

DÄrte Becher

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7003662/publications.pdf>

Version: 2024-02-01

259
papers

15,017
citations

19657

61
h-index

27406

106
g-index

274
all docs

274
docs citations

274
times ranked

16093
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	Yields and Immunomodulatory Effects of Pneumococcal Membrane Vesicles Differ with the Bacterial Growth Phase. <i>Advanced Healthcare Materials</i> , 2022, 11, e2101151.	7.6	12
3	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
4	Three Microbial Musketeers of the Seas: <i>Shewanella baltica</i> , <i>Aliivibrio fischeri</i> and <i>Vibrio harveyi</i> , and Their Adaptation to Different Salinity Probed by a Proteomic Approach. <i>International Journal of Molecular Sciences</i> , 2022, 23, 619.	4.1	2
5	Proteome analysis of the Gram-positive fish pathogen <i>Renibacterium salmoninarum</i> reveals putative role of membrane vesicles in virulence. <i>Scientific Reports</i> , 2022, 12, 3003.	3.3	5
6	<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
7	Diverse events have transferred genes for edible seaweed digestion from marine to human gut bacteria. <i>Cell Host and Microbe</i> , 2022, 30, 314-328.e11.	11.0	25
8	Migration of <i>Acanthamoeba</i> through <i>Legionella</i> biofilms is regulated by the bacterial <i>σ²⁴</i> network, effector proteins and the flagellum. <i>Environmental Microbiology</i> , 2022, , .	3.8	4
9	Expression of the Cyanobacterial 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
10	Connections between Exoproteome Heterogeneity and Virulence in the Oral Pathogen <i>Aggregatibacter actinomycetemcomitans</i> . <i>MSystems</i> , 2022, 7, .	3.8	5
11	Double trouble: <i>Bacillus</i> depends on a functional Tat machinery to avoid severe oxidative stress and starvation upon entry into a NaCl-depleted environment. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2021, 1868, 118914.	4.1	5
12	Bacterial symbiont subpopulations have different roles in a deep-sea symbiosis. <i>ELife</i> , 2021, 10, .	6.0	17
13	Metabolic Labeling of <i>Clostridioides difficile</i> . <i>Methods in Molecular Biology</i> , 2021, 2228, 271-282.	0.9	1
14	Diatom fucan polysaccharide precipitates carbon during algal blooms. <i>Nature Communications</i> , 2021, 12, 1150.	12.8	58
15	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
16	Proteomic Adaptation of <i>Clostridioides difficile</i> to Treatment with the Antimicrobial Peptide Nisin. <i>Cells</i> , 2021, 10, 372.	4.1	7
17	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
18	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

#	ARTICLE	IF	CITATIONS
19	Proteomic analysis of a hom-disrupted, cephamycin C overproducing <i>Streptomyces clavuligerus</i> . <i>Protein and Peptide Letters</i> , 2021, 28, 205-220.	0.9	3
20	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
21	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
22	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
23	A Small RNA Is Linking CRISPR-Cas and Zinc Transport. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 640440.	3.5	4
24	Reaching out in anticipation: bacterial membrane extensions represent a permanent investment in polysaccharide sensing and utilization. <i>Environmental Microbiology</i> , 2021, 23, 3149-3163.	3.8	10
25	What's a Biofilm? How the Choice of the Biofilm Model Impacts the Protein Inventory of <i>Clostridioides difficile</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 682111.	3.5	13
26	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
27	CdrS Is a Global Transcriptional Regulator Influencing Cell Division in <i>Haloferax volcanii</i> . <i>MBio</i> , 2021, 12, e0141621.	4.1	14
28	An Innovative Protocol for Metaproteomic Analyses of Microbial Pathogens in Cystic Fibrosis Sputum. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 724569.	3.9	6
29	Surviving Serum: the <i>Escherichia coli</i> <i>iss</i> Gene of Extraintestinal Pathogenic <i>E. coli</i> Is Required for the Synthesis of Group 4 Capsule. <i>Infection and Immunity</i> , 2021, 89, e0031621.	2.2	9
30	Another layer of complexity in <i>Staphylococcus aureus</i> methionine biosynthesis control: unusual RNase III-driven T-box riboswitch cleavage determines operon mRNA stability and decay. <i>Nucleic Acids Research</i> , 2021, 49, 2192-2212.	14.5	7
31	Influenza A H1N1 Induced Disturbance of the Respiratory and Fecal Microbiome of German Landrace Pigs – a Multi-Omics Characterization. <i>Microbiology Spectrum</i> , 2021, 9, e0018221.	3.0	14
32	The Metaproteomics Initiative: a coordinated approach for propelling the functional characterization of microbiomes. <i>Microbiome</i> , 2021, 9, 243.	11.1	36
33	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
34	Comparative proteomics of related symbiotic mussel species reveals high variability of host-symbiont interactions. <i>ISME Journal</i> , 2020, 14, 649-656.	9.8	15
35	A Multi-Omics Protocol for Swine Feces to Elucidate Longitudinal Dynamics in Microbiome Structure and Function. <i>Microorganisms</i> , 2020, 8, 1887.	3.6	15
36	A Lactococcal Phage Protein Promotes Viral Propagation and Alters the Host Proteomic Response During Infection. <i>Viruses</i> , 2020, 12, 797.	3.3	4

