

Lucia Grenga

List of Publications by Year in descending order

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Version: 2024-02-01

24
papers

635
citations

623734

14
h-index

752698

20
g-index

31
all docs

31
docs citations

31
times ranked

945
citing authors

#	ARTICLE	IF	CITATIONS
1	Proteotyping SARS-CoV-2 Virus from Nasopharyngeal Swabs: A Proof-of-Concept Focused on a 3 Min Mass Spectrometry Window. <i>Journal of Proteome Research</i> , 2020, 19, 4407-4416.	3.7	90
2	Evaluation of Sample Preparation Methods for Fast Proteotyping of Microorganisms by Tandem Mass Spectrometry. <i>Frontiers in Microbiology</i> , 2019, 10, 1985.	3.5	69
3	Shortlisting SARS-CoV-2 Peptides for Targeted Studies from Experimental Data-Dependent Acquisition Tandem Mass Spectrometry Data. <i>Proteomics</i> , 2020, 20, e2000107.	2.2	64
4	Shotgun proteomics analysis of SARS-CoV-2-infected cells and how it can optimize whole viral particle antigen production for vaccines. <i>Emerging Microbes and Infections</i> , 2020, 9, 1712-1721.	6.5	62
5	Adaptive Remodeling of the Bacterial Proteome by Specific Ribosomal Modification Regulates <i>Pseudomonas</i> Infection and Niche Colonisation. <i>PLoS Genetics</i> , 2016, 12, e1005837.	3.5	53
6	Pathogen proteotyping: A rapidly developing application of mass spectrometry to address clinical concerns. <i>Clinical Mass Spectrometry</i> , 2019, 14, 9-17.	1.9	49
7	One ligand, two regulators and three binding sites: How KDPG controls primary carbon metabolism in <i>Pseudomonas</i> . <i>PLoS Genetics</i> , 2017, 13, e1006839.	3.5	39
8	Quick change: post-transcriptional regulation in <i>Pseudomonas</i> . <i>FEMS Microbiology Letters</i> , 2017, 364, .	1.8	31
9	Pan-genome analysis identifies intersecting roles for <i>Pseudomonas</i> specialized metabolites in potato pathogen inhibition. <i>ELife</i> , 2021, 10, .	6.0	25
10	Quick microbial molecular phenotyping by differential shotgun proteomics. <i>Environmental Microbiology</i> , 2020, 22, 2996-3004.	3.8	24
11	The <i>Escherichia coli</i> FtsK functional domains involved in its interaction with its divisome protein partners. <i>FEMS Microbiology Letters</i> , 2008, 287, 163-167.	1.8	23
12	Taxonomical and functional changes in COVID-19 faecal microbiome could be related to SARS-CoV-2 faecal load. <i>Environmental Microbiology</i> , 2022, 24, 4299-4316.	3.8	20
13	Proteomics in the COVID-19 Battlefield: First Semester Check-Up. <i>Proteomics</i> , 2021, 21, 2000198.	2.2	18
14	Analyzing the Complex Regulatory Landscape of Hfq – an Integrative, Multi-Omics Approach. <i>Frontiers in Microbiology</i> , 2017, 8, 1784.	3.5	17
15	Control of mRNA translation by dynamic ribosome modification. <i>PLoS Genetics</i> , 2020, 16, e1008837.	3.5	13
16	Metaproteomics to Decipher CF Host-Microbiota Interactions: Overview, Challenges and Future Perspectives. <i>Genes</i> , 2021, 12, 892.	2.4	10
17	Heterogeneity of SARS-CoV-2 virus produced in cell culture revealed by shotgun proteomics and supported by genome sequencing. <i>Analytical and Bioanalytical Chemistry</i> , 2021, 413, 7265-7275.	3.7	7
18	Front Cover: Shortlisting SARS-CoV-2 Peptides for Targeted Studies from Experimental Data-Dependent Acquisition Tandem Mass Spectrometry Data. <i>Proteomics</i> , 2020, 20, 2070111.	2.2	2

#	ARTICLE	IF	CITATIONS
19	Front Cover: Proteomics in the COVID-19 Battlefield: First Semester Check-Up. <i>Proteomics</i> , 2021, 21, 2170001.	2.2	1
20	Characterisation of the MutS and MutL Proteins from the <i>Pseudomonas avellanae</i> Mismatch Repair (MMR) System. <i>Open Microbiology Journal</i> , 2012, 6, 45-52.	0.7	1
21	Control of mRNA translation by dynamic ribosome modification. , 2020, 16, e1008837.		0
22	Control of mRNA translation by dynamic ribosome modification. , 2020, 16, e1008837.		0
23	Control of mRNA translation by dynamic ribosome modification. , 2020, 16, e1008837.		0
24	Profiling SARS-CoV-2 Infection by High-Throughput Shotgun Proteomics. <i>Methods in Molecular Biology</i> , 2022, 2452, 167-182.	0.9	0