.0	43
11	Extracellular vesicle cross-talk between pulmonary artery smooth muscle cells and endothelium during excessive TGF- β signalling: implications for PAH vascular remodelling. <i>Cell Communication and Signaling</i> , 2019, 17, 143.	2.7	41
12	Identification of a circulating microvesicle protein network involved in ST-elevation myocardial infarction. <i>Thrombosis and Haemostasis</i> , 2014, 112, 716-726.	1.8	39
13	MALDI-Imaging Mass Spectrometry: a step forward in the anatomopathological characterization of stenotic aortic valve tissue. <i>Scientific Reports</i> , 2016, 6, 27106.	1.6	39
14	iTRAQ proteomic analysis of extracellular matrix remodeling in aortic valve disease. <i>Scientific Reports</i> , 2015, 5, 17290.	1.6	36
15	Citric Acid Metabolism in Resistant Hypertension. <i>Hypertension</i> , 2017, 70, 1049-1056.	1.3	36
16	KLK1 and ZG16B proteins and arginine-proline metabolism identified as novel targets to monitor atherosclerosis, acute coronary syndrome and recovery. <i>Metabolomics</i> , 2015, 11, 1056-1067.	1.4	35
17	Cytoskeleton deregulation and impairment in amino acids and energy metabolism in early atherosclerosis at aortic tissue with reflection in plasma. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2016, 1862, 725-732.	1.8	35
18	Recent advances in atherosclerosis-based proteomics: new biomarkers and a future perspective. <i>Expert Review of Proteomics</i> , 2008, 5, 679-691.	1.3	34

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19	Patients with calcific aortic stenosis exhibit systemic molecular evidence of ischemia, enhanced coagulation, oxidative stress and impaired cholesterol transport. <i>International Journal of Cardiology</i> , 2016, 225, 99-106.	0.8	34
20	Proteomic characterization of human coronary thrombus in patients with ST-segment elevation acute myocardial infarction. <i>Journal of Proteomics</i> , 2014, 109, 368-381.	1.2	33
21	Urinary exosomes reveal protein signatures in hypertensive patients with albuminuria. <i>Oncotarget</i> , 2017, 8, 44217-44231.	0.8	33
22	Hypertensive patients exhibit an altered metabolism. A specific metabolite signature in urine is able to predict albuminuria progression. <i>Translational Research</i> , 2016, 178, 25-37.e7.	2.2	28
23	Molecular anatomy of ascending aorta in atherosclerosis by MS Imaging: Specific lipid and protein patterns reflect pathology. <i>Journal of Proteomics</i> , 2015, 126, 245-251.	1.2	27
24	Tissue proteomics in atherosclerosis: elucidating the molecular mechanisms of cardiovascular diseases. <i>Expert Review of Proteomics</i> , 2009, 6, 395-409.	1.3	24
25	Urinary alpha-1 antitrypsin and CD59 glycoprotein predict albuminuria development in hypertensive patients under chronic renin-angiotensin system suppression. <i>Cardiovascular Diabetology</i> , 2016, 15, 8.	2.7	24
26	Atorvastatin modifies the protein profile of circulating human monocytes after an acute coronary syndrome. <i>Proteomics</i> , 2009, 9, 1982-1993.	1.3	23
27	Modification of the Secretion Pattern of Proteases, Inflammatory Mediators, and Extracellular Matrix Proteins by Human Aortic Valve is Key in Severe Aortic Stenosis. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2426-2439.	2.5	23
28	Valvular Aortic Stenosis: A Proteomic Insight. <i>Clinical Medicine Insights: Cardiology</i> , 2010, 4, CMC.S3884.	0.6	22
29	Kalirin and CHD7: novel endothelial dysfunction indicators in circulating extracellular vesicles from hypertensive patients with albuminuria. <i>Oncotarget</i> , 2017, 8, 15553-15562.	0.8	20
30	Pharmacological Blockade of NLRP3 Inflammasome/IL-1 β -Positive Loop Mitigates Endothelial Cell Senescence and Dysfunction. , 2022, 13, 284.		19
31	A novel methodology for the analysis of membrane and cytosolic subproteomes of erythrocytes by 2-DE. <i>Electrophoresis</i> , 2009, 30, 4095-4108.	1.3	18
32	Prediction of development and maintenance of high albuminuria during chronic renin-angiotensin suppression by plasma proteomics. <i>International Journal of Cardiology</i> , 2015, 196, 170-177.	0.8	18
33	Plasma Molecular Signatures in Hypertensive Patients With Renin-Angiotensin System Suppression. <i>Hypertension</i> , 2016, 68, 157-166.	1.3	18
34	A role for the membrane proteome in human chronic kidney disease erythrocytes. <i>Translational Research</i> , 2012, 160, 374-383.	2.2	17
35	Potential Roles of Extracellular Vesicles as Biomarkers and a Novel Treatment Approach in Multiple Sclerosis. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9011.	1.8	16
36	Vascular proteomics. <i>Proteomics - Clinical Applications</i> , 2007, 1, 1102-1122.	0.8	14