#	ARTICLE	IF	CITATIONS
37	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
38	<i>Verticillium longisporum</i> Elicits Media-Dependent Secretome Responses With Capacity to Distinguish Between Plant-Related Environments. <i>Frontiers in Microbiology</i> , 2020, 11, 1876.	3.5	18
39	Optimized Proteomics Workflow for the Detection of Small Proteins. <i>Journal of Proteome Research</i> , 2020, 19, 4004-4018.	3.7	28
40	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
41	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
42	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
43	Functional association of the stress-responsive LiaH protein and the minimal TatAyCy protein translocase in <i>Bacillus subtilis</i> . <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2020, 1867, 118719.	4.1	6
44	The Involvement of the McsB Arginine Kinase in Clp-Dependent Degradation of the MgsR Regulator in <i>Bacillus subtilis</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 900.	3.5	5
45	Dynamic proteomic analysis of <i>Phanerochaete chrysosporium</i> under copper stress. <i>Ecotoxicology and Environmental Safety</i> , 2020, 198, 110694.	6.0	13
46	Tryptic Shaving of <i>Staphylococcus aureus</i> Unveils Immunodominant Epitopes on the Bacterial Cell Surface. <i>Journal of Proteome Research</i> , 2020, 19, 2997-3010.	3.7	13
47	The Leader Peptide peTrpL Forms Antibiotic-Containing Ribonucleoprotein Complexes for Posttranscriptional Regulation of Multiresistance Genes. <i>MBio</i> , 2020, 11, .	4.1	10
48	Bacterioplankton reveal years-long retention of Atlantic deep-ocean water by the Tropic Seamount. <i>Scientific Reports</i> , 2020, 10, 4715.	3.3	8
49	Membrane Modulation of Super-Secreting <i>Bacillus</i> Expressing the Major <i>Staphylococcus aureus</i> Antigen – A Mass-Spectrometry-Based Absolute Quantification Approach. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 143.	4.1	8
50	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
51	Proteomic Adaptation of <i>Streptococcus pneumoniae</i> to the Human Antimicrobial Peptide LL-37. <i>Microorganisms</i> , 2020, 8, 413.	3.6	11
52	Verrucomicrobia use hundreds of enzymes to digest the algal polysaccharide fucoidan. <i>Nature Microbiology</i> , 2020, 5, 1026-1039.	13.3	182
53	Peptide-based quorum sensing systems in <i>Paenibacillus polymyxa</i> . <i>Life Science Alliance</i> , 2020, 3, e202000847.	2.8	11
54	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

#	ARTICLE	IF	CITATIONS
55	Polysaccharide utilization loci of North Sea <i>Flavobacteriia</i> as basis for using SusC/D-protein expression for predicting major phytoplankton glycans. <i>ISME Journal</i> , 2019, 13, 76-91.	9.8	139
56	Biphasic cellular adaptations and ecological implications of <i>Alteromonas macleodii</i> degrading a mixture of algal polysaccharides. <i>ISME Journal</i> , 2019, 13, 92-103.	9.8	74
57	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
58	In marine <i>Bacteroidetes</i> the bulk of glycan degradation during algae blooms is mediated by few clades using a restricted set of genes. <i>ISME Journal</i> , 2019, 13, 2800-2816.	9.8	125
59	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
60	A marine bacterial enzymatic cascade degrades the algal polysaccharide ulvan. <i>Nature Chemical Biology</i> , 2019, 15, 803-812.	8.0	97
61	Biopearling of Interconnected Outer Membrane Vesicle Chains by a Marine <i>Flavobacterium</i> . <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	20
62	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
63	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
64	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
65	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
66	Exoproteome Heterogeneity among Closely Related <i>Staphylococcus aureus</i> t437 Isolates and Possible Implications for Virulence. <i>Journal of Proteome Research</i> , 2019, 18, 2859-2874.	3.7	16
67	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
68	A homopolymeric adenosine tract in the promoter region of nspA influences factor H-mediated serum resistance in <i>Neisseria meningitidis</i> . <i>Scientific Reports</i> , 2019, 9, 2736.	3.3	4
69	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
70	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
71	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
72	Tuning the <i>Mycobacterium tuberculosis</i> Alternative Sigma Factor SigF through the Multidomain Regulator Rv1364c and Osmosensory Kinase Protein Kinase D. <i>Journal of Bacteriology</i> , 2019, 201, .	2.2	8

