

Paulo Costa Carvalho

List of Publications by Year in descending order

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Version: 2024-02-01

107
papers

3,260
citations

257450

24
h-index

168389

53
g-index

108
all docs

108
docs citations

108
times ranked

5879
citing authors

#	ARTICLE	IF	CITATIONS
1	Refolding of metacaspase 5 from <i>Trypanosoma cruzi</i> , structural characterization and the influence of c-terminal in protein recombinant production. <i>Protein Expression and Purification</i> , 2022, 191, 106007.	1.3	2
2	Cross-linking mass spectrometry reveals structural insights of the glutamine synthetase from <i>Leishmania braziliensis</i> . <i>Memórias Do Instituto Oswaldo Cruz</i> , 2022, 116, e210209.	1.6	0
3	A fingerprint of plasma proteome alteration after local tissue damage induced by <i>Bothrops leucurus</i> snake venom in mice. <i>Journal of Proteomics</i> , 2022, 253, 104464.	2.4	9
4	Simple, efficient and thorough shotgun proteomic analysis with PatternLab V. <i>Nature Protocols</i> , 2022, 17, 1553-1578.	12.0	26
5	Platelet proteome reveals features of cell death, antiviral response and viral replication in covid-19. <i>Cell Death Discovery</i> , 2022, 8, .	4.7	15
6	Proteomic changes in <i>Trypanosoma cruzi</i> epimastigotes treated with the proapoptotic compound PAC-1. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2021, 1869, 140582.	2.3	3
7	The impact of blood-processing time on the proteome of human peripheral blood mononuclear cells. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2021, 1869, 140581.	2.3	6
8	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.	2.4	10
9	Characterizing protein conformers by cross-linking mass spectrometry and pattern recognition. <i>Bioinformatics</i> , 2021, 37, 3035-3037.	4.1	2
10	DiagnoTop: A Computational Pipeline for Discriminating Bacterial Pathogens without Database Search. <i>Journal of the American Society for Mass Spectrometry</i> , 2021, 32, 1295-1299.	2.8	4
11	Proteogenomics Reveals Orthologous Alternatively Spliced Proteoforms in the Same Human and Mouse Brain Regions with Differential Abundance in an Alzheimer's Disease Mouse Model. <i>Cells</i> , 2021, 10, 1583.	4.1	4
12	Proteome remodeling in the <i>Mycobacterium tuberculosis</i> PknG knockout: Molecular evidence for the role of this kinase in cell envelope biogenesis and hypoxia response. <i>Journal of Proteomics</i> , 2021, 244, 104276.	2.4	6
13	Synthesis, LC-MS/MS analysis, and biological evaluation of two vaccine candidates against ticks based on the antigenic PO peptide from <i>R. sanguineus</i> linked to the p64K carrier protein from <i>Neisseria meningitidis</i> . <i>Analytical and Bioanalytical Chemistry</i> , 2021, 413, 5885-5900.	3.7	3
14	Leveraging the partition selection bias to achieve a high-quality clustering of mass spectra. <i>Journal of Proteomics</i> , 2021, 245, 104282.	2.4	0
15	Molecular Architecture of the Antiophidic Protein DM64 and its Binding Specificity to Myotoxin II From <i>Bothrops asper</i> Venom. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 787368.	3.5	2
16	Proteogenomic Analysis Reveals Proteins Involved in the First Step of Adipogenesis in Human Adipose-Derived Stem Cells. <i>Stem Cells International</i> , 2021, 2021, 1-14.	2.5	5
17	Glycolytic profile shift and antioxidant triggering in symbiont-free and H ₂ O ₂ -resistant <i>Strigomonas culicis</i> . <i>Free Radical Biology and Medicine</i> , 2020, 146, 392-401.	2.9	4
18	<i>De novo</i> sequencing of proteins by mass spectrometry. <i>Expert Review of Proteomics</i> , 2020, 17, 595-607.	3.0	19

