Luciana Pizzatti

List of Publications by Year in descending order

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ΙΠΟΙΔΝΙΑ ΡΙΖΖΑΤΤΙ

#	Article	IF	CITATIONS
1	Stability of human mesenchymal stem cells during <i>in vitro</i> culture: considerations for cell therapy. Cell Proliferation, 2013, 46, 10-22.	5.3	93
2	Wnt/β-catenin pathway regulates ABCB1 transcription in chronic myeloid leukemia. BMC Cancer, 2012, 12, 303.	2.6	89
3	Putative circulating markers of the early and advanced stages of breast cancer identified by high-resolution label-free proteomics. Cancer Letters, 2013, 330, 57-66.	7.2	52
4	Labelâ€free MS ^E proteomic analysis of chronic myeloid leukemia bone marrow plasma: disclosing new insights from therapy resistance. Proteomics, 2012, 12, 2618-2631.	2.2	42
5	Oxidative Stress, Redox Signaling and Cancer Chemoresistance: Putting Together the Pieces of the Puzzle. Current Medicinal Chemistry, 2014, 21, 3211-3226.	2.4	37
6	Identifying potential markers in Breast Cancer subtypes using plasma label-free proteomics. Journal of Proteomics, 2017, 151, 33-42.	2.4	35
7	Label-Free Proteomic Analysis of Breast Cancer Molecular Subtypes. Journal of Proteome Research, 2014, 13, 4752-4772.	3.7	34
8	Kaurenoic Acid Possesses Leishmanicidal Activity by Triggering a NLRP12/IL-1 <i>β</i> /cNOS/NO Pathway. Mediators of Inflammation, 2015, 2015, 1-10.	3.0	34
9	Altered protein profile in chronic myeloid leukemia chronic phase identified by a comparative proteomic study. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2006, 1764, 929-942.	2.3	28
10	SMAD 8 binding to mice Msx1 basal promoter is required for transcriptional activation. Biochemical Journal, 2006, 393, 141-150.	3.7	27
11	Clinical proteomics in cancer: Where we are. Cancer Letters, 2016, 382, 231-239.	7.2	27
12	SUZ12 is a candidate target of the non anonical WNT pathway in the progression of chronic myeloid leukemia. Genes Chromosomes and Cancer, 2010, 49, 107-118.	2.8	26
13	Doping control analysis at the Rio 2016 Olympic and Paralympic Games. Drug Testing and Analysis, 2017, 9, 1658-1672.	2.6	26
14	Label-Free Proteomics Revealed Oxidative Stress and Inflammation as Factors That Enhance Chemoresistance in Luminal Breast Cancer. Oxidative Medicine and Cellular Longevity, 2019, 2019, 1-15.	4.0	25
15	Knock-down of Kaiso induces proliferation and blocks granulocytic differentiation in blast crisis of chronic myeloid leukemia. Cancer Cell International, 2012, 12, 28.	4.1	22
16	The positive is inside the negative: HER2-negative tumors can express the HER2 intracellular domain and present a HER2-positive phenotype. Cancer Letters, 2015, 357, 186-195.	7.2	22
17	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
18	Proteomic Workflows for High-Quality Quantitative Proteome and Post-Translational Modification Analysis of Clinically Relevant Samples from Formalin-Fixed Paraffin-Embedded Archives. Journal of Proteome Research, 2021, 20, 1027-1039.	3.7	20

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19	The Human Melanoma Proteome Atlas—Complementing the melanoma transcriptome. Clinical and Translational Medicine, 2021, 11, e451.	4.0	20
20	A comparative proteomic study identified LRPPRC and MCM7 as putative actors in imatinib mesylate cross-resistance in Lucena cell line. Proteome Science, 2012, 10, 23.	1.7	18
21	Short infusion of paclitaxel imbalances plasmatic lipid metabolism and correlates with cardiac markers of acute damage in patients with breast cancer. Cancer Chemotherapy and Pharmacology, 2017, 80, 469-478.	2.3	18
22	Toxicoproteomics Disclose Pesticides as Downregulators of TNF-α, IL-1β and Estrogen Receptor Pathways in Breast Cancer Women Chronically Exposed. Frontiers in Oncology, 2020, 10, 1698.	2.8	14
23	The human melanoma proteome atlas—Defining the molecular pathology. Clinical and Translational Medicine, 2021, 11, e473.	4.0	14
24	Gene doping and genomic science in sports: where are we?. Bioanalysis, 2020, 12, 801-811.	1.5	12
25	How can Proteomics Reach Cancer Biomarkers?. Current Proteomics, 2013, 10, 136-149.	0.3	12
26	Similar proteomic profiles of human mesenchymal stromal cells from different donors. Cytotherapy, 2009, 11, 268-277.	0.7	11
27	Early downregulation of acute phase proteins after doxorubicin exposition in patients with breast cancer. Tumor Biology, 2016, 37, 3775-3783.	1.8	10
28	Mechanisms of kidney repair by human mesenchymal stromal cells after ischemia: A comprehensive view using labelâ€free <scp>MS</scp> ^E . Proteomics, 2014, 14, 1480-1493.	2.2	9
29	RUNX1T1 is overexpressed in imatinib mesylate-resistant cells. Molecular Medicine Reports, 2009, 2, 657-61.	2.4	7
30	Running ahead of doping: analytical advances and challenges faced by modern laboratories ahead of Rio 2016. Bioanalysis, 2016, 8, 1753-1756.	1.5	6
31	SPARC-like1 mRNA is overexpressed in human uterine leiomyoma. Molecular Medicine Reports, 0, , .	2.4	5
32	SPARC-like1 mRNA is overexpressed in human uterine leiomyoma. Molecular Medicine Reports, 2008, 1, 571-4.	2.4	5
33	Mapping the Melanoma Plasma Proteome (MPP) Using Single-Shot Proteomics Interfaced with the WiMT Database. Cancers, 2021, 13, 6224.	3.7	4
34	Otx2 is a putative candidate to activate mice Msx1 gene from distal enhancer. Biochemical and Biophysical Research Communications, 2007, 358, 655-660.	2.1	3
35	Polymorphisms at CYP enzymes, NR112 and NR113 in association with virologic response to antiretroviral therapy in Brazilian HIV-positive individuals. Pharmacogenomics Journal, 2021, , .	2.0	1
36	Changes in protein expression due to deleterious mutations in the FA/BRCA pathway. Biochemical and Biophysical Research Communications, 2007, 364, 755-760.	2.1	0

#	Article	IF	CITATIONS
37	Investigation of a new oxazolidine derivative in human resistance acute leukemia cells: deciphering its mechanism of action by label-free proteomic. Naunyn-Schmiedeberg's Archives of Pharmacology, 2021, 394, 1153-1166.	3.0	0

Networks Establishing Hematopoietic Stem Cell Multipotency and Self-Renewal. , 0, , .