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37	An optimum method designed for 2â€D DIGE analysis of human arterial intima and media layers isolated by laser microdissection. <i>Proteomics - Clinical Applications</i> , 2009, 3, 1174-1184.	0.8	14
38	A clinical perspective on the utility of alpha 1 antichymotrypsin for the early diagnosis of calcific aortic stenosis. <i>Clinical Proteomics</i> , 2017, 14, 12.	1.1	14
39	Lipid and protein maps defining arterial layers in atherosclerotic aorta. <i>Data in Brief</i> , 2015, 4, 328-331.	0.5	13
40	Immune system deregulation in hypertensive patients chronically RAS suppressed developing albuminuria. <i>Scientific Reports</i> , 2017, 7, 8894.	1.6	13
41	Obtenci3n de un protocolo 3ptimo para el an3lisis prote3mico de v3lvulas a3rticas humanas sanas y esten3ticas. <i>Revista Espanola De Cardiologia</i> , 2010, 63, 46-53.	0.6	9
42	Human Adenovirus Serotype 5 Is Sensitive to IgM-Independent Neutralization In Vitro and In Vivo. <i>Viruses</i> , 2019, 11, 616.	1.5	7
43	Cardiovascular Proteomics. <i>Current Proteomics</i> , 2006, 3, 147-170.	0.1	6
44	A comprehensive study of calcific aortic stenosis: from rabbit to human samples. <i>DMM Disease Models and Mechanisms</i> , 2018, 11, .	1.2	6
45	NLRP3 Inflammasome in Vascular Disease: A Recurrent Villain to Combat Pharmacologically. <i>Antioxidants</i> , 2022, 11, 269.	2.2	6
46	Development of an Optimal Protocol for the Proteomic Analysis of Stenotic and Healthy Aortic Valves. <i>Revista Espanola De Cardiologia (English Ed)</i> , 2010, 63, 46-53.	0.4	5
47	Pharmacoproteomics in Cardiac Hypertrophy and Atherosclerosis. <i>Cardiovascular & Hematological Disorders Drug Targets</i> , 2009, 9, 141-148.	0.2	4
48	Secretome of Human Aortic Valves. <i>Methods in Molecular Biology</i> , 2013, 1005, 237-243.	0.4	4
49	Characterization of Membrane and Cytosolic Proteins of Erythrocytes. <i>Methods in Molecular Biology</i> , 2013, 1000, 71-80.	0.4	4
50	Contribution of proteomics to the management of vascular disorders. <i>Translational Proteomics</i> , 2015, 7, 3-14.	1.2	3
51	Laser Microdissection and Saturation Labeling DIGE Method for the Analysis of Human Arteries. <i>Methods in Molecular Biology</i> , 2013, 1000, 21-32.	0.4	2
52	Two-Dimensional Electrophoresis and Identification by Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2017, 1592, 71-78.	0.4	1
53	Proteomic Analysis of Blood Extracellular Vesicles in Cardiovascular Disease by LC-MS/MS Analysis. <i>Methods in Molecular Biology</i> , 2017, 1619, 141-149.	0.4	1
54	Characterization and Analysis of Human Arterial Tissue Secretome by 2-DE and nLC-MS/MS. <i>Methods in Molecular Biology</i> , 2013, 1000, 81-90.	0.4	0

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55	Proteomics Toward Biomarkers Discovery and Risk Assessment. , 2013, , 115-130.		0