#	ARTICLE	IF	CITATIONS
73	Transcriptomic and proteomic insight into the mechanism of cyclooctasulfurâ€versus thiosulfateâ€oxidation by the chemolithoautotroph <i>Sulfurimonas denitrificans</i> . <i>Environmental Microbiology</i> , 2019, 21, 244-258.	3.8	16
74	<i>Escherichia coli</i> Can Adapt Its Protein Translocation Machinery for Enhanced Periplasmic Recombinant Protein Production. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019, 7, 465.	4.1	8
75	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
76	Proteomic response of <i>Streptococcus pneumoniae</i> to iron limitation. <i>International Journal of Medical Microbiology</i> , 2018, 308, 713-721.	3.6	26
77	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
78	From the wound to the bench: exoproteome interplay between wound-colonizing <i>Staphylococcus aureus</i> strains and co-existing bacteria. <i>Virulence</i> , 2018, 9, 363-378.	4.4	15
79	Adaptation of <i>Staphylococcus aureus</i> to Airway Environments in Patients With Cystic Fibrosis by Upregulation of Superoxide Dismutase M and Iron-Scavenging Proteins. <i>Journal of Infectious Diseases</i> , 2018, 217, 1453-1461.	4.0	20
80	Global quantification of phosphoproteins combining metabolic labeling and gelâ€based proteomics in <i>B. pumilus</i> . <i>Electrophoresis</i> , 2018, 39, 334-343.	2.4	6
81	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
82	The Proteomic Response of <i>Bacillus pumilus</i> Cells to Glucose Starvation. <i>Proteomics</i> , 2018, 18, 1700109.	2.2	10
83	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
84	Proteomic Signatures of <i>Clostridium difficile</i> Stressed with Metronidazole, Vancomycin, or Fidaxomicin. <i>Cells</i> , 2018, 7, 213.	4.1	14
85	Iron Regulation in <i>Clostridioides difficile</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 3183.	3.5	49
86	Alphaâ€and betaâ€mannan utilization by marine <i>Bacteroidetes</i> . <i>Environmental Microbiology</i> , 2018, 20, 4127-4140.	3.8	31
87	NspA contributes to resistance against complement in invasive meningococci of the sequence type 41/44 clonal complex. <i>Molecular Immunology</i> , 2018, 102, 169-170.	2.2	0
88	A Metabolic Labeling Strategy for Relative Protein Quantification in <i>Clostridioides difficile</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 2371.	3.5	4
89	A Secreted Bacterial Peptidylarginine Deiminase Can Neutralize Human Innate Immune Defenses. <i>MBio</i> , 2018, 9, .	4.1	55
90	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

#	ARTICLE	IF	CITATIONS
91	Adaptive mechanisms that provide competitive advantages to marine bacteroidetes during microalgal blooms. <i>ISME Journal</i> , 2018, 12, 2894-2906.	9.8	84
92	Proteomic analysis of bacterial (outer) membrane vesicles: progress and clinical potential. <i>Expert Review of Proteomics</i> , 2018, 15, 623-626.	3.0	6
93	Metaproteogenomic Profiling of Microbial Communities Colonizing Actively Venting Hydrothermal Chimneys. <i>Frontiers in Microbiology</i> , 2018, 9, 680.	3.5	36
94	The <i>Escherichia coli</i> Type III Secretion System 2 Has a Global Effect on Cell Surface. <i>MBio</i> , 2018, 9, .	4.1	27
95	An ancient family of mobile genomic islands introducing cephalosporinase and carbapenemase genes in <i>Enterobacteriaceae</i> . <i>Virulence</i> , 2018, 9, 1377-1389.	4.4	9
96	Aquatic adaptation of a laterally acquired pectin degradation pathway in marine gammaproteobacteria. <i>Environmental Microbiology</i> , 2017, 19, 2320-2333.	3.8	57
97	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
98	An Easy and Fast Protocol for Affinity Bead-Based Protein Enrichment and Storage of Proteome Samples. <i>Methods in Enzymology</i> , 2017, 585, 1-13.	1.0	6
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	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
101	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
102	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
103	<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
104	Nitrogen fixation in a chemoautotrophic lucinid symbiosis. <i>Nature Microbiology</i> , 2017, 2, 16193.	13.3	56
105	Metabolic and physiological interdependencies in the <i>Bathymodiolus azoricus</i> symbiosis. <i>ISME Journal</i> , 2017, 11, 463-477.	9.8	116
106	Sample Preparation for Mass-Spectrometry Based Absolute Protein Quantification in Antibiotic Stress Research. <i>Methods in Molecular Biology</i> , 2017, 1520, 281-289.	0.9	1
107	Proteome-wide alterations in an industrial clavulanic acid producing strain of <i>Streptomyces clavuligerus</i> . <i>Synthetic and Systems Biotechnology</i> , 2017, 2, 39-48.	3.7	18
108	Insight into the evolution of microbial metabolism from the deep-branching bacterium, <i>Thermovibrio ammonificans</i> . <i>ELife</i> , 2017, 6, .	6.0	40

