

# DÄrte Becher

## List of Publications by Year in descending order

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259  
papers

15,017  
citations

19657

61  
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27406

106  
g-index

274  
all docs

274  
docs citations

274  
times ranked

16093  
citing authors

#	ARTICLE	IF	CITATIONS
1	Substrate-Controlled Succession of Marine Bacterioplankton Populations Induced by a Phytoplankton Bloom. <i>Science</i> , 2012, 336, 608-611.	12.6	1,304
2	Condition-Dependent Transcriptome Reveals High-Level Regulatory Architecture in <i>Bacillus subtilis</i> . <i>Science</i> , 2012, 335, 1103-1106.	12.6	809
3	Polysulfides Link H <sub>2</sub> S to Protein Thiol Oxidation. <i>Antioxidants and Redox Signaling</i> , 2013, 19, 1749-1765.	5.4	410
4	Cellulose and hemicellulose decomposition by forest soil bacteria proceeds by the action of structurally variable enzymatic systems. <i>Scientific Reports</i> , 2016, 6, 25279.	3.3	328
5	Small cationic antimicrobial peptides delocalize peripheral membrane proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E1409-18.	7.1	283
6	A comprehensive proteome map of growing <i>Bacillus subtilis</i> cells. <i>Proteomics</i> , 2004, 4, 2849-2876.	2.2	282
7	Grad-seq guides the discovery of ProQ as a major small RNA-binding protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 11591-11596.	7.1	267
8	Global Network Reorganization During Dynamic Adaptations of <i>Bacillus subtilis</i> . <i>Metabolism</i> . <i>Science</i> , 2012, 335, 1099-1103.	12.6	255
9	Exploring functional contexts of symbiotic sustain within lichen-associated bacteria by comparative omics. <i>ISME Journal</i> , 2015, 9, 412-424.	9.8	238
10	Physiological Proteomics of the Uncultured Endosymbiont of <i>Riftia pachyptila</i> . <i>Science</i> , 2007, 315, 247-250.	12.6	207
11	Metaproteomics of a gutless marine worm and its symbiotic microbial community reveal unusual pathways for carbon and energy use. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E1173-82.	7.1	191
12	Systems-wide temporal proteomic profiling in glucose-starved <i>Bacillus subtilis</i> . <i>Nature Communications</i> , 2010, 1, 137.	12.8	188
13	Niches of two polysaccharide-degrading <i>Polaribacter</i> isolates from the North Sea during a spring diatom bloom. <i>ISME Journal</i> , 2015, 9, 1410-1422.	9.8	182
14	Verrucomicrobia use hundreds of enzymes to digest the algal polysaccharide fucoidan. <i>Nature Microbiology</i> , 2020, 5, 1026-1039.	13.3	182
15	Functional characterization of polysaccharide utilization loci in the marine <i>Bacteroidetes</i> <i>Gramella forsetii</i> KT0803. <i>ISME Journal</i> , 2014, 8, 1492-1502.	9.8	177
16	A Comprehensive Proteomics and Transcriptomics Analysis of <i>Bacillus subtilis</i> Salt Stress Adaptation. <i>Journal of Bacteriology</i> , 2010, 192, 870-882.	2.2	175
17	S-Bacillithiolation Protects Against Hypochlorite Stress in <i>Bacillus subtilis</i> as Revealed by Transcriptomics and Redox Proteomics. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.009506.	3.8	154
18	Oxygenation Cascade in Conversion of n-Alkanes to $\omega$ -Dioic Acids Catalyzed by Cytochrome P450 52A3. <i>Journal of Biological Chemistry</i> , 1998, 273, 32528-32534.	3.4	145

