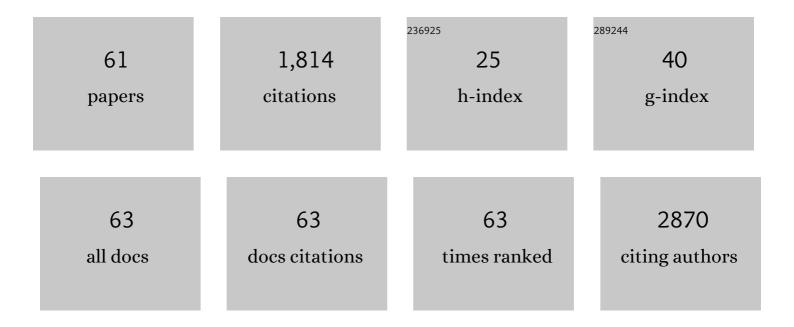
## Gustavo H M F Souza

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Proteomic analysis of dorsolateral prefrontal cortex indicates the involvement of cytoskeleton, oligodendrocyte, energy metabolism and new potential markers in schizophrenia. Journal of Psychiatric Research, 2009, 43, 978-986.	3.1	165
2	Purification and characterization of a keratinolytic metalloprotease from Chryseobacterium sp. kr6. Journal of Biotechnology, 2007, 128, 693-703.	3.8	118
3	A chitin-like component in Aedes aegypti eggshells, eggs and ovaries. Insect Biochemistry and Molecular Biology, 2007, 37, 1249-1261.	2.7	94
4	Detection and expression analysis of recombinant proteins in plantâ€derived complex mixtures using nanoUPLCâ€MS <sup>E</sup> . Journal of Separation Science, 2011, 34, 2618-2630.	2.5	86
5	Baseline resolution of isomers by traveling wave ion mobility mass spectrometry: investigating the effects of polarizable drift gases and ionic charge distribution. Journal of Mass Spectrometry, 2013, 48, 989-997.	1.6	77
6	Proteomic analysis of seminal plasma in adolescents with and without varicocele. Fertility and Sterility, 2013, 99, 92-98.	1.0	67
7	Label-Free Quantitative Proteomics of Embryogenic and Non-Embryogenic Callus during Sugarcane Somatic Embryogenesis. PLoS ONE, 2015, 10, e0127803.	2.5	65
8	Secretome of the preimplantation human embryo by bottom-up label-free proteomics. Analytical and Bioanalytical Chemistry, 2011, 401, 1331-9.	3.7	53
9	Longissimus dorsi muscle label-free quantitative proteomic reveals biological mechanisms associated with intramuscular fat deposition. Journal of Proteomics, 2018, 179, 30-41.	2.4	53
10	Biological and biochemical characterization of new basic phospholipase A2 BmTX-I isolated from Bothrops moojeni snake venom. Toxicon, 2008, 51, 1509-1519.	1.6	46
11	Expression of functional recombinant human growth hormone in transgenic soybean seeds. Transgenic Research, 2011, 20, 811-826.	2.4	44
12	Labelâ€free MS <sup>E</sup> proteomic analysis of chronic myeloid leukemia bone marrow plasma: disclosing new insights from therapy resistance. Proteomics, 2012, 12, 2618-2631.	2.2	42
13	Diacerhein downregulate proinflammatory cytokines expression and decrease the autoimmune diabetes frequency in nonobese diabetic (NOD) mice. International Immunopharmacology, 2008, 8, 782-791.	3.8	40
14	Accumulation of functional recombinant human coagulation factor IX in transgenic soybean seeds. Transgenic Research, 2011, 20, 841-855.	2.4	39
15	LC-MSE, Multiplex MS/MS, Ion Mobility, and Label-Free Quantitation in Clinical Proteomics. Methods in Molecular Biology, 2017, 1546, 57-73.	0.9	36
16	Peptidomics of Acanthoscurria gomesiana spider venom reveals new toxins with potential antimicrobial activity. Journal of Proteomics, 2017, 151, 232-242.	2.4	36
17	Evaluation of metal-ion stress in sunflower (Helianthus annuus L.) leaves through proteomic changes. Metallomics, 2009, 1, 107-113.	2.4	34
18	Purification, sequencing and structural analysis of two acidic phospholipases A2 from the venom of Bothrops insularis (jararaca ilhoa). Biochimie, 2006, 88, 1947-1959.	2.6	32

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19	Differential Metabolism of a Two-Carbon Substrate by Members of the Paracoccidioides Genus. Frontiers in Microbiology, 2017, 8, 2308.	3.5	32
20	Peptide fingerprinting of snake venoms by direct infusion nanoâ€electrospray ionization mass spectrometry: potential use in venom identification and taxonomy. Journal of Mass Spectrometry, 2008, 43, 594-599.	1.6	30
