

# Manfredo Quadroni

## List of Publications by Year in descending order

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Version: 2024-02-01

23  
papers

818  
citations

706676

14  
h-index

721071

23  
g-index

25  
all docs

25  
docs citations

25  
times ranked

1783  
citing authors

#	ARTICLE	IF	CITATIONS
1	Quantitative proteomic analysis to capture the role of heat-accumulated proteins in moss plant acquired thermotolerance. <i>Plant, Cell and Environment</i> , 2021, 44, 2117-2133.	2.8	21
2	Robust and sensitive peptidomics workflow for plasma based on specific extraction, lipid removal, capillary LC setup and multinozzle ESI emitter. <i>Talanta</i> , 2021, 223, 121617.	2.9	2
3	Bacterial Hsp90 Facilitates the Degradation of Aggregation-Prone Hsp70-Hsp40 Substrates. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 653073.	1.6	18
4	Phosphorylation in the Charged Linker Modulates Interactions and Secretion of Hsp90. <i>Cells</i> , 2021, 10, 1701.	1.8	6
5	The Hsp70-Hsp90 co-chaperone Hop/Stip1 shifts the proteostatic balance from folding towards degradation. <i>Nature Communications</i> , 2020, 11, 5975.	5.8	78
6	OCIAD1 is a host mitochondrial substrate of the hepatitis C virus NS3-4A protease. <i>PLoS ONE</i> , 2020, 15, e0236447.	1.1	7
7	Human shelterin protein POT1 prevents severe telomere instability induced by homologous recombination-mediated DNA repair. <i>EMBO Journal</i> , 2020, 39, e104500.	3.5	30
8	Ribonuclease inhibitor 1 regulates erythropoiesis by controlling GATA1 translation. <i>Journal of Clinical Investigation</i> , 2018, 128, 1597-1614.	3.9	20
9	MsViz: A Graphical Software Tool for In-Depth Manual Validation and Quantitation of Post-translational Modifications. <i>Journal of Proteome Research</i> , 2017, 16, 3092-3101.	1.8	9
10	Nuclear Proteomics Uncovers Diurnal Regulatory Landscapes in Mouse Liver. <i>Cell Metabolism</i> , 2017, 25, 102-117.	7.2	164
11	Fine-Tuning of Optimal TCR Signaling in Tumor-Redirected CD8 T Cells by Distinct TCR Affinity-Mediated Mechanisms. <i>Frontiers in Immunology</i> , 2017, 8, 1564.	2.2	41
12	Chemical crosslinking and mass spectrometry to elucidate the topology of integral membrane proteins. <i>PLoS ONE</i> , 2017, 12, e0186840.	1.1	11
13	ALM2 inflammasome is activated by pharmacological disruption of nuclear envelope integrity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E4671-80.	3.3	106
14	Identification of Antigenic Proteins from <i>Lichtheimia corymbifera</i> for Farmer's Lung Disease Diagnosis. <i>PLoS ONE</i> , 2016, 11, e0160888.	1.1	11
15	Quantitative proteomics of rat livers shows that unrestricted feeding is stressful for proteostasis with implications on life span. <i>Aging</i> , 2016, 8, 1735-1758.	1.4	18
16	Quantitative proteomics of heat-treated human cells show an across-the-board mild depletion of housekeeping proteins to massively accumulate few HSPs. <i>Cell Stress and Chaperones</i> , 2015, 20, 605-620.	1.2	69
17	Hsp90 inhibition induces both protein-specific and global changes in the ubiquitinome. <i>Journal of Proteomics</i> , 2015, 120, 215-229.	1.2	16
18	Proteome-Wide Effect of 17- $\beta$ -Estradiol and Lipoxin A4 in an Endometriotic Epithelial Cell Line. <i>Frontiers in Endocrinology</i> , 2015, 6, 192.	1.5	3

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19	Database Construction and Peptide Identification Strategies for Proteogenomic Studies on Sequenced Genomes. <i>Current Topics in Medicinal Chemistry</i> , 2014, 14, 425-434.	1.0	17
20	Dynamic Impacts of the Inhibition of the Molecular Chaperone Hsp90 on the T-Cell Proteome Have Implications for Anti-Cancer Therapy. <i>PLoS ONE</i> , 2013, 8, e80425.	1.1	44
21	Secreted glutamic protease rescues aspartic protease Pep deficiency in <i>Aspergillus fumigatus</i> during growth in acidic protein medium. <i>Microbiology (United Kingdom)</i> , 2011, 157, 1541-1550.	0.7	13
22	Multiplication of an ancestral gene encoding secreted fungalysin preceded species differentiation in the dermatophytes <i>Trichophyton</i> and <i>Microsporum</i> . <i>Microbiology (United Kingdom)</i> , 2004, 150, 301-310.	0.7	103
23	Quantify this! Report on a round table discussion on quantitative mass spectrometry in proteomics. <i>Proteomics</i> , 2004, 4, 2211-2215.	1.3	10