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19	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
20	Polysaccharide utilization loci of North Sea <i>Flavobacteriia</i> as basis for using SusC/D-protein expression for predicting major phytoplankton glycans. ISME Journal, 2019, 13, 76-91.	9.8	139
21	Global impact of protein arginine phosphorylation on the physiology of <i>Bacillus subtilis</i> . Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 7451-7456.	7.1	133
22	The Genome of the Obligate Intracellular Parasite <i>Trachipleistophora hominis</i> : New Insights into Microsporidian Genome Dynamics and Reductive Evolution. PLoS Pathogens, 2012, 8, e1002979.	4.7	127
23	Quantitative prediction of genome-wide resource allocation in bacteria. Metabolic Engineering, 2015, 32, 232-243.	7.0	125
24	In marine <i>Bacteroidetes</i> the bulk of glycan degradation during algae blooms is mediated by few clades using a restricted set of genes. ISME Journal, 2019, 13, 2800-2816.	9.8	125
25	Profiling the surfacome of <i>Staphylococcus aureus</i> . Proteomics, 2010, 10, 3082-3096.	2.2	119
26	Molecular mechanisms underlying the close association between soil <i>Burkholderia</i> and fungi. ISME Journal, 2016, 10, 253-264.	9.8	118
27	Metabolic and physiological interdependencies in the <i>Bathymodiolus azoricus</i> symbiosis. ISME Journal, 2017, 11, 463-477.	9.8	116
28	The influence of agr and $\sigma^B$ in growth phase dependent regulation of virulence factors in <i>Staphylococcus aureus</i> . Proteomics, 2004, 4, 3034-3047.	2.2	114
29	Efficient, Global-Scale Quantification of Absolute Protein Amounts by Integration of Targeted Mass Spectrometry and Two-Dimensional Gel-Based Proteomics. Analytical Chemistry, 2011, 83, 2677-2684.	6.5	110
30	Involvement of protein acetylation in glucose-induced transcription of a stress-responsive promoter. Molecular Microbiology, 2011, 81, 1190-1204.	2.5	109
31	Functional analysis of novel Rab GTPases identified in the proteome of purified <i>Legionella</i> -containing vacuoles from macrophages. Cellular Microbiology, 2014, 16, n/a-n/a.	2.1	106
32	Towards the development of <i>Bacillus subtilis</i> as a cell factory for membrane proteins and protein complexes. Microbial Cell Factories, 2008, 7, 10.	4.0	104
33	Comprehensive Absolute Quantification of the Cytosolic Proteome of <i>Bacillus subtilis</i> by Data Independent, Parallel Fragmentation in Liquid Chromatography/Mass Spectrometry (LC/MSE). Molecular and Cellular Proteomics, 2014, 13, 1008-1019.	3.8	102
34	Acetylation of the Response Regulator RcsB Controls Transcription from a Small RNA Promoter. Journal of Bacteriology, 2013, 195, 4174-4186.	2.2	99
35	Comparative Proteome Analysis of Spontaneous Outer Membrane Vesicles and Purified Outer Membranes of <i>Neisseria meningitidis</i> . Journal of Bacteriology, 2013, 195, 4425-4435.	2.2	98
36	A marine bacterial enzymatic cascade degrades the algal polysaccharide ulvan. Nature Chemical Biology, 2019, 15, 803-812.	8.0	97

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37	Heme biosynthesis is coupled to electron transport chains for energy generation. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 10436-10441.	7.1	95
38	Picking Vanished Proteins from the Void: How to Collect and Ship/Share Extremely Dilute Proteins in a Reproducible and Highly Efficient Manner. Analytical Chemistry, 2014, 86, 7421-7427.	6.5	95
39	Distinct Roles of Phenol-Soluble Modulins in Spreading of Staphylococcus aureus on Wet Surfaces. Applied and Environmental Microbiology, 2013, 79, 886-895.	3.1	90
40	S-Cysteinylation Is a General Mechanism for Thiol Protection of Bacillus subtilis Proteins after Oxidative Stress. Journal of Biological Chemistry, 2007, 282, 25981-25985.	3.4	89
41	<i>S-</i> Bacillithiolation Protects Conserved and Essential Proteins Against Hypochlorite Stress in <i>Firmicutes</i> Bacteria. Antioxidants and Redox Signaling, 2013, 18, 1273-1295.	5.4	88
42	Oxidative stress triggers thiol oxidation in the glyceraldehyde-3-phosphate dehydrogenase of Staphylococcus aureus. Molecular Microbiology, 2004, 52, 133-140.	2.5	87
43	The <i>E. coli</i> sirtuin CobB shows no preference for enzymatic and nonenzymatic lysine acetylation substrate sites. MicrobiologyOpen, 2015, 4, 66-83.	3.0	87
44	Depletion of thiol-containing proteins in response to quinones in <i>Bacillus subtilis</i> . Molecular Microbiology, 2008, 69, 1513-1529.	2.5	85
45	The Phosphoproteome of the Minimal Bacterium Mycoplasma pneumoniae. Molecular and Cellular Proteomics, 2010, 9, 1228-1242.	3.8	85
46	Adaptive mechanisms that provide competitive advantages to marine bacteroidetes during microalgal blooms. ISME Journal, 2018, 12, 2894-2906.	9.8	84
47	Gel-free and Gel-based Proteomics in Bacillus subtilis. Molecular and Cellular Proteomics, 2006, 5, 1183-1192.	3.8	83
48	Virulence Factors Produced by Staphylococcus aureus Biofilms Have a Moonlighting Function Contributing to Biofilm Integrity. Molecular and Cellular Proteomics, 2019, 18, 1036-1053.	3.8	82
49	Protein aggregation in Escherichia coli: role of proteases. FEMS Microbiology Letters, 2002, 207, 9-12.	1.8	80
50	Proteome analyses of Staphylococcus aureus in growing and non-growing cells: A physiological approach. International Journal of Medical Microbiology, 2005, 295, 547-565.	3.6	79
51	Dynamics of protein phosphorylation on Ser/Thr/Tyr in <i>Bacillus subtilis</i> . Proteomics, 2007, 7, 3509-3526.	2.2	78
52	Quantitative Cell Surface Proteome Profiling for SigB-Dependent Protein Expression in the Human Pathogen <i>Staphylococcus aureus</i> via Biotinylation Approach. Journal of Proteome Research, 2010, 9, 1579-1590.	3.7	77
53	Proteins unique to intraphagosomally grown Mycobacterium tuberculosis. Proteomics, 2006, 6, 2485-2494.	2.2	75
54	Biphasic cellular adaptations and ecological implications of <i>Alteromonas macleodii</i> degrading a mixture of algal polysaccharides. ISME Journal, 2019, 13, 92-103.	9.8	74