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19	Proteomics reveals that quinoa bioester promotes replenishing effects in epidermal tissue. <i>Scientific Reports</i> , 2020, 10, 19392.	3.3	4
20	Editorial. <i>Journal of Proteomics</i> , 2020, 228, 103937.	2.4	0
21	Mixed-Data Acquisition: Next-Generation Quantitative Proteomics Data Acquisition. <i>Journal of Proteomics</i> , 2020, 222, 103803.	2.4	8
22	RawVegetable – A data assessment tool for proteomics and cross-linking mass spectrometry experiments. <i>Journal of Proteomics</i> , 2020, 225, 103864.	2.4	10
23	Proteomics pinpoints alterations in grade I meningiomas of male versus female patients. <i>Scientific Reports</i> , 2020, 10, 10335.	3.3	10
24	Unveiling the partners of the DRBD2-mRNP complex, an RBP in <i>Trypanosoma cruzi</i> and ortholog to the yeast SR-protein Gbp2. <i>BMC Microbiology</i> , 2019, 19, 128.	3.3	17
25	Thymic Microenvironment Is Modified by Malnutrition and <i>Leishmania infantum</i> Infection. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 252.	3.9	25
26	Proteomic profiling of splenic interstitial fluid of malnourished mice infected with <i>Leishmania infantum</i> reveals defects on cell proliferation and pro-inflammatory response. <i>Journal of Proteomics</i> , 2019, 208, 103492.	2.4	7
27	A quantitation module for isotope-labeled peptides integrated into PatternLab for proteomics. <i>Journal of Proteomics</i> , 2019, 202, 103371.	2.4	1
28	Differential proteomic comparison of breast cancer secretome using a quantitative paired analysis workflow. <i>BMC Cancer</i> , 2019, 19, 365.	2.6	11
29	Top-Down Garbage Collector: a tool for selecting high-quality top-down proteomics mass spectra. <i>Bioinformatics</i> , 2019, 35, 3489-3490.	4.1	4
30	Data on antigen recognition hindrance by antibodies covalently immobilized to Protein G magnetic beads by dimethyl pimelimidate (DMP) cross-linking. <i>Data in Brief</i> , 2019, 22, 516-521.	1.0	1
31	Quantitative Proteomic Map of the Trypanosomatid <i>Strigomonas culicis</i> : The Biological Contribution of its Endosymbiotic Bacterium. <i>Protist</i> , 2019, 170, 125698.	1.5	5
32	Comprehensive identification of protein disulfide bonds with pepsin/trypsin digestion, Orbitrap HCD and Spectrum Identification Machine. <i>Journal of Proteomics</i> , 2019, 198, 78-86.	2.4	9
33	Interactome analysis of the human Cap-specific mRNA (nucleoside 2'-O-methyltransferase 1 (hMTr1) protein. <i>Journal of Cellular Biochemistry</i> , 2019, 120, 5597-5611.	2.6	5
34	<i>Trypanosoma cruzi</i> immunoproteome: Calpain-like CAP5.5 differentially detected throughout distinct stages of human Chagas disease cardiomyopathy. <i>Journal of Proteomics</i> , 2019, 194, 179-190.	2.4	12
35	New substrates and interactors of the mycobacterial Serine/Threonine protein kinase PknG identified by a tailored interactomic approach. <i>Journal of Proteomics</i> , 2019, 192, 321-333.	2.4	30
36	Characterization of homodimer interfaces with cross-linking mass spectrometry and isotopically labeled proteins. <i>Nature Protocols</i> , 2018, 13, 431-458.	12.0	47

