## Fernando De la Cuesta

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

54	1,154	21	<b>32</b>
papers	citations	h-index	g-index
58 ext. papers	1,388 ext. citations	4.6 avg, IF	3.68 L-index

#	Paper	IF	Citations
54	Pharmacological Blockade of NLRP3 Inflammasome/IL-1EPositive Loop Mitigates Endothelial Cell Senescence and Dysfunction. <b>2022</b> , 13, 284-297		4
53	Transcriptional dynamics of pluripotent stem cell-derived endothelial cell differentiation revealed by single-cell RNA sequencing. <i>European Heart Journal</i> , <b>2020</b> , 41, 1024-1036	9.5	15
52	Human Adenovirus Serotype 5 Is Sensitive to IgM-Independent Neutralization In Vitro and In Vivo. <i>Viruses</i> , <b>2019</b> , 11,	6.2	5
51	Extracellular vesicle cross-talk between pulmonary artery smooth muscle cells and endothelium during excessive TGF-Isignalling: implications for PAH vascular remodelling. <i>Cell Communication and Signaling</i> , <b>2019</b> , 17, 143	7.5	24
50	A comprehensive study of calcific aortic stenosis: from rabbit to human samples. <i>DMM Disease Models and Mechanisms</i> , <b>2018</b> , 11,	4.1	5
49	Two-Dimensional Electrophoresis and Identification by Mass Spectrometry. <i>Methods in Molecular Biology</i> , <b>2017</b> , 1592, 71-78	1.4	1
48	Immune system deregulation in hypertensive patients chronically RAS suppressed developing albuminuria. <i>Scientific Reports</i> , <b>2017</b> , 7, 8894	4.9	11
47	Citric Acid Metabolism in Resistant Hypertension: Underlying Mechanisms and Metabolic Prediction of Treatment Response. <i>Hypertension</i> , <b>2017</b> , 70, 1049-1056	8.5	25
46	Proteomic Analysis of Blood Extracellular Vesicles in Cardiovascular Disease by LC-MS/MS Analysis. <i>Methods in Molecular Biology</i> , <b>2017</b> , 1619, 141-149	1.4	1
45	A clinical perspective on the utility of alpha 1 antichymotrypsin for the early diagnosis of calcific aortic stenosis. <i>Clinical Proteomics</i> , <b>2017</b> , 14, 12	5	10
44	Kalirin and CHD7: novel endothelial dysfunction indicators in circulating extracellular vesicles from hypertensive patients with albuminuria. <i>Oncotarget</i> , <b>2017</b> , 8, 15553-15562	3.3	17
43	Urinary exosomes reveal protein signatures in hypertensive patients with albuminuria. <i>Oncotarget</i> , <b>2017</b> , 8, 44217-44231	3.3	23
42	Hypertensive patients exhibit an altered metabolism. A specific metabolite signature in urine is able to predict albuminuria progression. <i>Translational Research</i> , <b>2016</b> , 178, 25-37.e7	11	19
41	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> , <b>2016</b> , 225, 99-106	3.2	24
40	Plasma Molecular Signatures in Hypertensive Patients With Renin-Angiotensin System Suppression: New Predictors of Renal Damage and De Novo Albuminuria Indicators. <i>Hypertension</i> , <b>2016</b> , 68, 157-66	8.5	14
39	Urinary alpha-1 antitrypsin and CD59 glycoprotein predict albuminuria development in hypertensive patients under chronic renin-angiotensin system suppression. <i>Cardiovascular Diabetology</i> , <b>2016</b> , 15, 8	8.7	21
38	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> . <b>2016</b> . 1862. 725-732	6.9	20