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55	Evolutionary Events Associated with an Outbreak of Meningococcal Disease in Men Who Have Sex with Men. <i>PLoS ONE</i> , 2016, 11, e0154047.	2.5	71
56	Regulation of quinone detoxification by the thiol stress sensing DUF24/MarR-like repressor, YodB in <i>Bacillus subtilis</i> . <i>Molecular Microbiology</i> , 2008, 67, 1108-1124.	2.5	70
57	A Trigger Enzyme in <i>Mycoplasma pneumoniae</i> : Impact of the Glycerophosphodiesterase GlpQ on Virulence and Gene Expression. <i>PLoS Pathogens</i> , 2011, 7, e1002263.	4.7	68
58	Protein S-Mycothiolation Functions as Redox-Switch and Thiol Protection Mechanism in <i>Corynebacterium glutamicum</i> Under Hypochlorite Stress. <i>Antioxidants and Redox Signaling</i> , 2014, 20, 589-605.	5.4	68
59	The dynamic protein partnership of RNA polymerase in <i>Bacillus subtilis</i> . <i>Proteomics</i> , 2011, 11, 2992-3001.	2.2	67
60	Metabolic Reprogramming of <i>Clostridioides difficile</i> During the Stationary Phase With the Induction of Toxin Production. <i>Frontiers in Microbiology</i> , 2018, 9, 1970.	3.5	67
61	Diamide Triggers Mainly S Thiolations in the Cytoplasmic Proteomes of <i>Bacillus subtilis</i> and <i>Staphylococcus aureus</i> . <i>Journal of Bacteriology</i> , 2009, 191, 7520-7530.	2.2	66
62	Quantitative proteomics in the field of microbiology. <i>Proteomics</i> , 2014, 14, 547-565.	2.2	66
63	A proteomic view of cell physiology of <i>Bacillus licheniformis</i> . <i>Proteomics</i> , 2004, 4, 1465-1490.	2.2	64
64	Extracytoplasmic Proteases Determining the Cleavage and Release of Secreted Proteins, Lipoproteins, and Membrane Proteins in <i>Bacillus subtilis</i> . <i>Journal of Proteome Research</i> , 2013, 12, 4101-4110.	3.7	64
65	A Metaproteomics Approach to Elucidate Host and Pathogen Protein Expression during Catheter-Associated Urinary Tract Infections (CAUTIs). <i>Molecular and Cellular Proteomics</i> , 2015, 14, 989-1008.	3.8	63
66	A proteomic view of cell physiology and virulence of <i>Staphylococcus aureus</i> . <i>International Journal of Medical Microbiology</i> , 2010, 300, 76-87.	3.6	62
67	Extracellular Proteome and Citrullinome of the Oral Pathogen <i>Porphyromonas gingivalis</i> . <i>Journal of Proteome Research</i> , 2016, 15, 4532-4543.	3.7	62
68	Effects of hypoxia-reoxygenation stress on mitochondrial proteome and bioenergetics of the hypoxia-tolerant marine bivalve <i>Crassostrea gigas</i> . <i>Journal of Proteomics</i> , 2019, 194, 99-111.	2.4	62
69	Quantitative Proteomic View on Secreted, Cell Surface-Associated, and Cytoplasmic Proteins of the Methicillin-Resistant Human Pathogen <i>Staphylococcus aureus</i> under Iron-Limited Conditions. <i>Journal of Proteome Research</i> , 2011, 10, 1657-1666.	3.7	59
70	Penicillin-binding protein folding is dependent on the PrsA peptidyl-prolyl cis-trans isomerase in <i>Bacillus subtilis</i> . <i>Molecular Microbiology</i> , 2010, 77, 108-127.	2.5	58
71	Diatom fucan polysaccharide precipitates carbon during algal blooms. <i>Nature Communications</i> , 2021, 12, 1150.	12.8	58
72	Towards the entire proteome of the model bacterium <i>Bacillus subtilis</i> by gel-based and gel-free approaches. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2007, 849, 129-140.	2.3	57