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37	XPLex: An Effective, Multiplex Cross-Linking Chemistry for Acidic Residues. <i>Analytical Chemistry</i> , 2018, 90, 6043-6050.	6.5	18
38	Comparing intestinal versus diffuse gastric cancer using a PEFf-oriented proteomic pipeline. <i>Journal of Proteomics</i> , 2018, 171, 63-72.	2.4	11
39	Proteomic Deep Mining the Venom of the Red-Headed Krait, <i>Bungarus flaviceps</i> . <i>Toxins</i> , 2018, 10, 373.	3.4	16
40	A proteomic glimpse into the oncogenesis of prostate cancer. <i>Journal of Applied Biomedicine</i> , 2018, 16, 328-336.	1.7	3
41	Assessing the partners of the RBP9-mRNP complex in <i>Trypanosoma cruzi</i> using shotgun proteomics and RNA-seq. <i>RNA Biology</i> , 2018, 15, 1-13.	3.1	10
42	Identification of potential targets for an anticoagulant pectin. <i>Journal of Proteomics</i> , 2017, 151, 243-250.	2.4	2
43	Profiling the proteomics in honeybee worker brains submitted to the proboscis extension reflex. <i>Journal of Proteomics</i> , 2017, 151, 131-144.	2.4	7
44	An in-depth snake venom proteopeptidome characterization: Benchmarking <i>Bothrops jararaca</i> . <i>Journal of Proteomics</i> , 2017, 151, 214-231.	2.4	50
45	Dataset of proteins mapped on HepG2 cells and those differentially abundant after expression of the dengue non-structural 1 protein. <i>Data in Brief</i> , 2017, 10, 248-263.	1.0	3
46	DiagnoProt: a tool for discovery of new molecules by mass spectrometry. <i>Bioinformatics</i> , 2017, 33, 1883-1885.	4.1	7
47	Proteomic assessment of colorectal cancers and respective resection margins from patients of the Amazon state of Brazil. <i>Journal of Proteomics</i> , 2017, 154, 59-68.	2.4	4
48	Proteomic Analysis of Peripheral Blood Mononuclear Cells after a High-Fat, High-Carbohydrate Meal with Orange Juice. <i>Journal of Proteome Research</i> , 2017, 16, 4086-4092.	3.7	21
49	A multi-protease, multi-dissociation, bottom-up-to-top-down proteomic view of the <i>Loxosceles intermedia</i> venom. <i>Scientific Data</i> , 2017, 4, 170090.	5.3	21
50	Proteomic profiling of extracellular vesicles secreted from <i>Toxoplasma gondii</i> . <i>Proteomics</i> , 2017, 17, 1600477.	2.2	31
51	The effect of the dengue non-structural 1 protein expression over the HepG2 cell proteins in a proteomic approach. <i>Journal of Proteomics</i> , 2017, 152, 339-354.	2.4	6
52	Quantitative proteomic analysis of the <i>Saccharomyces cerevisiae</i> industrial strains CAT-1 and PE-2. <i>Journal of Proteomics</i> , 2017, 151, 114-121.	2.4	18
53	Platelet proteome reveals novel pathways of platelet activation and platelet-mediated immunoregulation in dengue. <i>PLoS Pathogens</i> , 2017, 13, e1006385.	4.7	76
54	The EAL-domain protein FcsR regulates flagella, chemotaxis and type III secretion system in <i>Pseudomonas aeruginosa</i> by a phosphodiesterase independent mechanism. <i>Scientific Reports</i> , 2017, 7, 10281.	3.3	19

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55	Considerations about gastric cancer proteomics. <i>Revista Do Colegio Brasileiro De Cirurgioes</i> , 2016, 43, 395-397.	0.6	2
56	A Time-Based and Intratumoral Proteomic Assessment of a Recurrent Glioblastoma Multiforme. <i>Frontiers in Oncology</i> , 2016, 6, 183.	2.8	13
57	Time-course proteome analysis of developing extrafloral nectaries of <i>Ricinus communis</i> . <i>Proteomics</i> , 2016, 16, 629-633.	2.2	17
58	An Evaluation of the Crystal Structure of C-terminal Truncated Apolipoprotein A-I in Solution Reveals Structural Dynamics Related to Lipid Binding. <i>Journal of Biological Chemistry</i> , 2016, 291, 5439-5451.	3.4	16
59	Integrated analysis of shotgun proteomic data with PatternLab for proteomics 4.0. <i>Nature Protocols</i> , 2016, 11, 102-117.	12.0	257
60	The Role of the <i>Trypanosoma cruzi</i> TcNRBD1 Protein in Translation. <i>PLoS ONE</i> , 2016, 11, e0164650.	2.5	10
61	Using PepExplorer to Filter and Organize <i>De Novo</i> Peptide Sequencing Results. <i>Current Protocols in Bioinformatics</i> , 2015, 51, 13.27.1-13.27.9.	25.8	4
62	Colorectal cancer DNA methylation patterns from patients in Manaus, Brazil. <i>Biological Research</i> , 2015, 48, 50.	3.4	7
63	Computational proteomics: Integrating mass spectral data into a biological context. <i>Journal of Proteomics</i> , 2015, 129, 1-2.	2.4	0
64	Proteomic profiling of nipple aspirate fluid (NAF): Exploring the complementarity of different peptide fractionation strategies. <i>Journal of Proteomics</i> , 2015, 117, 86-94.	2.4	18
65	SIM-XL: A powerful and user-friendly tool for peptide cross-linking analysis. <i>Journal of Proteomics</i> , 2015, 129, 51-55.	2.4	73
66	A scoring model for phosphopeptide site localization and its impact on the question of whether to use MSA. <i>Journal of Proteomics</i> , 2015, 129, 42-50.	2.4	9
67	Proteomic Analysis of the Endosperm Ontogeny of <i>Jatropha curcas</i> L. Seeds. <i>Journal of Proteome Research</i> , 2015, 14, 2557-2568.	3.7	21
68	Seeing beyond the tip of the iceberg: A deep analysis of the venom of the Brazilian Rattlesnake, <i>Crotalus durissus terrificus</i> . <i>EuPA Open Proteomics</i> , 2015, 8, 144-156.	2.5	21
69	Reevaluating the <i>Trypanosoma cruzi</i> proteomic map: The shotgun description of bloodstream trypomastigotes. <i>Journal of Proteomics</i> , 2015, 115, 58-65.	2.4	44
70	Interrogating the Venom of the Viperid Snake <i>Sistrurus catenatus edwardsii</i> by a Combined Approach of Electrospray and MALDI Mass Spectrometry. <i>PLoS ONE</i> , 2015, 10, e0092091.	2.5	26
71	On best practices in the development of bioinformatics software. <i>Frontiers in Genetics</i> , 2014, 5, 199.	2.3	53
72	Editorial (Thematic Issue: Genomics and Proteomics behind Drug Design). <i>Current Topics in Medicinal Chemistry</i> , 2014, 14, 343-343.	2.1	0

