

Benito Cañas

List of Publications by Year in descending order

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46
papers

2,457
citations

126907

33
h-index

265206

42
g-index

46
all docs

46
docs citations

46
times ranked

2509
citing authors

#	ARTICLE	IF	CITATIONS
1	Trends in sample preparation for classical and second generation proteomics. Journal of Chromatography A, 2007, 1153, 235-258.	3.7	167
2	Species Differentiation of Seafood Spoilage and Pathogenic Gram-Negative Bacteria by MALDI-TOF Mass Fingerprinting. Journal of Proteome Research, 2010, 9, 3169-3183.	3.7	144
3	Elemental Bioimaging in Kidney by LA-ICP-MS As a Tool to Study Nephrotoxicity and Renal Protective Strategies in Cisplatin Therapies. Analytical Chemistry, 2011, 83, 7933-7940.	6.5	130
4	Mass spectrometry technologies for proteomics. Briefings in Functional Genomics & Proteomics, 2006, 4, 295-320.	3.8	102
5	Analytical methodologies for metallomics studies of antitumor Pt-containing drugs. Metallomics, 2010, 2, 19-38.	2.4	98
6	Rapid direct detection of the major fish allergen, parvalbumin, by selected MS/MS ion monitoring mass spectrometry. Journal of Proteomics, 2012, 75, 3211-3220.	2.4	94
7	Identification of commercial hake and grenadier species by proteomic analysis of the parvalbumin fraction. Proteomics, 2006, 6, 5278-5287.	2.2	90
8	Rapid species identification of seafood spoilage and pathogenic Gram-positive bacteria by MALDI-TOF mass fingerprinting. Electrophoresis, 2011, 32, 2951-2965.	2.4	85
9	Fast Monitoring of Species-Specific Peptide Biomarkers Using High-Intensity-Focused-Ultrasound-Assisted Tryptic Digestion and Selected MS/MS Ion Monitoring. Analytical Chemistry, 2011, 83, 5688-5695.	6.5	81
10	Improved in-gel approaches to generate peptide maps of integral membrane proteins with matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. Journal of Mass Spectrometry, 2002, 37, 322-330.	1.6	80
11	De Novo Mass Spectrometry Sequencing and Characterization of Species-Specific Peptides from Nucleoside Diphosphate Kinase B for the Classification of Commercial Fish Species Belonging to the Family Merlucciidae. Journal of Proteome Research, 2007, 6, 3070-3080.	3.7	74
12	Staphylococcus aureus Exotoxins and Their Detection in the Dairy Industry and Mastitis. Toxins, 2020, 12, 537.	3.4	74
13	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
14	Food authentication of commercially-relevant shrimp and prawn species: From classical methods to Foodomics. Electrophoresis, 2012, 33, 2201-2211.	2.4	62
15	SpectraBank: An open access tool for rapid microbial identification by MALDI-TOF MS fingerprinting. Electrophoresis, 2012, 33, 2138-2142.	2.4	61
16	Extensive De Novo Sequencing of New Parvalbumin Isoforms Using a Novel Combination of Bottom-Up Proteomics, Accurate Molecular Mass Measurement by FTICR-MS, and Selected MS/MS Ion Monitoring. Journal of Proteome Research, 2010, 9, 4393-4406.	3.7	60
17	Safety Assessment of Fresh and Processed Seafood Products by MALDI-TOF Mass Fingerprinting. Food and Bioprocess Technology, 2011, 4, 907-918.	4.7	59
18	Identification and classification of seafood-borne pathogenic and spoilage bacteria: 16S rRNA sequencing versus MALDI-TOF MS fingerprinting. Electrophoresis, 2013, 34, 877-887.	2.4	59