21	Label-Free Proteome Analysis of Plasma from Patients with Breast Cancer: Stage-Specific Protein Expression. Frontiers in Oncology, 2017, 7, 14.	2.8	30
22	Label-free proteomic analysis to confirm the predicted proteome of Corynebacterium pseudotuberculosis under nitrosative stress mediated by nitric oxide. BMC Genomics, 2014, 15, 1065.	2.8	29
23	Proteomics in quality control: Whey protein-based supplements. Journal of Proteomics, 2016, 147, 48-55.	2.4	28
24	Differential seminal plasma proteome according to semen retrieval in men with spinal cord injury. Fertility and Sterility, 2013, 100, 959-969.e3.	1.0	27
25	Comparative metallomics for transgenic and non-transgenic soybeans. Journal of Analytical Atomic Spectrometry, 2007, 22, 1501.	3.0	25
26	Evaluation of sample preparation protocols for proteomic analysis of sunflower leaves. Talanta, 2010, 80, 1545-1551.	5.5	24
27	ESI-MS/MS Identification of a Bradykinin-Potentiating Peptide from Amazon Bothrops atrox Snake Venom Using a Hybrid Qq-oaTOF Mass Spectrometer. Toxins, 2013, 5, 327-335.	3.4	23
28	Delineation of the pan-proteome of fish-pathogenic Streptococcus agalactiae strains using a label-free shotgun approach. BMC Genomics, 2019, 20, 11.	2.8	23
29	Characterization of the mechanisms underlying the inflammatory response to Polistes lanio lanio (paper wasp) venom in mouse dorsal skin. Toxicon, 2009, 53, 42-52.	1.6	22
30	Differential expression of albumins and globulins of wheat flours of different technological qualities revealed by nanoUPLC-UDMSE. Food Chemistry, 2018, 239, 1027-1036.	8.2	22
31	Non-targeted sportomics analyses by mass spectrometry to understand exercise-induced metabolic stress in soccer players. International Journal of Mass Spectrometry, 2017, 418, 1-5.	1.5	21
32	Discovering the infectome of human endothelial cells challenged with Aspergillus fumigatus applying a mass spectrometry label-free approach. Journal of Proteomics, 2014, 97, 126-140.	2.4	20
33	Immune Response Resetting in Ongoing Sepsis. Journal of Immunology, 2019, 203, 1298-1312.	0.8	20
34	Separation of glycosidic catiomers by TWIMâ€MS using CO <sub>2</sub> as a drift gas. Journal of Mass Spectrometry, 2015, 50, 336-343.	1.6	19
35	Comparative proteomic analysis of four biotechnological strains <i>Lactococcus lactis</i> through labelâ€free quantitative proteomics. Microbial Biotechnology, 2019, 12, 265-274.	4.2	19
36	Immunogenic and allergenic profile of wheat flours from different technological qualities revealed by ion mobility mass spectrometry. Journal of Food Composition and Analysis, 2018, 73, 67-75.	3.9	18

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37	Mass spectrometry fingerprinting of media used for <i>in vitro</i> production of bovine embryos. Rapid Communications in Mass Spectrometry, 2009, 23, 1313-1320.	1.5	17
38	Structural and kinetic characterization of a maize aldose reductase. Plant Physiology and Biochemistry, 2009, 47, 98-104.	5.8	17
39	Effect of endometriosis on the protein expression pattern of follicular fluid from patients submitted to controlled ovarian hyperstimulation for in vitro fertilization. Human Reproduction, 2010, 25, 1755-1766.	0.9	17
40	Label-free quantitative proteomics of Corynebacterium pseudotuberculosis isolates reveals differences between Biovars ovis and equi strains. BMC Genomics, 2017, 18, 451.	2.8	17
41	A shift in the virulence potential of Corynebacterium pseudotuberculosis biovar ovis after passage in a murine host demonstrated through comparative proteomics. BMC Microbiology, 2017, 17, 55.	3.3	16