#	ARTICLE	IF	CITATIONS
109	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
110	Signatures of cytoplasmic proteins in the exoproteome distinguish community- and hospital-associated methicillin-resistant <i>Staphylococcus aureus</i> USA300 lineages. <i>Virulence</i> , 2017, 8, 891-907.	4.4	19
111	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
112	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
113	A SDD1-like subtilase is exuded by tobacco roots. <i>Functional Plant Biology</i> , 2016, 43, 141.	2.1	8
114	Proteomic analysis of the <i>Simkania</i> containing vacuole: the central role of retrograde transport. <i>Molecular Microbiology</i> , 2016, 99, 151-171.	2.5	23
115	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
116	Impact of Moderate Temperature Changes on <i>Neisseria meningitidis</i> Adhesion Phenotypes and Proteome. <i>Infection and Immunity</i> , 2016, 84, 3484-3495.	2.2	10
117	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
118	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
119	Proteomics of septicemic <i>Escherichia coli</i> . <i>Proteomics - Clinical Applications</i> , 2016, 10, 1020-1024.	1.6	1
120	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
121	Updating the proteome of the uncultivable hemotrophic <i>Mycoplasma</i> in experimentally infected pigs. <i>Proteomics</i> , 2016, 16, 609-613.	2.2	3
122	Decoding the complete arsenal for cellulose and hemicellulose deconstruction in the highly efficient cellulose decomposer <i>Paenibacillus O199</i> . <i>Biotechnology for Biofuels</i> , 2016, 9, 104.	6.2	56
123	Molecular mechanisms underlying the close association between soil <i>Burkholderia</i> and fungi. <i>ISME Journal</i> , 2016, 10, 253-264.	9.8	118
124	Comparative proteome analysis of <i>Actinoplanes</i> sp. SE50/110 grown with maltose or glucose shows minor differences for acarbose biosynthesis proteins but major differences for saccharide transporters. <i>Journal of Proteomics</i> , 2016, 131, 140-148.	2.4	21
125	Global analysis of the impact of linezolid onto virulence factor production in <i>S. aureus</i> USA300. <i>International Journal of Medical Microbiology</i> , 2016, 306, 131-140.	3.6	9
126	Methods and applications of absolute protein quantification in microbial systems. <i>Journal of Proteomics</i> , 2016, 136, 222-233.	2.4	16

#	ARTICLE	IF	CITATIONS
127	Life Stage-specific Proteomes of <i>Legionella pneumophila</i> Reveal a Highly Differential Abundance of Virulence-associated Dot/Icm effectors. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 177-200.	3.8	27
128	The <i>E. coli</i> sirtuin CobB shows no preference for enzymatic and nonenzymatic lysine acetylation substrate sites. <i>MicrobiologyOpen</i> , 2015, 4, 66-83.	3.0	87
129	Multi-Organism Proteomes (iMOP): Advancing our Understanding of Human Biology. <i>Proteomics</i> , 2015, 15, 2885-2894.	2.2	2
130	High-resolution proteome maps of <i>Bacillus licheniformis</i> cells growing in minimal medium. <i>Proteomics</i> , 2015, 15, 2629-2633.	2.2	6
131	Characterization of <i>Helicobacter pylori</i> VacA-containing vacuoles (VCVs), VacA intracellular trafficking and interference with calcium signalling in T lymphocytes. <i>Cellular Microbiology</i> , 2015, 17, 1811-1832.	2.1	24
132	Purification and proteomics of pathogen-modified vacuoles and membranes. <i>Frontiers in Cellular and Infection Microbiology</i> , 2015, 5, 48.	3.9	56
133	<i>Enterococcus faecalis</i> Glycolipids Modulate Lipoprotein-Content of the Bacterial Cell Membrane and Host Immune Response. <i>PLoS ONE</i> , 2015, 10, e0132949.	2.5	8
134	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
135	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
136	Antibacterial Metabolites and Bacteriolytic Enzymes Produced by <i>Bacillus pumilus</i> During Bacteriolysis of <i>Arthrobacter citreus</i> . <i>Marine Biotechnology</i> , 2015, 17, 290-304.	2.4	15
137	Time-Resolved Analysis of Cytosolic and Surface-Associated Proteins of <i>Staphylococcus aureus</i> HG001 under Planktonic and Biofilm Conditions. <i>Journal of Proteome Research</i> , 2015, 14, 3804-3822.	3.7	13
138	Comprehensive proteome analysis of <i>Actinoplanes</i> sp. SE50/110 highlighting the location of proteins encoded by the acarbose and the pyochelin biosynthesis gene cluster. <i>Journal of Proteomics</i> , 2015, 125, 1-16.	2.4	17
139	First description of small proteins encoded by sRNAs in <i>Methanosarcina mazei</i> strain GÄ1. <i>Biochimie</i> , 2015, 117, 138-148.	2.6	30
140	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
141	Versatile vector suite for the extracytoplasmic production and purification of heterologous His-tagged proteins in <i>Lactococcus lactis</i> . <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 9037-9048.	3.6	14
142	Quantitative prediction of genome-wide resource allocation in bacteria. <i>Metabolic Engineering</i> , 2015, 32, 232-243.	7.0	125
143	Systematic Analysis of Mycobacterial Acylation Reveals First Example of Acylation-mediated Regulation of Enzyme Activity of a Bacterial Phosphatase. <i>Journal of Biological Chemistry</i> , 2015, 290, 26218-26234.	3.4	53
144	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