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73	Redox Regulation in <i>Bacillus subtilis</i> : The Bacilliredoxins BrxA(YphP) and BrxB(YqiW) Function in De-Bacillithiolation of S-Bacillithiolated OhrR and MetE. Antioxidants and Redox Signaling, 2014, 21, 357-367.	5.4	57
74	Aquatic adaptation of a laterally acquired pectin degradation pathway in marine gammaproteobacteria. Environmental Microbiology, 2017, 19, 2320-2333.	3.8	57
75	Stress Responses of the Industrial Workhorse <i>Bacillus licheniformis</i> to Osmotic Challenges. PLoS ONE, 2013, 8, e80956.	2.5	56
76	Purification and proteomics of pathogen-modified vacuoles and membranes. Frontiers in Cellular and Infection Microbiology, 2015, 5, 48.	3.9	56
77	Decoding the complete arsenal for cellulose and hemicellulose deconstruction in the highly efficient cellulose decomposer <i>Paenibacillus O199</i> . Biotechnology for Biofuels, 2016, 9, 104.	6.2	56
78	Nitrogen fixation in a chemoautotrophic lucinid symbiosis. Nature Microbiology, 2017, 2, 16193.	13.3	56
79	Cometabolic Degradation of Dibenzofuran by Biphenyl-Cultivated <i>Ralstonia</i> sp. Strain SBUG 290. Applied and Environmental Microbiology, 2000, 66, 4528-4531.	3.1	55
80	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
81	A Secreted Bacterial Peptidylarginine Deiminase Can Neutralize Human Innate Immune Defenses. MBio, 2018, 9, .	4.1	55
82	Complementary Analysis of the Vegetative Membrane Proteome of the Human Pathogen <i>Staphylococcus aureus</i> . Molecular and Cellular Proteomics, 2008, 7, 1460-1468.	3.8	54
83	Structural insights into the redox-switch mechanism of the MarR/DUF24-type regulator HypR. Nucleic Acids Research, 2012, 40, 4178-4192.	14.5	54
84	Comparative Proteomics of Purified Pathogen Vacuoles Correlates Intracellular Replication of <i>Legionella pneumophila</i> with the Small GTPase Ras-related protein 1 (Rap1). Molecular and Cellular Proteomics, 2017, 16, 622-641.	3.8	54
85	Inhibition of Acetyl Phosphate-dependent Transcription by an Acetylatable Lysine on RNA Polymerase. Journal of Biological Chemistry, 2012, 287, 32147-32160.	3.4	53
86	Systematic Analysis of Mycobacterial Acylation Reveals First Example of Acylation-mediated Regulation of Enzyme Activity of a Bacterial Phosphatase. Journal of Biological Chemistry, 2015, 290, 26218-26234.	3.4	53
87	Immunoproteomic analysis of <i>Bordetella pertussis</i> and identification of new immunogenic proteins. Vaccine, 2009, 27, 542-548.	3.8	52
88	Highly phosphorylated bacterial proteins. Proteomics, 2004, 4, 3068-3077.	2.2	51
89	Metaproteomics to unravel major microbial players in leaf litter and soil environments: challenges and perspectives. Proteomics, 2013, 13, 2895-2909.	2.2	51
90	The role of peptide deformylase in protein biosynthesis: A proteomic study. Proteomics, 2003, 3, 299-306.	2.2	50