42	Ion Mobilityâ€Enhanced Dataâ€Independent Acquisitions Enable a Deep Proteomic Landscape of Oligodendrocytes. Proteomics, 2017, 17, 1700209.	2.2	15
43	Structural and functional characterization of myotoxin, Cr-IV 1, a phospholipase A2 D49 from the venom of the snake Calloselasma rhodostoma. Biologicals, 2008, 36, 168-176.	1.4	14
44	Intrinsic Mobility of Gaseous Cationic and Anionic Aggregates of Ionic Liquids. ChemPhysChem, 2011, 12, 1444-1447.	2.1	14
45	Relationship Between Expression of Voltage-Dependent Anion Channel (VDAC) Isoforms and Type of Hexokinase Binding Sites on Brain Mitochondria. Journal of Molecular Neuroscience, 2010, 41, 48-54.	2.3	13
46	Quantitative Proteomic Analysis Reveals Changes in the Benchmark Corynebacterium pseudotuberculosis Biovar Equi Exoproteome after Passage in a Murine Host. Frontiers in Cellular and Infection Microbiology, 2017, 7, 325.	3.9	12
47	Neuromuscular action of venom from the South American colubrid snake Philodryas patagoniensis. Comparative Biochemistry and Physiology Part - C: Toxicology and Pharmacology, 2008, 148, 31-38.	2.6	11
48	Saliva proteomics from children with caries at different severity stages. Oral Diseases, 2020, 26, 1219-1229.	3.0	11
49	Investigating the Potential of Ion Mobility-Mass Spectrometry for Microalgae Biomass Characterization. Analytical Chemistry, 2019, 91, 9266-9276.	6.5	10
50	The catalytic mechanism of indole-3-glycerol phosphate synthase (IGPS) investigated by electrospray ionization (tandem) mass spectrometry. Tetrahedron Letters, 2008, 49, 5914-5917.	1.4	9
51	Modifications to the composition of the hyphal outer layer of Aspergillus fumigatus modulates HUVEC proteins related to inflammatory and stress responses. Journal of Proteomics, 2017, 151, 83-96.	2.4	9
52	Albumin Is Synthesized in Epididymis and Aggregates in a High Molecular Mass Glycoprotein Complex Involved in Sperm-Egg Fertilization. PLoS ONE, 2014, 9, e103566.	2.5	9
53	Proteomic analysis of Chromobacterium violaceum and its adaptability to stress. BMC Microbiology, 2015, 15, 272.	3.3	7
54	Dataset of differentially regulated proteins in HUVECs challenged with wild type and UGM1 mutant Aspergillus fumigatus strains. Data in Brief, 2016, 9, 24-31.	1.0	6

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55	Data from proteomic analysis of bovine Longissimus dorsi muscle associated with intramuscular fat content. Data in Brief, 2018, 19, 1314-1317.	1.0	6
56	Vanilla bahiana, a contribution from the Atlantic Forest biodiversity for the production of vanilla: A proteomic approach through high-definition nanoLC/MS. Food Research International, 2019, 120, 148-156.	6.2	6
57	Quantitative Proteomic Analysis of MARC-145 Cells Infected with a Mexican Porcine Reproductive and Respiratory Syndrome Virus Strain Using a Label-Free Based DIA approach. Journal of the American Society for Mass Spectrometry, 2020, 31, 1302-1312.	2.8	6
58	Electrophoresis and spectrometric analyses of adaptation-related proteins in thermally stressed Chromobacterium violaceum. Genetics and Molecular Research, 2013, 12, 5057-5071.	0.2	5
59	Tri―and dipeptides identification in whey protein and porcine liver protein hydrolysates by fast LC–MS/MS neutral loss screening and <i>de novo</i> sequencing. Journal of Mass Spectrometry, 2021, 56, e4701.	1.6	4
60	Proteome alterations associated with the oleic acid and cis-9, trans-11 conjugated linoleic acid content in bovine skeletal muscle. Journal of Proteomics, 2020, 222, 103792.	2.4	2
61	Human Blood Plasma Investigation Employing 2D UPLC-UDMSE Data-Independent Acquisition Proteomics. Methods in Molecular Biology, 2021, 2259, 153-165.	0.9	1