#	ARTICLE	IF	CITATIONS
145	Exploring functional contexts of symbiotic sustain within lichen-associated bacteria by comparative omics. ISME Journal, 2015, 9, 412-424.	9.8	238
146	Functional characterization of polysaccharide utilization loci in the marine <i>Bacteroidetes</i> <i>Gramella forsetii</i> ™ KT0803. ISME Journal, 2014, 8, 1492-1502.	9.8	177
147	Archaeal Ubiquitin-like SAMP3 is Isopeptide-linked to Proteins via a UbaA-dependent Mechanism. Molecular and Cellular Proteomics, 2014, 13, 220-239.	3.8	25
148	Fur Is the Master Regulator of the Extraintestinal Pathogenic Escherichia coli Response to Serum. MBio, 2014, 5, .	4.1	31
149	The oxygen-independent metabolism of cyclic monoterpenes in <i>Castellaniella defragrans</i> 65Phen. BMC Microbiology, 2014, 14, 164.	3.3	19
150	The phosphoproteome and its physiological dynamics in <i>Staphylococcus aureus</i> . International Journal of Medical Microbiology, 2014, 304, 121-132.	3.6	48
151	Protein <i>S-</i> Mycothiolation Functions as Redox-Switch and Thiol Protection Mechanism in <i>Corynebacterium glutamicum</i> Under Hypochlorite Stress. Antioxidants and Redox Signaling, 2014, 20, 589-605.	5.4	68
152	Small cationic antimicrobial peptides delocalize peripheral membrane proteins. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E1409-18.	7.1	283
153	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
154	Redox Regulation in <i>Bacillus subtilis</i> : The Bacilliredoxins BrxA(YphP) and BrxB(YqiW) Function in De-Bacillithiolation of <i>S-</i> Bacillithiolated OhrR and MetE. Antioxidants and Redox Signaling, 2014, 21, 357-367.	5.4	57
155	The <i>Staphylococcus aureus</i> proteome. International Journal of Medical Microbiology, 2014, 304, 110-120.	3.6	39
156	Cell physiology of the biotechnological relevant bacterium <i>Bacillus pumilus</i> —An omics-based approach. Journal of Biotechnology, 2014, 192, 204-214.	3.8	13
157	A Highly Unstable Transcript Makes CwO D,L-Endopeptidase Expression Responsive to Growth Conditions in <i>Bacillus subtilis</i> . Journal of Bacteriology, 2014, 196, 237-247.	2.2	18
158	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
159	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
160	Highly Precise Quantification of Protein Molecules per Cell During Stress and Starvation Responses in <i>Bacillus subtilis</i> . Molecular and Cellular Proteomics, 2014, 13, 2260-2276.	3.8	44
161	Quantitative proteomics in the field of microbiology. Proteomics, 2014, 14, 547-565.	2.2	66
162	Influence of Impaired Lipoprotein Biogenesis on Surface and Exoproteome of <i>Streptococcus pneumoniae</i> . Journal of Proteome Research, 2014, 13, 650-667.	3.7	45

