

Sandra MaaÃ

List of Publications by Year in descending order

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Version: 2024-02-01

53
papers

1,162
citations

394390

19
h-index

434170

31
g-index

55
all docs

55
docs citations

55
times ranked

1438
citing authors

#	ARTICLE	IF	CITATIONS
1	The global proteome and ubiquitinome of bacterial and viral co-infected bronchial epithelial cells. <i>Journal of Proteomics</i> , 2022, 250, 104387.	2.4	1
2	Atp ^H is an inhibitor of FOF1 ATP synthase to arrest ATP hydrolysis during low-energy conditions in cyanobacteria. <i>Current Biology</i> , 2022, 32, 136-148.e5.	3.9	22
3	<i>Streptococcus pneumoniae</i> and Influenza A Virus Co-Infection Induces Altered Polyubiquitination in A549 Cells. <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 817532.	3.9	2
4	Migration of <i>Acanthamoeba</i> through <i>Legionella</i> biofilms is regulated by the bacterial <i>QsoX</i> network, effector proteins and the flagellum. <i>Environmental Microbiology</i> , 2022, , .	3.8	4
5	Expression of the Cyanobacterial F _o F ₁ ATP Synthase Regulator Atp ^H Depends on Small DNA-Binding Proteins and Differential mRNA Stability. <i>Microbiology Spectrum</i> , 2022, 10, e0256221.	3.0	5
6	Connections between Exoproteome Heterogeneity and Virulence in the Oral Pathogen <i>Aggregatibacter actinomycetemcomitans</i> . <i>MSystems</i> , 2022, 7, .	3.8	5
7	Metabolic Labeling of <i>Clostridioides difficile</i> . <i>Methods in Molecular Biology</i> , 2021, 2228, 271-282.	0.9	1
8	Reprogramming of sRNA target specificity by the leader peptide peTrpL in response to antibiotic exposure. <i>Nucleic Acids Research</i> , 2021, 49, 2894-2915.	14.5	9
9	Proteomic Adaptation of <i>Clostridioides difficile</i> to Treatment with the Antimicrobial Peptide Nisin. <i>Cells</i> , 2021, 10, 372.	4.1	7
10	A conserved, buried cysteine near the P-site is accessible to cysteine modifications and increases ROS stability in the P-type plasma membrane H ⁺ -ATPase. <i>Biochemical Journal</i> , 2021, 478, 619-632.	3.7	9
11	Proteomic Charting of Imipenem Adaptive Responses in a Highly Carbapenem Resistant Clinical <i>Enterobacter roggenkampii</i> Isolate. <i>Antibiotics</i> , 2021, 10, 501.	3.7	1
12	The Rhinobiome of Exacerbated Wheezers and Asthmatics: Insights From a German Pediatric Exacerbation Network. <i>Frontiers in Allergy</i> , 2021, 2, 667562.	2.8	7
13	A Small RNA Is Linking CRISPR-Cas and Zinc Transport. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 640440.	3.5	4
14	Bottom-up and top-down proteomic approaches for the identification, characterization, and quantification of the low molecular weight proteome with focus on short open reading frame-encoded peptides. <i>Proteomics</i> , 2021, 21, e2100008.	2.2	32
15	CdrS Is a Global Transcriptional Regulator Influencing Cell Division in <i>Haloferax volcanii</i> . <i>MBio</i> , 2021, 12, e0141621.	4.1	14
16	Another layer of complexity in <i>Staphylococcus aureus</i> methionine biosynthesis control: unusual RNase III-driven T-box riboswitch cleavage determines <i>met</i> operon mRNA stability and decay. <i>Nucleic Acids Research</i> , 2021, 49, 2192-2212.	14.5	7
17	Redirected Stress Responses in a Genome-Minimized <i>Bacillus</i> Strain with Enhanced Capacity for Protein Secretion. <i>MSystems</i> , 2021, 6, e0065521.	3.8	5
18	A Lactococcal Phage Protein Promotes Viral Propagation and Alters the Host Proteomic Response During Infection. <i>Viruses</i> , 2020, 12, 797.	3.3	4

