

Gabriel PadrÃ³n

List of Publications by Year in descending order

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Version: 2024-02-01

30
papers

623
citations

758635

12
h-index

642321

23
g-index

32
all docs

32
docs citations

32
times ranked

766
citing authors

#	ARTICLE	IF	CITATIONS
1	Nitric Oxide Resistance in <i>Leishmania (Viannia) braziliensis</i> Involves Regulation of Glucose Consumption, Glutathione Metabolism and Abundance of Pentose Phosphate Pathway Enzymes. <i>Antioxidants</i> , 2022, 11, 277.	2.2	6
2	The OxyR and SoxR transcriptional regulators are involved in a broad oxidative stress response in <i>Paraburkholderia xenovorans</i> LB400. <i>Biological Research</i> , 2022, 55, 7.	1.5	1
3	In-Depth Quantitative Proteomics Characterization of In Vitro Selected Miltefosine Resistance in <i>Leishmania infantum</i> . <i>Proteomes</i> , 2022, 10, 10.	1.7	2
4	Quantitative analysis of proteins secreted by <i>Leishmania (Viannia) braziliensis</i> strains associated to distinct clinical manifestations of American Tegumentary Leishmaniasis. <i>Journal of Proteomics</i> , 2021, 232, 104077.	1.2	10
5	Biodistribution and pharmacokinetic profiles of an altered peptide ligand derived from heat-shock proteins 60 in Lewis rats. <i>Cell Stress and Chaperones</i> , 2020, 25, 133-140.	1.2	5
6	In-depth quantitative proteomics uncovers specie-specific metabolic programs in <i>Leishmania (Viannia)</i> species. <i>PLoS Neglected Tropical Diseases</i> , 2020, 14, e0008509.	1.3	10
7	Title is missing!. , 2020, 14, e0008509.		0
8	Title is missing!. , 2020, 14, e0008509.		0
9	Title is missing!. , 2020, 14, e0008509.		0
10	Title is missing!. , 2020, 14, e0008509.		0
11	The Combination of the CIGB-300 Anticancer Peptide and Cisplatin Modulates Proteins Related to Cell Survival, DNA Repair and Metastasis in a Lung Cancer Cell Line Model. <i>Current Proteomics</i> , 2019, 16, 338-349.	0.1	0
12	In-Depth Quantitative Proteomic Analysis of Trophozoites and Pseudocysts of <i>Trichomonas vaginalis</i> . <i>Journal of Proteome Research</i> , 2018, 17, 3704-3718.	1.8	21
13	APL1, an altered peptide ligand derived from human heat-shock protein 60, increases the frequency of Tregs and its suppressive capacity against antigen responding effector CD4 ⁺ T cells from rheumatoid arthritis patients. <i>Cell Stress and Chaperones</i> , 2016, 21, 735-744.	1.2	17
14	Proteomic Study to Survey the CIGB-552 Antitumor Effect. <i>BioMed Research International</i> , 2015, 2015, 1-18.	0.9	6
15	Computational proteomics: Integrating mass spectral data into a biological context. <i>Journal of Proteomics</i> , 2015, 129, 1-2.	1.2	0
16	Two decades of proteomics in Latin America: A personal view. <i>Journal of Proteomics</i> , 2014, 107, 83-92.	1.2	7
17	Computational proteomics pitfalls and challenges: HavanaBioinfo 2012 Workshop report. <i>Journal of Proteomics</i> , 2013, 87, 134-138.	1.2	19
18	Proteomic Profile Regulated by the Anticancer Peptide CIGB-300 in Non-Small Cell Lung Cancer (NSCLC) Cells. <i>Journal of Proteome Research</i> , 2010, 9, 5473-5483.	1.8	26

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19	Anaerobic growth promotes synthesis of colonization factors encoded at the <i>Vibrio</i> pathogenicity island in <i>Vibrio cholerae</i> El Tor. <i>Research in Microbiology</i> , 2009, 160, 48-56.	1.0	27
20	Proteomics Based on Peptide Fractionation by SDS-Free PAGE. <i>Journal of Proteome Research</i> , 2008, 7, 2427-2434.	1.8	18
21	Selective isolation of multiple positively charged peptides for 2-DE-free quantitative proteomics. <i>Proteomics</i> , 2006, 6, 4444-4455.	1.3	18
22	SCAPE: A New Tool for the Selective Capture of Peptides in Protein Identification. <i>Journal of Proteome Research</i> , 2005, 4, 491-496.	1.8	24
23	Identification of nuclear proteins of small cell lung cancer cell line H82: An improved procedure for the analysis of silver-stained proteins. <i>Electrophoresis</i> , 2003, 24, 237-252.	1.3	26
24	Automated interpretation of low-energy collision-induced dissociation spectra by SeqMS, a software aid for de novo sequencing by tandem mass spectrometry. <i>Electrophoresis</i> , 2000, 21, 1694-1699.	1.3	72
25	Differentiating β - and γ -aspartic acids by electrospray ionization and low-energy tandem mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2000, 14, 2092-2102.	0.7	67
26	The metastable decomposition of a peptide containing oxidized methionine(s) in matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 1999, 13, 1075-1076.	0.7	12
27	Structural characterization of <i>Acetobacter diazotrophicus</i> levansucrase by matrix-assisted laser desorption/ionization mass spectrometry: identification of an N-terminal blocking group and a free-thiol cysteine residue. , 1999, 34, 169-174.		11
28	Automated interpretation of high-energy collision-induced dissociation spectra of singly protonated peptides by 'seqms', a software aid for de novo sequencing by tandem mass spectrometry. , 1998, 12, 1867-1878.		43
29	Effect of the position of a basic amino acid on C-terminal rearrangement of protonated peptides upon collision-induced dissociation. , 1996, 31, 150-158.		55
30	A method for determination of N-glycosylation sites in glycoproteins by collision-induced dissociation analysis in fast atom bombardment mass spectrometry: Identification of the positions of carbohydrate-linked asparagine in recombinant α -amylase by treatment with peptide-N-glycosidase F in ^{18}O -labeled water. <i>Analytical Biochemistry</i> , 1992, 205, 151-158.	1.1	116