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91	Global relative and absolute quantitation in microbial proteomics. <i>Current Opinion in Microbiology</i> , 2012, 15, 364-372.	5.1	50
92	Abundant toxin-related genes in the genomes of beneficial symbionts from deep-sea hydrothermal vent mussels. <i>ELife</i> , 2015, 4, e07966.	6.0	50
93	Characterization of a thaumarchaeal symbiont that drives incomplete nitrification in the tropical sponge <i>Lanthella basta</i> . <i>Environmental Microbiology</i> , 2019, 21, 3831-3854.	3.8	50
94	Two-dimensional reference map of <i>Agrobacterium tumefaciens</i> proteins. <i>Proteomics</i> , 2004, 4, 1061-1073.	2.2	49
95	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
96	Iron Regulation in <i>Clostridioides difficile</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 3183.	3.5	49
97	Probing the active site of homoserinetrans-succinylase. <i>FEBS Letters</i> , 2004, 577, 386-392.	2.8	48
98	The phosphoproteome and its physiological dynamics in <i>Staphylococcus aureus</i> . <i>International Journal of Medical Microbiology</i> , 2014, 304, 121-132.	3.6	48
99	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
100	From complementarity to comprehensiveness – targeting the membrane proteome of growing <i>Bacillus subtilis</i> by divergent approaches. <i>Proteomics</i> , 2008, 8, 4123-4136.	2.2	46
101	Influence of Impaired Lipoprotein Biogenesis on Surface and Exoproteome of <i>Streptococcus pneumoniae</i> . <i>Journal of Proteome Research</i> , 2014, 13, 650-667.	3.7	45
102	Differential effect of YidC depletion on the membrane proteome of <i>Escherichia coli</i> under aerobic and anaerobic growth conditions. <i>Proteomics</i> , 2010, 10, 3235-3247.	2.2	44
103	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
104	Staphylococcal PknB as the First Prokaryotic Representative of the Proline-Directed Kinases. <i>PLoS ONE</i> , 2010, 5, e9057.	2.5	44
105	Genomic and proteomic profiles of biofilms on microplastics are decoupled from artificial surface properties. <i>Environmental Microbiology</i> , 2021, 23, 3099-3115.	3.8	43
106	Life and Death of Proteins: A Case Study of Glucose-starved <i>Staphylococcus aureus</i> . <i>Molecular and Cellular Proteomics</i> , 2012, 11, 558-570.	3.8	42
107	A global <i>Staphylococcus aureus</i> proteome resource applied to the in vivo characterization of host-pathogen interactions. <i>Scientific Reports</i> , 2017, 7, 9718.	3.3	42
108	Changing expression patterns of TonB-dependent transporters suggest shifts in polysaccharide consumption over the course of a spring phytoplankton bloom. <i>ISME Journal</i> , 2021, 15, 2336-2350.	9.8	42

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109	Genome and proteome characterization of the psychrophilic Flavobacterium bacteriophage 11b. <i>Extremophiles</i> , 2007, 11, 95-104.	2.3	41
110	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
111	Heat Shock Proteome of <i>Agrobacterium tumefaciens</i> : Evidence for New Control Systems. <i>Journal of Bacteriology</i> , 2002, 184, 1772-1778.	2.2	40
112	In vitro Phosphorylation of Key Metabolic Enzymes from <i>Bacillus subtilis</i> : PrkC Phosphorylates Enzymes from Different Branches of Basic Metabolism. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2010, 18, 129-140.	1.0	40
113	CtsR inactivation during thiol-specific stress in low GC, Gram+ bacteria. <i>Molecular Microbiology</i> , 2011, 79, 772-785.	2.5	40
114	Global proteome analysis of vancomycin stress in <i>Staphylococcus aureus</i> . <i>International Journal of Medical Microbiology</i> , 2013, 303, 624-634.	3.6	40
115	Ser/Thr protein kinase PrkC-mediated regulation of GroEL is critical for biofilm formation in <i>Bacillus anthracis</i> . <i>Npj Biofilms and Microbiomes</i> , 2017, 3, 7.	6.4	40
116	Insight into the evolution of microbial metabolism from the deep-branching bacterium, <i>Thermovibrio ammonificans</i> . <i>ELife</i> , 2017, 6, .	6.0	40
117	The <i>Staphylococcus aureus</i> proteome. <i>International Journal of Medical Microbiology</i> , 2014, 304, 110-120.	3.6	39
118	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
119	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
120	In vivo phosphorylation patterns of key stressosome proteins define a second feedback loop that limits activation of <i>Bacillus subtilis</i> $\sigma^B$ . <i>Molecular Microbiology</i> , 2011, 80, 798-810.	2.5	37
121	Activity Control of the ClpC Adaptor McsB in <i>Bacillus subtilis</i> . <i>Journal of Bacteriology</i> , 2011, 193, 3887-3893.	2.2	37
122	The Stability of Cytadherence Proteins in <i>Mycoplasma pneumoniae</i> Requires Activity of the Protein Kinase PrkC. <i>Infection and Immunity</i> , 2010, 78, 184-192.	2.2	36
123	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
124	A quantitative assessment of the membrane-integral sub-proteome of a bacterial magnetic organelle. <i>Journal of Proteomics</i> , 2018, 172, 89-99.	2.4	36
125	Metaproteogenomic Profiling of Microbial Communities Colonizing Actively Venting Hydrothermal Chimneys. <i>Frontiers in Microbiology</i> , 2018, 9, 680.	3.5	36
126	Proteomic analysis of the food spoiler <i>Pseudomonas fluorescens</i> ITEM 17298 reveals the antibiofilm activity of the pepsin-digested bovine lactoferrin. <i>Food Microbiology</i> , 2019, 82, 177-193.	4.2	36