#	ARTICLE	IF	CITATIONS
163	Coping with Anoxia: A Comprehensive Proteomic and Transcriptomic Survey of Denitrification. <i>Journal of Proteome Research</i> , 2014, 13, 4325-4338.	3.7	8
164	Metaproteomics to unravel major microbial players in leaf litter and soil environments: challenges and perspectives. <i>Proteomics</i> , 2013, 13, 2895-2909.	2.2	51
165	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
166	Dynamic protein phosphorylation during the growth of <i>Xanthomonas campestris</i> pv. <i>campestris</i> B100 revealed by a gel-based proteomics approach. <i>Journal of Biotechnology</i> , 2013, 167, 111-122.	3.8	16
167	Distinct Roles of Phenol-Soluble Modulins in Spreading of <i>Staphylococcus aureus</i> on Wet Surfaces. <i>Applied and Environmental Microbiology</i> , 2013, 79, 886-895.	3.1	90
168	Polysulfides Link H ₂ S to Protein Thiol Oxidation. <i>Antioxidants and Redox Signaling</i> , 2013, 19, 1749-1765.	5.4	410
169	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
170	Novel Twin-Arginine Translocation Pathway-Dependent Phenotypes of <i>Bacillus subtilis</i> Unveiled by Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2013, 12, 796-807.	3.7	26
171	S-Bacillithiolation Protects Conserved and Essential Proteins Against Hypochlorite Stress in Firmicutes Bacteria. <i>Antioxidants and Redox Signaling</i> , 2013, 18, 1273-1295.	5.4	88
172	Global Relative Quantification with Liquid Chromatography-Matrix-assisted Laser Desorption Ionization Time-of-flight (LC-MALDI-TOF) Cross-validation with LTQ-Orbitrap Proves Reliability and Reveals Complementary Ionization Preferences. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2911-2920.	3.8	11
173	Acetylation of the Response Regulator RcsB Controls Transcription from a Small RNA Promoter. <i>Journal of Bacteriology</i> , 2013, 195, 4174-4186.	2.2	99
174	Comparative Proteome Analysis of Spontaneous Outer Membrane Vesicles and Purified Outer Membranes of <i>Neisseria meningitidis</i> . <i>Journal of Bacteriology</i> , 2013, 195, 4425-4435.	2.2	98
175	A Two-Component System (XydS/R) Controls the Expression of Genes Encoding CBM6-Containing Proteins in Response to Straw in <i>Clostridium cellulolyticum</i> . <i>PLoS ONE</i> , 2013, 8, e56063.	2.5	25
176	Stress Responses of the Industrial Workhorse <i>Bacillus licheniformis</i> to Osmotic Challenges. <i>PLoS ONE</i> , 2013, 8, e80956.	2.5	56
177	The Genome of the Obligate Intracellular Parasite <i>Trachipleistophora hominis</i> : New Insights into Microsporidian Genome Dynamics and Reductive Evolution. <i>PLoS Pathogens</i> , 2012, 8, e1002979.	4.7	127
178	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
179	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
180	Global impact of protein arginine phosphorylation on the physiology of <i>Bacillus subtilis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 7451-7456.	7.1	133

#	ARTICLE	IF	CITATIONS
181	Inhibition of Acetyl Phosphate-dependent Transcription by an Acetyltable Lysine on RNA Polymerase. <i>Journal of Biological Chemistry</i> , 2012, 287, 32147-32160.	3.4	53
182	Structural insights into the redox-switch mechanism of the MarR/DUF24-type regulator HypR. <i>Nucleic Acids Research</i> , 2012, 40, 4178-4192.	14.5	54
183	Global Network Reorganization During Dynamic Adaptations of <i>Bacillus subtilis</i> Metabolism. <i>Science</i> , 2012, 335, 1099-1103.	12.6	255
184	Partially overlapping substrate specificities of staphylococcal group A sortases. <i>Proteomics</i> , 2012, 12, 3049-3062.	2.2	19
185	Condition-Dependent Transcriptome Reveals High-Level Regulatory Architecture in <i>Bacillus subtilis</i> . <i>Science</i> , 2012, 335, 1103-1106.	12.6	809
186	Global relative and absolute quantitation in microbial proteomics. <i>Current Opinion in Microbiology</i> , 2012, 15, 364-372.	5.1	50
187	Cell surface proteome of the marine planctomycete <i>Scopelodopirellula baltica</i> . <i>Proteomics</i> , 2012, 12, 1781-1791.	2.2	13
188	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
189	Substrate-Controlled Succession of Marine Bacterioplankton Populations Induced by a Phytoplankton Bloom. <i>Science</i> , 2012, 336, 608-611.	12.6	1,304
190	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
191	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
192	Mapping of Interactions between Human Macrophages and <i>Staphylococcus aureus</i> Reveals an Involvement of MAP Kinase Signaling in the Host Defense. <i>Journal of Proteome Research</i> , 2011, 10, 4018-4032.	3.7	27
193	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
194	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
195	CtsR inactivation during thiol-specific stress in low GC, Gram+ bacteria. <i>Molecular Microbiology</i> , 2011, 79, 772-785.	2.5	40
196	<i>In vivo</i> phosphorylation patterns of key stressosome proteins define a second feedback loop that limits activation of <i>Bacillus subtilis</i> . <i>Molecular Microbiology</i> , 2011, 80, 798-810.	2.5	37
197	Involvement of protein acetylation in glucose-induced transcription of a stress-responsive promoter. <i>Molecular Microbiology</i> , 2011, 81, 1190-1204.	2.5	109
198	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