## (2013-2016)

37	MALDI-Imaging Mass Spectrometry: a step forward in the anatomopathological characterization of stenotic aortic valve tissue. <i>Scientific Reports</i> , <b>2016</b> , 6, 27106	4.9	30
36	KLK1 and ZG16B proteins and arginine-proline metabolism identified as novel targets to monitor atherosclerosis, acute coronary syndrome and recovery. <i>Metabolomics</i> , <b>2015</b> , 11, 1056-1067	4.7	31
35	Contribution of proteomics to the management of vascular disorders. <i>Translational Proteomics</i> , <b>2015</b> , 7, 3-14		2
34	Molecular anatomy of ascending aorta in atherosclerosis by MS Imaging: Specific lipid and protein patterns reflect pathology. <i>Journal of Proteomics</i> , <b>2015</b> , 126, 245-51	3.9	23
33	Prediction of development and maintenance of high albuminuria during chronic renin-angiotensin suppression by plasma proteomics. <i>International Journal of Cardiology</i> , <b>2015</b> , 196, 170-7	3.2	16
32	Lipid and protein maps defining arterial layers in atherosclerotic aorta. <i>Data in Brief</i> , <b>2015</b> , 4, 328-31	1.2	12
31	iTRAQ proteomic analysis of extracellular matrix remodeling in aortic valve disease. <i>Scientific Reports</i> , <b>2015</b> , 5, 17290	4.9	26
30	Kidney tissue proteomics reveals regucalcin downregulation in response to diabetic nephropathy with reflection in urinary exosomes. <i>Translational Research</i> , <b>2015</b> , 166, 474-484.e4	11	43
29	Identification of a urine metabolomic signature in patients with advanced-stage chronic kidney disease. <i>Kidney International</i> , <b>2014</b> , 85, 103-11	9.9	102
28	Diabetic nephropathy induces changes in the proteome of human urinary exosomes as revealed by label-free comparative analysis. <i>Journal of Proteomics</i> , <b>2014</b> , 96, 92-102	3.9	101
27	Proteomic characterization of human coronary thrombus in patients with ST-segment elevation acute myocardial infarction. <i>Journal of Proteomics</i> , <b>2014</b> , 109, 368-81	3.9	18
26	Identification of a circulating microvesicle protein network involved in ST-elevation myocardial infarction. <i>Thrombosis and Haemostasis</i> , <b>2014</b> , 112, 716-26	7	31
25	Deregulation of smooth muscle cell cytoskeleton within the human atherosclerotic coronary media layer. <i>Journal of Proteomics</i> , <b>2013</b> , 82, 155-65	3.9	41
24	Secretome of human aortic valves. <i>Methods in Molecular Biology</i> , <b>2013</b> , 1005, 237-43	1.4	1
23	Characterization of membrane and cytosolic proteins of erythrocytes. <i>Methods in Molecular Biology</i> , <b>2013</b> , 1000, 71-80	1.4	3
22	Laser microdissection and saturation labeling DIGE method for the analysis of human arteries. <i>Methods in Molecular Biology</i> , <b>2013</b> , 1000, 21-32	1.4	1
21	Characterization and analysis of human arterial tissue secretome by 2-DE and nLC-MS/MS. <i>Methods in Molecular Biology</i> , <b>2013</b> , 1000, 81-90	1.4	
20	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> , <b>2013</b> , 12, 2426-39	7.6	17

Proteomics Toward Biomarkers Discovery and Risk Assessment **2013**, 115-130

18	Secretome analysis of atherosclerotic and non-atherosclerotic arteries reveals dynamic extracellular remodeling during pathogenesis. <i>Journal of Proteomics</i> , <b>2012</b> , 75, 2960-71	3.9	49
17	A role for the membrane proteome in human chronic kidney disease erythrocytes. <i>Translational Research</i> , <b>2012</b> , 160, 374-83	11	14
16	Metabolomic profiling for identification of novel potential biomarkers in cardiovascular diseases. Journal of Biomedicine and Biotechnology, <b>2011</b> , 2011, 790132		62
15	A proteomic focus on the alterations occurring at the human atherosclerotic coronary intima. <i>Molecular and Cellular Proteomics</i> , <b>2011</b> , 10, M110.003517	7.6	57
14	Development of an optimal protocol for the proteomic analysis of stenotic and healthy aortic valves. <i>Revista Espanola De Cardiologia (English Ed )</i> , <b>2010</b> , 63, 46-53	0.7	3
13	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> , <b>2010</b> , 9, 4420-32	5.6	39
12	Obtencifi de un protocolo fitimo para el anlisis protefhico de vlvulas afticas humanas sanas y estenficas. <i>Revista Espanola De Cardiologia</i> , <b>2010</b> , 63, 46-53	1.5	8
11	Valvular aortic stenosis: a proteomic insight. Clinical Medicine Insights: Cardiology, 2010, 4, 1-7	3.2	14
10	A novel methodology for the analysis of membrane and cytosolic sub-proteomes of erythrocytes by 2-DE. <i>Electrophoresis</i> , <b>2009</b> , 30, 4095-108	3.6	18
9	Atorvastatin modifies the protein profile of circulating human monocytes after an acute coronary syndrome. <i>Proteomics</i> , <b>2009</b> , 9, 1982-93	4.8	22
8	An optimum method designed for 2-D DIGE analysis of human arterial intima and media layers isolated by laser microdissection. <i>Proteomics - Clinical Applications</i> , <b>2009</b> , 3, 1174-84	3.1	12
7	Tissue proteomics in atherosclerosis: elucidating the molecular mechanisms of cardiovascular diseases. <i>Expert Review of Proteomics</i> , <b>2009</b> , 6, 395-409	4.2	17
6	Pharmacoproteomics in cardiac hypertrophy and atherosclerosis. <i>Cardiovascular &amp; Hematological Disorders Drug Targets</i> , <b>2009</b> , 9, 141-8	1.1	2
5	Recent advances in atherosclerosis-based proteomics: new biomarkers and a future perspective. <i>Expert Review of Proteomics</i> , <b>2008</b> , 5, 679-91	4.2	32
4	Vascular proteomics. <i>Proteomics - Clinical Applications</i> , <b>2007</b> , 1, 1102-22	3.1	13
3	Circulating human monocytes in the acute coronary syndrome express a characteristic proteomic profile. <i>Journal of Proteome Research</i> , <b>2007</b> , 6, 876-86	5.6	48
2	Cardiovascular Proteomics. <i>Current Proteomics</i> , <b>2006</b> , 3, 147-170	0.7	6

## LIST OF PUBLICATIONS

1 Cardiovascular Proteomics341-379