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127	The Metaproteomics Initiative: a coordinated approach for propelling the functional characterization of microbiomes. <i>Microbiome</i> , 2021, 9, 243.	11.1	36
128	The redox-sensing regulator YodB senses quinones and diamide <i>via</i> a thiol-disulfide switch in <i>Bacillus subtilis</i> . <i>Proteomics</i> , 2010, 10, 3155-3164.	2.2	35
129	Status quo in physiological proteomics of the uncultured <i>Riftia pachyptila</i> endosymbiont. <i>Proteomics</i> , 2011, 11, 3106-3117.	2.2	34
130	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
131	An exclusion list based label-free proteome quantification approach using an LTQ Orbitrap. <i>Rapid Communications in Mass Spectrometry</i> , 2012, 26, 701-709.	1.5	33
132	Identification and optimization of PrsA in <i>Bacillus subtilis</i> for improved yield of amylase. <i>Microbial Cell Factories</i> , 2019, 18, 158.	4.0	33
133	Surface shaving as a versatile tool to profile global interactions between human serum proteins and the <i>Staphylococcus aureus</i> cell surface. <i>Proteomics</i> , 2011, 11, 2921-2930.	2.2	32
134	Sample Preservation and Storage Significantly Impact Taxonomic and Functional Profiles in Metaproteomics Studies of the Human Gut Microbiome. <i>Microorganisms</i> , 2019, 7, 367.	3.6	32
135	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
136	Fur Is the Master Regulator of the Extraintestinal Pathogenic <i>Escherichia coli</i> Response to Serum. <i>MBio</i> , 2014, 5, .	4.1	31
137	Alpha- and beta-mannan utilization by marine <i>Bacteroidetes</i> . <i>Environmental Microbiology</i> , 2018, 20, 4127-4140.	3.8	31
138	Detailed proteome analysis of growing cells of the planctomycete <i>Rhodopirellula baltica</i> SH1 <sup>T</sup> . <i>Proteomics</i> , 2008, 8, 1608-1623.	2.2	30
139	First description of small proteins encoded by spRNAs in <i>Methanosarcina mazei</i> strain GÅ1. <i>Biochimie</i> , 2015, 117, 138-148.	2.6	30
140	Effect of selected environmental factors on degradation and mineralization of biaryl compounds by the bacterium <i>Ralstonia pickettii</i> in soil and compost. <i>Chemosphere</i> , 1998, 36, 2321-2335.	8.2	29
141	Analyses of Soluble and Membrane Proteomes of <i>Ralstonia eutropha</i> H16 Reveal Major Changes in the Protein Complement in Adaptation to Lithoautotrophy. <i>Journal of Proteome Research</i> , 2011, 10, 2767-2776.	3.7	29
142	Optimized Proteomics Workflow for the Detection of Small Proteins. <i>Journal of Proteome Research</i> , 2020, 19, 4004-4018.	3.7	28
143	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
144	Changing the phospholipid composition of <i>Staphylococcus aureus</i> causes distinct changes in membrane proteome and membrane-sensory regulators. <i>Proteomics</i> , 2010, 10, 1685-1693.	2.2	27

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