#	ARTICLE	IF	CITATIONS
199	Characterization of proteome alterations in <i>Phanerochaete chrysosporium</i> in response to lead exposure. <i>Proteome Science</i> , 2011, 9, 12.	1.7	21
200	A guide through the computational analysis of isotope-labeled mass spectrometry-based quantitative proteomics data: an application study. <i>Proteome Science</i> , 2011, 9, 30.	1.7	23
201	<i>Bacillus subtilis</i> YqjG is required for genetic competence development. <i>Proteomics</i> , 2011, 11, 270-282.	2.2	22
202	The dynamic protein partnership of RNA polymerase in <i>Bacillus subtilis</i> . <i>Proteomics</i> , 2011, 11, 2992-3001.	2.2	67
203	Status quo in physiological proteomics of the uncultured <i>Riftia pachyptila</i> endosymbiont. <i>Proteomics</i> , 2011, 11, 3106-3117.	2.2	34
204	From the genome sequence to the protein inventory of <i>Bacillus subtilis</i> . <i>Proteomics</i> , 2011, 11, 2971-2980.	2.2	21
205	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
206	Activity Control of the ClpC Adaptor McsB in <i>Bacillus subtilis</i> . <i>Journal of Bacteriology</i> , 2011, 193, 3887-3893.	2.2	37
207	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
208	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
209	Profiling the surfacome of <i>Staphylococcus aureus</i> . <i>Proteomics</i> , 2010, 10, 3082-3096.	2.2	119
210	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
211	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
212	Penicillin binding protein folding is dependent on the PrsA peptidylprolyl <i>cis</i> - <i>trans</i> isomerase in <i>Bacillus subtilis</i> . <i>Molecular Microbiology</i> , 2010, 77, 108-127.	2.5	58
213	The Phosphoproteome of the Minimal Bacterium <i>Mycoplasma pneumoniae</i> . <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1228-1242.	3.8	85
214	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
215	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
216	Heme biosynthesis is coupled to electron transport chains for energy generation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 10436-10441.	7.1	95

#	ARTICLE	IF	CITATIONS
217	Systems-wide temporal proteomic profiling in glucose-starved <i>Bacillus subtilis</i> . <i>Nature Communications</i> , 2010, 1, 137.	12.8	188
218	Quantitative Cell Surface Proteome Profiling for SigB-Dependent Protein Expression in the Human Pathogen <i>Staphylococcus aureus</i> via Biotinylation Approach. <i>Journal of Proteome Research</i> , 2010, 9, 1579-1590.	3.7	77
219	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
220	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
221	<i>Staphylococcal PknB as the First Prokaryotic Representative of the Proline-Directed Kinases</i> . <i>PLoS ONE</i> , 2010, 5, e9057.	2.5	44
222	A Proteomic View of an Important Human Pathogen – Towards the Quantification of the Entire <i>Staphylococcus aureus</i> Proteome. <i>PLoS ONE</i> , 2009, 4, e8176.	2.5	139
223	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
224	Analysis of ultra acidic proteins by the use of anodic acidic gels. <i>Analytical Biochemistry</i> , 2009, 385, 208-214.	2.4	5
225	Immunoproteomic analysis of <i>Bordetella pertussis</i> and identification of new immunogenic proteins. <i>Vaccine</i> , 2009, 27, 542-548.	3.8	52
226	Detailed proteome analysis of growing cells of the planctomycete <i>Rhodopirellula baltica</i> SH1 ^T . <i>Proteomics</i> , 2008, 8, 1608-1623.	2.2	30
227	Monitoring of changes in the membrane proteome during stationary phase adaptation of <i>Bacillus subtilis</i> using <i>in vivo</i> labeling techniques. <i>Proteomics</i> , 2008, 8, 2062-2076.	2.2	55
228	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
229	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
230	Towards the development of <i>Bacillus subtilis</i> as a cell factory for membrane proteins and protein complexes. <i>Microbial Cell Factories</i> , 2008, 7, 10.	4.0	104
231	Depletion of thiol-containing proteins in response to quinones in <i>Bacillus subtilis</i> . <i>Molecular Microbiology</i> , 2008, 69, 1513-1529.	2.5	85
232	Complementary Analysis of the Vegetative Membrane Proteome of the Human Pathogen <i>Staphylococcus aureus</i> . <i>Molecular and Cellular Proteomics</i> , 2008, 7, 1460-1468.	3.8	54
233	S-Cysteinylation Is a General Mechanism for Thiol Protection of <i>Bacillus subtilis</i> Proteins after Oxidative Stress. <i>Journal of Biological Chemistry</i> , 2007, 282, 25981-25985.	3.4	89
234	Physiological Proteomics of the Uncultured Endosymbiont of <i>Riftia pachyptila</i> . <i>Science</i> , 2007, 315, 247-250.	12.6	207