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73	The influence of iron on the proteomic profile of <i>Chromobacterium violaceum</i> . <i>BMC Microbiology</i> , 2014, 14, 267.	3.3	7
74	Expression of the mevalonate pathway enzymes in the <i>Lutzomyia longipalpis</i> (Diptera: Psychodidae) sex pheromone gland demonstrated by an integrated proteomic approach. <i>Journal of Proteomics</i> , 2014, 96, 117-132.	2.4	15
75	Deciphering the Human Brain Proteome: Characterization of the Anterior Temporal Lobe and Corpus Callosum As Part of the Chromosome 15-centric Human Proteome Project. <i>Journal of Proteome Research</i> , 2014, 13, 147-157.	3.7	16
76	Exploring the Proteomic Landscape of a Gastric Cancer Biopsy with the Shotgun Imaging Analyzer. <i>Journal of Proteome Research</i> , 2014, 13, 314-320.	3.7	18
77	PepExplorer: A Similarity-driven Tool for Analyzing de Novo Sequencing Results. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2480-2489.	3.8	33
78	Proteome Analysis of the Inner Integument from Developing <i>Jatropha curcas</i> L. Seeds. <i>Journal of Proteome Research</i> , 2014, 13, 3562-3570.	3.7	14
79	Comparative Proteomic Analysis of the Aging Soleus and Extensor Digitorum Longus Rat Muscles Using TMT Labeling and Mass Spectrometry. <i>Journal of Proteome Research</i> , 2013, 12, 4532-4546.	3.7	24
80	Proteome Analysis of Plastids from Developing Seeds of <i>Jatropha curcas</i> L.. <i>Journal of Proteome Research</i> , 2013, 12, 5137-5145.	3.7	17
81	HI-Bone: A Scoring System for Identifying Phenylisothiocyanate-Derivatized Peptides Based on Precursor Mass and High Intensity Fragment Ions. <i>Analytical Chemistry</i> , 2013, 85, 3515-3520.	6.5	7
82	Effectively addressing complex proteomic search spaces with peptide spectrum matching. <i>Bioinformatics</i> , 2013, 29, 1343-1344.	4.1	20
83	Single-Step Inline Hydroxyapatite Enrichment Facilitates Identification and Quantitation of Phosphopeptides from Mass-Limited Proteomes with MudPIT. <i>Journal of Proteome Research</i> , 2012, 11, 2697-2709.	3.7	56
84	Improving the TFold test for differential shotgun proteomics. <i>Bioinformatics</i> , 2012, 28, 1652-1654.	4.1	73
85	Toward objective evaluation of proteomic algorithms. <i>Nature Methods</i> , 2012, 9, 455-456.	19.0	35
86	PatternLab: From Mass Spectra to Label-Free Differential Shotgun Proteomics. <i>Current Protocols in Bioinformatics</i> , 2012, 40, Unit13.19.	25.8	39
87	Are Gastric Cancer Resection Margin Proteomic Profiles More Similar to Those from Controls or Tumors?. <i>Journal of Proteome Research</i> , 2012, 11, 5836-5842.	3.7	24
88	Proteomic Profiling of the Influence of Iron Availability on <i>Cryptococcus gattii</i> . <i>Journal of Proteome Research</i> , 2012, 11, 189-205.	3.7	20
89	Search engine processor: Filtering and organizing peptide spectrum matches. <i>Proteomics</i> , 2012, 12, 944-949.	2.2	107
90	Tools and challenges for diversity-driven proteomics in Brazil. <i>Proteomics</i> , 2012, 12, 2601-2606.	2.2	4