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19	Exoproteomic profiling uncovers critical determinants for virulence of livestock-associated and human-originated <i>Staphylococcus aureus</i> ST398 strains. <i>Virulence</i> , 2020, 11, 947-963.	4.4	12
20	Optimized Proteomics Workflow for the Detection of Small Proteins. <i>Journal of Proteome Research</i> , 2020, 19, 4004-4018.	3.7	28
21	A global data-driven census of <i>Salmonella</i> small proteins and their potential functions in bacterial virulence. <i>MicroLife</i> , 2020, 1, .	2.1	34
22	Proteomic Adaptation of <i>Streptococcus pneumoniae</i> to the Antimicrobial Peptide Human Beta Defensin 3 (hBD3) in Comparison to Other Cell Surface Stresses. <i>Microorganisms</i> , 2020, 8, 1697.	3.6	2
23	The Leader Peptide peTrpL Forms Antibiotic-Containing Ribonucleoprotein Complexes for Posttranscriptional Regulation of Multiresistance Genes. <i>MBio</i> , 2020, 11, .	4.1	10
24	Membrane Modulation of Super-Secreting <i>Bacillus</i> Expressing the Major <i>Staphylococcus aureus</i> Antigen A: A Mass-Spectrometry-Based Absolute Quantification Approach. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 143.	4.1	8
25	Comprehensive Spectral Library from the Pathogenic Bacterium <i>Streptococcus pneumoniae</i> with Focus on Phosphoproteins. <i>Journal of Proteome Research</i> , 2020, 19, 1435-1446.	3.7	4
26	Proteomic Adaptation of <i>Streptococcus pneumoniae</i> to the Human Antimicrobial Peptide LL-37. <i>Microorganisms</i> , 2020, 8, 413.	3.6	11
27	Peptide-based quorum sensing systems in <i>Paenibacillus polymyxa</i> . <i>Life Science Alliance</i> , 2020, 3, e202000847.	2.8	11
28	Toward the Quantitative Characterization of Arginine Phosphorylations in <i>Staphylococcus aureus</i> . <i>Journal of Proteome Research</i> , 2019, 18, 265-279.	3.7	10
29	Ariadne's Thread in the Analytical Labyrinth of Membrane Proteins: Integration of Targeted and Shotgun Proteomics for Global Absolute Quantification of Membrane Proteins. <i>Analytical Chemistry</i> , 2019, 91, 11972-11980.	6.5	7
30	Investigating <i>Lactococcus lactis</i> MG1363 Response to Phage p2 Infection at the Proteome Level. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 704-714.	3.8	12
31	Subcellular Protein Fractionation in <i>Legionella pneumophila</i> and Preparation of the Derived Sub-proteomes for Analysis by Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2019, 1921, 445-464.	0.9	0
32	Virulence Factors Produced by <i>Staphylococcus aureus</i> Biofilms Have a Moonlighting Function Contributing to Biofilm Integrity. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1036-1053.	3.8	82
33	The Disulfide Stress Response and Protein S-thioallylation Caused by Allicin and Diallyl Polysulfanes in <i>Bacillus subtilis</i> as Revealed by Transcriptomics and Proteomics. <i>Antioxidants</i> , 2019, 8, 605.	5.1	23
34	Proteomic Investigation Uncovers Potential Targets and Target Sites of Pneumococcal Serine-Threonine Kinase StkP and Phosphatase PhpP. <i>Frontiers in Microbiology</i> , 2019, 10, 3101.	3.5	28
35	Proteomic response of <i>Streptococcus pneumoniae</i> to iron limitation. <i>International Journal of Medical Microbiology</i> , 2018, 308, 713-721.	3.6	26
36	Spectral Library Based Analysis of Arginine Phosphorylations in <i>Staphylococcus aureus</i> . <i>Molecular and Cellular Proteomics</i> , 2018, 17, 335-348.	3.8	41

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37	Proteomic Signatures of <i>Clostridium difficile</i> Stressed with Metronidazole, Vancomycin, or Fidaxomicin. <i>Cells</i> , 2018, 7, 213.	4.1	14
38	Iron Regulation in <i>Clostridioides difficile</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 3183.	3.5	49
39	Absolute Protein Quantification Using AQUA-Calibrated 2D-PAGE. <i>Methods in Molecular Biology</i> , 2018, 1841, 141-162.	0.9	3
40	Enrichment of Cell Surface-Associated Proteins in Gram-Positive Bacteria by Biotinylation or Trypsin Shaving for Mass Spectrometry Analysis. <i>Methods in Molecular Biology</i> , 2018, 1841, 35-43.	0.9	5
41	A Metabolic Labeling Strategy for Relative Protein Quantification in <i>Clostridioides difficile</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 2371.	3.5	4
42	Monitoring global protein thiol-oxidation and protein S-mycothiolation in <i>Mycobacterium smegmatis</i> under hypochlorite stress. <i>Scientific Reports</i> , 2017, 7, 1195.	3.3	47
43	The glyceraldehyde-3-phosphate dehydrogenase GapDH of <i>Corynebacterium diphtheriae</i> is redox-controlled by protein S-mycothiolation under oxidative stress. <i>Scientific Reports</i> , 2017, 7, 5020.	3.3	24
44	The protein inventory of <i>Clostridium difficile</i> grown in complex and minimal medium. <i>Proteomics - Clinical Applications</i> , 2016, 10, 1068-1072.	1.6	36
45	Costs of life - Dynamics of the protein inventory of <i>Staphylococcus aureus</i> during anaerobiosis. <i>Scientific Reports</i> , 2016, 6, 28172.	3.3	38
46	Methods and applications of absolute protein quantification in microbial systems. <i>Journal of Proteomics</i> , 2016, 136, 222-233.	2.4	16
47	Genome-Wide Analysis of Phosphorylated PhoP Binding to Chromosomal DNA Reveals Several Novel Features of the PhoPR-Mediated Phosphate Limitation Response in <i>Bacillus subtilis</i> . <i>Journal of Bacteriology</i> , 2015, 197, 1492-1506.	2.2	23
48	Adaptation of <i>Bacillus subtilis</i> carbon core metabolism to simultaneous nutrient limitation and osmotic challenge: a multi-omics perspective. <i>Environmental Microbiology</i> , 2014, 16, 1898-1917.	3.8	83
49	Comprehensive Absolute Quantification of the Cytosolic Proteome of <i>Bacillus subtilis</i> by Data Independent, Parallel Fragmentation in Liquid Chromatography/Mass Spectrometry (LC/MSE). <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1008-1019.	3.8	102
50	Highly Precise Quantification of Protein Molecules per Cell During Stress and Starvation Responses in <i>Bacillus subtilis</i> . <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2260-2276.	3.8	44
51	The new horizon in 2D electrophoresis: New technology to increase resolution and sensitivity. <i>Electrophoresis</i> , 2013, 34, 1510-1518.	2.4	27
52	Efficient, Global-Scale Quantification of Absolute Protein Amounts by Integration of Targeted Mass Spectrometry and Two-Dimensional Gel-Based Proteomics. <i>Analytical Chemistry</i> , 2011, 83, 2677-2684.	6.5	110
53	A comprehensive analysis of <i>Bordetella pertussis</i> surface proteome and identification of new immunogenic proteins. <i>Vaccine</i> , 2011, 29, 3583-3595.	3.8	49