

DÄrte Becher

List of Publications by Year in descending order

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259
papers

15,017
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19608

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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. | 1.2 | 1 |
| 2 | Yields and Immunomodulatory Effects of Pneumococcal Membrane Vesicles Differ with the Bacterial Growth Phase. <i>Advanced Healthcare Materials</i> , 2022, 11, e2101151. | 3.9 | 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. | 1.8 | 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. | 1.8 | 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. | 1.6 | 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. | 1.8 | 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. | 5.1 | 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, . . | 1.8 | 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. | 1.2 | 5 |
| 10 | Connections between Exoproteome Heterogeneity and Virulence in the Oral Pathogen <i>Aggregatibacter actinomycetemcomitans</i> . <i>MSystems</i> , 2022, 7, . | 1.7 | 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. | 1.9 | 5 |
| 12 | Bacterial symbiont subpopulations have different roles in a deep-sea symbiosis. <i>ELife</i> , 2021, 10, . | 2.8 | 17 |
| 13 | Metabolic Labeling of <i>Clostridioides difficile</i> . <i>Methods in Molecular Biology</i> , 2021, 2228, 271-282. | 0.4 | 1 |
| 14 | Diatom fucan polysaccharide precipitates carbon during algal blooms. <i>Nature Communications</i> , 2021, 12, 1150. | 5.8 | 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. | 6.5 | 9 |
| 16 | Proteomic Adaptation of <i>Clostridioides difficile</i> to Treatment with the Antimicrobial Peptide Nisin. <i>Cells</i> , 2021, 10, 372. | 1.8 | 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. | 1.7 | 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. | 4.4 | 42 |

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|----|---|-----|-----------|
| 19 | Proteomic analysis of a hom-disrupted, cephamycin C overproducing <i>Streptomyces clavuligerus</i> . <i>Protein and Peptide Letters</i> , 2021, 28, 205-220. | 0.4 | 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. | 1.5 | 1 |
| 21 | The Rhinobiome of Exacerbated Wheezers and Asthmatics: Insights From a German Pediatric Exacerbation Network. <i>Frontiers in Allergy</i> , 2021, 2, 667562. | 1.2 | 7 |
| 22 | Genomic and proteomic profiles of biofilms on microplastics are decoupled from artificial surface properties. <i>Environmental Microbiology</i> , 2021, 23, 3099-3115. | 1.8 | 43 |
| 23 | A Small RNA Is Linking CRISPR-Cas and Zinc Transport. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 640440. | 1.6 | 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. | 1.8 | 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. | 1.5 | 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. | 1.3 | 32 |
| 27 | CdrS Is a Global Transcriptional Regulator Influencing Cell Division in <i>Haloferax volcanii</i> . <i>MBio</i> , 2021, 12, e0141621. | 1.8 | 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. | 1.8 | 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. | 1.0 | 9 |
| 30 | 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. | 6.5 | 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. | 1.2 | 14 |
| 32 | The Metaproteomics Initiative: a coordinated approach for propelling the functional characterization of microbiomes. <i>Microbiome</i> , 2021, 9, 243. | 4.9 | 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. | 1.7 | 5 |
| 34 | Comparative proteomics of related symbiotic mussel species reveals high variability of host-symbiont interactions. <i>ISME Journal</i> , 2020, 14, 649-656. | 4.4 | 15 |
| 35 | A Multi-Omics Protocol for Swine Feces to Elucidate Longitudinal Dynamics in Microbiome Structure and Function. <i>Microorganisms</i> , 2020, 8, 1887. | 1.6 | 15 |
| 36 | A Lactococcal Phage Protein Promotes Viral Propagation and Alters the Host Proteomic Response During Infection. <i>Viruses</i> , 2020, 12, 797. | 1.5 | 4 |

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|----|---|-----|-----------|
| 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. | 1.8 | 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. | 1.5 | 18 |
| 39 | Optimized Proteomics Workflow for the Detection of Small Proteins. <i>Journal of Proteome Research</i> , 2020, 19, 4004-4018. | 1.8 | 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, . | 1.0 | 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. | 1.6 | 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, . | 1.3 | 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. | 1.9 | 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. | 1.5 | 5 |
| 45 | Dynamic proteomic analysis of <i>Phanerochaete chrysosporium</i> under copper stress. <i>Ecotoxicology and Environmental Safety</i> , 2020, 198, 110694. | 2.9 | 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. | 1.8 | 13 |
| 47 | The Leader Peptide peTrpL Forms Antibiotic-Containing Ribonucleoprotein Complexes for Posttranscriptional Regulation of Multiresistance Genes. <i>MBio</i> , 2020, 11, . | 1.8 | 10 |
| 48 | Bacterioplankton reveal years-long retention of Atlantic deep-ocean water by the Tropic Seamount. <i>Scientific Reports</i> , 2020, 10, 4715. | 1.6 | 8 |
| 49 | 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. | 2.0 | 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. | 1.8 | 4 |
| 51 | Proteomic Adaptation of <i>Streptococcus pneumoniae</i> to the Human Antimicrobial Peptide LL-37. <i>Microorganisms</i> , 2020, 8, 413. | 1.6 | 11 |
| 52 | Verrucomicrobia use hundreds of enzymes to digest the algal polysaccharide fucoidan. <i>Nature Microbiology</i> , 2020, 5, 1026-1039. | 5.9 | 182 |
| 53 | Peptide-based quorum sensing systems in <i>Paenibacillus polymyxa</i> . <i>Life Science Alliance</i> , 2020, 3, e202000847. | 1.3 | 11 |
| 54 | Toward the Quantitative Characterization of Arginine Phosphorylations in <i>Staphylococcus aureus</i> . <i>Journal of Proteome Research</i> , 2019, 18, 265-279. | 1.8 | 10 |

