

Andreas Otto

List of Publications by Year in descending order

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Version: 2024-02-01

37
papers

1,706
citations

361413

20
h-index

330143

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37
all docs

37
docs citations

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times ranked

2321
citing authors

#	ARTICLE	IF	CITATIONS
1	Surviving Serum: the Escherichia coli <i>iss</i> Gene of Extraintestinal Pathogenic E. coli Is Required for the Synthesis of Group 4 Capsule. <i>Infection and Immunity</i> , 2021, 89, e0031621.	2.2	9
2	A Lactococcal Phage Protein Promotes Viral Propagation and Alters the Host Proteomic Response During Infection. <i>Viruses</i> , 2020, 12, 797.	3.3	4
3	SppI Forms a Membrane Protein Complex with SppA and Inhibits Its Protease Activity in <i>Bacillus subtilis</i> . <i>MSphere</i> , 2020, 5, .	2.9	3
4	Bacterioplankton reveal years-long retention of Atlantic deep-ocean water by the Tropic Seamount. <i>Scientific Reports</i> , 2020, 10, 4715.	3.3	8
5	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
6	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
7	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
8	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
9	A homopolymeric adenosine tract in the promoter region of <i>nspA</i> influences factor H-mediated serum resistance in <i>Neisseria meningitidis</i> . <i>Scientific Reports</i> , 2019, 9, 2736.	3.3	4
10	Differential daptomycin resistance development in <i>Staphylococcus aureus</i> strains with active and mutated <i>gra</i> regulatory systems. <i>International Journal of Medical Microbiology</i> , 2018, 308, 335-348.	3.6	38
11	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
12	Proteomic Signatures of <i>Clostridium difficile</i> Stressed with Metronidazole, Vancomycin, or Fidaxomicin. <i>Cells</i> , 2018, 7, 213.	4.1	14
13	Iron Regulation in <i>Clostridioides difficile</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 3183.	3.5	49
14	A Metabolic Labeling Strategy for Relative Protein Quantification in <i>Clostridioides difficile</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 2371.	3.5	4
15	Tracking gene expression and oxidative damage of O ₂ -stressed <i>Clostridioides difficile</i> by a multi-omics approach. <i>Anaerobe</i> , 2018, 53, 94-107.	2.1	21
16	Comparative Proteomics of Purified Pathogen Vacuoles Correlates Intracellular Replication of <i>Legionella pneumophila</i> with the Small GTPase Ras-related protein 1 (Rap1). <i>Molecular and Cellular Proteomics</i> , 2017, 16, 622-641.	3.8	54
17	<i>Bacillus pumilus</i> KatX2 confers enhanced hydrogen peroxide resistance to a <i>Bacillus subtilis</i> PkatA::katX2 mutant strain. <i>Microbial Cell Factories</i> , 2017, 16, 72.	4.0	2
18	Identification of new protein-coding genes with a potential role in the virulence of the plant pathogen <i>Xanthomonas euvesicatoria</i> . <i>BMC Genomics</i> , 2017, 18, 625.	2.8	13

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19	Grad-seq guides the discovery of ProQ as a major small RNA-binding protein. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 11591-11596.	7.1	267
20	Impact of Moderate Temperature Changes on Neisseria meningitidis Adhesion Phenotypes and Proteome. Infection and Immunity, 2016, 84, 3484-3495.	2.2	10
21	The protein inventory of <i>Clostridium difficile</i> grown in complex and minimal medium. Proteomics - Clinical Applications, 2016, 10, 1068-1072.	1.6	36
22	Comparative proteome analysis of Actinoplanes sp. SE50/110 grown with maltose or glucose shows minor differences for acarbose biosynthesis proteins but major differences for saccharide transporters. Journal of Proteomics, 2016, 131, 140-148.	2.4	21
23	Comprehensive proteome analysis of Actinoplanes sp. SE50/110 highlighting the location of proteins encoded by the acarbose and the pyochelin biosynthesis gene cluster. Journal of Proteomics, 2015, 125, 1-16.	2.4	17
24	A Metaproteomics Approach to Elucidate Host and Pathogen Protein Expression during Catheter-Associated Urinary Tract Infections (CAUTIs). Molecular and Cellular Proteomics, 2015, 14, 989-1008.	3.8	63
25	The phosphoproteome and its physiological dynamics in Staphylococcus aureus. International Journal of Medical Microbiology, 2014, 304, 121-132.	3.6	48
26	The Staphylococcus aureus proteome. International Journal of Medical Microbiology, 2014, 304, 110-120.	3.6	39
27	Quantitative proteomics in the field of microbiology. Proteomics, 2014, 14, 547-565.	2.2	66
28	Global proteome analysis of vancomycin stress in Staphylococcus aureus. International Journal of Medical Microbiology, 2013, 303, 624-634.	3.6	40
29	Novel Twin-Arginine Translocation Pathway-Dependent Phenotypes of <i>Bacillus subtilis</i> Unveiled by Quantitative Proteomics. Journal of Proteome Research, 2013, 12, 796-807.	3.7	26
30	Global relative and absolute quantitation in microbial proteomics. Current Opinion in Microbiology, 2012, 15, 364-372.	5.1	50
31	Analyses of Soluble and Membrane Proteomes of <i>Ralstonia eutropha</i> H16 Reveal Major Changes in the Protein Complement in Adaptation to Lithoautotrophy. Journal of Proteome Research, 2011, 10, 2767-2776.	3.7	29
32	A Comprehensive Proteomics and Transcriptomics Analysis of <i>Bacillus subtilis</i> Salt Stress Adaptation. Journal of Bacteriology, 2010, 192, 870-882.	2.2	175
33	Systems-wide temporal proteomic profiling in glucose-starved <i>Bacillus subtilis</i> . Nature Communications, 2010, 1, 137.	12.8	188
34	A Proteomic View of an Important Human Pathogen – Towards the Quantification of the Entire <i>Staphylococcus aureus</i> Proteome. PLoS ONE, 2009, 4, e8176.	2.5	139
35	Monitoring of changes in the membrane proteome during stationary phase adaptation of <i>Bacillus subtilis</i> using <i>in vivo</i> labeling techniques. Proteomics, 2008, 8, 2062-2076.	2.2	55
36	Towards the entire proteome of the model bacterium <i>Bacillus subtilis</i> by gel-based and gel-free approaches. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2007, 849, 129-140.	2.3	57

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37	Gel-free and Gel-based Proteomics in <i>Bacillus subtilis</i> . <i>Molecular and Cellular Proteomics</i> , 2006, 5, 1183-1192.	3.8	83