#	ARTICLE	IF	CITATIONS
235	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
236	<i>Phanerochaete chrysosporium</i> soluble proteome as a prelude for the analysis of heavy metal stress response. <i>Proteomics</i> , 2007, 7, 1249-1260.	2.2	22
237	Dynamics of protein phosphorylation on Ser/Thr/Tyr in <i>Bacillus subtilis</i> . <i>Proteomics</i> , 2007, 7, 3509-3526.	2.2	78
238	Genome and proteome characterization of the psychrophilic <i>Flavobacterium</i> bacteriophage 11b. <i>Extremophiles</i> , 2007, 11, 95-104.	2.3	41
239	Visual analysis of gel-free proteome data. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2006, 12, 497-508.	4.4	15
240	Proteins unique to intraphagosomally grown <i>Mycobacterium tuberculosis</i> . <i>Proteomics</i> , 2006, 6, 2485-2494.	2.2	75
241	Gel-free and Gel-based Proteomics in <i>Bacillus subtilis</i> . <i>Molecular and Cellular Proteomics</i> , 2006, 5, 1183-1192.	3.8	83
242	The bphC gene-encoded 2,3-dihydroxybiphenyl-1,2-dioxygenase is involved in complete degradation of dibenzofuran by the biphenyl-degrading bacterium <i>Ralstonia</i> sp. SBUC 290. <i>Journal of Applied Microbiology</i> , 2005, 98, 635-645.	3.1	22
243	Proteome analyses of <i>Staphylococcus aureus</i> in growing and non-growing cells: A physiological approach. <i>International Journal of Medical Microbiology</i> , 2005, 295, 547-565.	3.6	79
244	Oxidative stress triggers thiol oxidation in the glyceraldehyde-3-phosphate dehydrogenase of <i>Staphylococcus aureus</i> . <i>Molecular Microbiology</i> , 2004, 52, 133-140.	2.5	87
245	Two-dimensional reference map of <i>Agrobacterium tumefaciens</i> proteins. <i>Proteomics</i> , 2004, 4, 1061-1073.	2.2	49
246	A proteomic view of cell physiology of <i>Bacillus licheniformis</i> . <i>Proteomics</i> , 2004, 4, 1465-1490.	2.2	64
247	Highly phosphorylated bacterial proteins. <i>Proteomics</i> , 2004, 4, 3068-3077.	2.2	51
248	A comprehensive proteome map of growing <i>Bacillus subtilis</i> cells. <i>Proteomics</i> , 2004, 4, 2849-2876.	2.2	282
249	The influence of agr and σ^B in growth phase dependent regulation of virulence factors in <i>Staphylococcus aureus</i> . <i>Proteomics</i> , 2004, 4, 3034-3047.	2.2	114
250	Probing the active site of homoserine trans-succinylase. <i>FEBS Letters</i> , 2004, 577, 386-392.	2.8	48
251	Nucleophosmin is a component of the fructoselysine-specific receptor in cell membranes of Mono Mac 6 and U937 monocyte-like cells. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2004, 1670, 132-136.	2.4	14
252	Proteome analysis of plant-induced proteins of <i>Agrobacterium tumefaciens</i> . <i>FEMS Microbiology Ecology</i> , 2003, 44, 355-360.	2.7	23

#	ARTICLE	IF	CITATIONS
253	The role of peptide deformylase in protein biosynthesis: A proteomic study. <i>Proteomics</i> , 2003, 3, 299-306.	2.2	50
254	Analysis of Automatically Generated Peptide Mass Fingerprints of Cellular Proteins and Antigens from <i>Helicobacter pylori</i> 26695 Separated by Two-dimensional Electrophoresis. <i>Molecular and Cellular Proteomics</i> , 2003, 2, 1271-1283.	3.8	25
255	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
256	Protein aggregation in <i>Escherichia coli</i> : role of proteases. <i>FEMS Microbiology Letters</i> , 2002, 207, 9-12.	1.8	80
257	Cometabolic Degradation of Dibenzofuran by Biphenyl-Cultivated <i>Ralstonia</i> sp. Strain SBUG 290. <i>Applied and Environmental Microbiology</i> , 2000, 66, 4528-4531.	3.1	55
258	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
259	Oxygenation Cascade in Conversion of n-Alkanes to ω -Dioic Acids Catalyzed by Cytochrome P450 52A3. <i>Journal of Biological Chemistry</i> , 1998, 273, 32528-32534.	3.4	145