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91	Improvements in Proteomic Metrics of Low Abundance Proteins through Proteome Equalization Using ProteoMiner Prior to MudPIT. <i>Journal of Proteome Research</i> , 2011, 10, 3690-3700.	3.7	86
92	Chemo-Resistant Protein Expression Pattern of Glioblastoma Cells (A172) to Perillyl Alcohol. <i>Journal of Proteome Research</i> , 2011, 10, 153-160.	3.7	23
93	Can the false discovery rate be misleading?. <i>Proteomics</i> , 2011, 11, 4105-4108.	2.2	34
94	Analyzing marginal cases in differential shotgun proteomics. <i>Bioinformatics</i> , 2011, 27, 275-276.	4.1	474
95	Dynamic proteomic overview of glioblastoma cells (A172) exposed to perillyl alcohol. <i>Journal of Proteomics</i> , 2010, 73, 1018-1027.	2.4	23
96	PYR/PYL/RCAR family members are major <i>in vivo</i> ABI1 protein phosphatase 2C interacting proteins in Arabidopsis. <i>Plant Journal</i> , 2010, 61, 290-299.	5.7	451
97	XDIA: improving on the label-free data-independent analysis. <i>Bioinformatics</i> , 2010, 26, 847-848.	4.1	104
98	Analyzing Shotgun Proteomic Data with PatternLab for Proteomics. <i>Current Protocols in Bioinformatics</i> , 2010, 30, Unit 13.13.1-15.	25.8	24
99	YADA: a tool for taking the most out of high-resolution spectra. <i>Bioinformatics</i> , 2009, 25, 2734-2736.	4.1	67
100	Charge Prediction Machine: Tool for Inferring Precursor Charge States of Electron Transfer Dissociation Tandem Mass Spectra. <i>Analytical Chemistry</i> , 2009, 81, 1996-2003.	6.5	15
101	GO Explorer: A gene-ontology tool to aid in the interpretation of shotgun proteomics data. <i>Proteome Science</i> , 2009, 7, 6.	1.7	35
102	Caititu: A tool to graphically represent peptide sequence coverage and domain distribution. <i>Journal of Proteomics</i> , 2008, 71, 486-489.	2.4	19
103	PatternLab for proteomics: a tool for differential shotgun proteomics. <i>BMC Bioinformatics</i> , 2008, 9, 316.	2.6	127
104	Marcadores s3ricos e espectrometria de massa no diagn3stico do c4ncer. <i>Jornal Brasileiro De Patologia E Medicina Laboratorial</i> , 2006, 42, 431.	0.3	2
105	Efeito do 4lcool per4lico na express4o g4nica de c4lulas de adenocarcinoma de pulm4o humano. <i>Jornal Brasileiro De Pneumologia</i> , 2005, 31, 511-515.	0.7	2
106	Detec4o molecular da reativa4o simult4nea de VZV e HSV em paciente com hist4ria cl4nica de roseola infantum. <i>Jornal Brasileiro De Patologia E Medicina Laboratorial</i> , 2003, 39, 207.	0.3	1
107	Using SIM-XL to identify and annotate cross-linked peptides analyzed by mass spectrometry. <i>Protocol Exchange</i> , 0, , .	0.3	4