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19	Mass Spectrometry Characterization of Species-Specific Peptides from Arginine Kinase for the Identification of Commercially Relevant Shrimp Species. <i>Journal of Proteome Research</i> , 2009, 8, 5356-5362.	3.7	58
20	Human proteome enhancement: High-recovery method and improved two-dimensional map of colostrum fat globule membrane proteins. <i>Electrophoresis</i> , 2001, 22, 1810-1818.	2.4	57
21	Differential characterization of biogenic amine-producing bacteria involved in food poisoning using MALDI-TOF mass fingerprinting. <i>Electrophoresis</i> , 2010, 31, 1116-1127.	2.4	55
22	Combined in-gel tryptic digestion and CNBr cleavage for the generation of peptide maps of an integral membrane protein with MALDI-TOF mass spectrometry. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2002, 1555, 111-115.	1.0	51
23	Characterization of <i>Staphylococcus aureus</i> strains isolated from Italian dairy products by MALDI-TOF mass fingerprinting. <i>Electrophoresis</i> , 2012, 33, 2355-2364.	2.4	51
24	Selected tandem mass spectrometry ion monitoring for the fast identification of seafood species. <i>Journal of Chromatography A</i> , 2011, 1218, 4445-4451.	3.7	50
25	Top-Down Mass Spectrometric Approach for the Full Characterization of Insulin-Cisplatin Adducts. <i>Analytical Chemistry</i> , 2009, 81, 3507-3516.	6.5	49
26	Proteomics for the assessment of quality and safety of fishery products. <i>Food Research International</i> , 2013, 54, 972-979.	6.2	48
27	Novel insights into the bottom-up mass spectrometry proteomics approach for the characterization of Pt-binding proteins: The insulin-cisplatin case study. <i>Analyst</i> , 2010, 135, 1288.	3.5	44
28	The sarcoplasmic fish proteome: Pathways, metabolic networks and potential bioactive peptides for nutritional inferences. <i>Journal of Proteomics</i> , 2013, 78, 211-220.	2.4	43
29	Identification of commercial prawn and shrimp species of food interest by native isoelectric focusing. <i>Food Chemistry</i> , 2010, 121, 569-574.	8.2	42
30	Comparative analysis of protein extraction methods for the identification of seafood-borne pathogenic and spoilage bacteria by MALDI-TOF mass spectrometry. <i>Analytical Methods</i> , 2010, 2, 1941.	2.7	41
31	Arginine Kinase Peptide Mass Fingerprinting as a Proteomic Approach for Species Identification and Taxonomic Analysis of Commercially Relevant Shrimp Species. <i>Journal of Agricultural and Food Chemistry</i> , 2009, 57, 5665-5672.	5.2	37
32	Characterization of Pt-protein complexes by nHPLC-ESI-LTQ MS/MS using a gel-based bottom-up approach. <i>Talanta</i> , 2012, 88, 599-608.	5.5	36
33	LA-ICP-MS and nHPLC-ESI-LTQ-FT-MS/MS for the analysis of cisplatin-protein complexes separated by two dimensional gel electrophoresis in biological samples. <i>Journal of Analytical Atomic Spectrometry</i> , 2012, 27, 1474.	3.0	36
34	Species identification of the Northern shrimp (<i>Pandalus borealis</i>) by polymerase chain reaction-restriction fragment length polymorphism and proteomic analysis. <i>Analytical Biochemistry</i> , 2012, 421, 56-67.	2.4	33
35	Characterization of Foodborne Strains of <i>Staphylococcus aureus</i> by Shotgun Proteomics: Functional Networks, Virulence Factors and Species-Specific Peptide Biomarkers. <i>Frontiers in Microbiology</i> , 2017, 8, 2458.	3.5	32
36	OFFGEL isoelectric focusing and polyacrylamide gel electrophoresis separation of platinum-binding proteins. <i>Journal of Chromatography A</i> , 2011, 1218, 1281-1290.	3.7	29

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37	Advanced proteomics and systems biology applied to study food allergy. <i>Current Opinion in Food Science</i> , 2018, 22, 9-16.	8.0	18
38	Fast Global Phosphoproteome Profiling of Jurkat T Cells by HIFU-TiO ₂ -SCX-LC-MS/MS. <i>Analytical Chemistry</i> , 2017, 89, 8853-8862.	6.5	17
39	Characterization of Bacteriophage Peptides of Pathogenic <i>Streptococcus</i> by LC-ESI-MS/MS: Bacteriophage Phylogenomics and Their Relationship to Their Host. <i>Frontiers in Microbiology</i> , 2020, 11, 1241.	3.5	12
40	Discrimination of South African Commercial Fish Species (<i>Merluccius</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 627 Td (<i>capensis</i>) and Aquatic Food Product Technology, 2009, 18, 67-78.	1.4	10
41	Proteomic Characterization of Bacteriophage Peptides from the Mastitis Producer <i>Staphylococcus aureus</i> by LC-ESI-MS/MS and the Bacteriophage Phylogenomic Analysis. <i>Foods</i> , 2021, 10, 799.	4.3	9
42	Fish Authentication. , 2013, , 205-222.		5
43	Proteomics Tools for Food Fingerprints. <i>Comprehensive Analytical Chemistry</i> , 2014, , 201-222.	1.3	4
44	Proteomic Identification of Commercial Fish Species. , 2017, , 317-330.		2
45	Rapid Shotgun Analysis. <i>Methods in Molecular Biology</i> , 2021, 2259, 259-268.	0.9	0
46	A Method to Compare MALDI-TOF MS PMF Spectra and Its Application in Phyloproteomics. <i>Lecture Notes in Computer Science</i> , 2009, , 1147-1153.	1.3	0