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|----|---|-----|-----------|
| 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. | 4.4 | 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. | 4.4 | 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. | 3.2 | 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. | 4.4 | 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. | 1.8 | 50 |
| 60 | A marine bacterial enzymatic cascade degrades the algal polysaccharide ulvan. <i>Nature Chemical Biology</i> , 2019, 15, 803-812. | 3.9 | 97 |
| 61 | Biopearling of Interconnected Outer Membrane Vesicle Chains by a Marine <i>Flavobacterium</i> . <i>Applied and Environmental Microbiology</i> , 2019, 85, . | 1.4 | 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. | 1.9 | 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. | 1.6 | 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. | 2.5 | 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. | 0.4 | 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. | 1.8 | 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. | 2.5 | 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. | 1.6 | 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. | 2.1 | 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. | 2.2 | 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. | 1.2 | 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, . | 1.0 | 8 |

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|----|--|-----|-----------|
| 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. | 1.8 | 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. | 2.0 | 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. | 1.5 | 28 |
| 76 | Proteomic response of <i>Streptococcus pneumoniae</i> to iron limitation. <i>International Journal of Medical Microbiology</i> , 2018, 308, 713-721. | 1.5 | 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. | 1.5 | 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. | 1.8 | 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. | 1.9 | 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. | 1.3 | 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. | 1.2 | 36 |
| 82 | The Proteomic Response of <i>Bacillus pumilus</i> Cells to Glucose Starvation. <i>Proteomics</i> , 2018, 18, 1700109. | 1.3 | 10 |
| 83 | Spectral Library Based Analysis of Arginine Phosphorylations in <i>Staphylococcus aureus</i> . <i>Molecular and Cellular Proteomics</i> , 2018, 17, 335-348. | 2.5 | 41 |
| 84 | Proteomic Signatures of <i>Clostridium difficile</i> Stressed with Metronidazole, Vancomycin, or Fidaxomicin. <i>Cells</i> , 2018, 7, 213. | 1.8 | 14 |
| 85 | Iron Regulation in <i>Clostridioides difficile</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 3183. | 1.5 | 49 |
| 86 | Alphaâ€and betaâ€mannan utilization by marine <i>Bacteroidetes</i> . <i>Environmental Microbiology</i> , 2018, 20, 4127-4140. | 1.8 | 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. | 1.0 | 0 |
| 88 | A Metabolic Labeling Strategy for Relative Protein Quantification in <i>Clostridioides difficile</i> . <i>Frontiers in Microbiology</i> , 2018, 9, 2371. | 1.5 | 4 |
| 89 | A Secreted Bacterial Peptidylarginine Deiminase Can Neutralize Human Innate Immune Defenses. <i>MBio</i> , 2018, 9, . | 1.8 | 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. | 1.5 | 67 |

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| 91 | Adaptive mechanisms that provide competitive advantages to marine bacteroidetes during microalgal blooms. <i>ISME Journal</i> , 2018, 12, 2894-2906. | 4.4 | 84 |
| 92 | Proteomic analysis of bacterial (outer) membrane vesicles: progress and clinical potential. <i>Expert Review of Proteomics</i> , 2018, 15, 623-626. | 1.3 | 6 |
| 93 | Metaproteogenomic Profiling of Microbial Communities Colonizing Actively Venting Hydrothermal Chimneys. <i>Frontiers in Microbiology</i> , 2018, 9, 680. | 1.5 | 36 |
| 94 | The <i>Escherichia coli</i> Type III Secretion System 2 Has a Global Effect on Cell Surface. <i>MBio</i> , 2018, 9, . | 1.8 | 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. | 1.8 | 9 |
| 96 | Aquatic adaptation of a laterally acquired pectin degradation pathway in marine gammaproteobacteria. <i>Environmental Microbiology</i> , 2017, 19, 2320-2333. | 1.8 | 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. | 2.5 | 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. | 0.4 | 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. | 1.6 | 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. | 2.9 | 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. | 1.6 | 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. | 1.6 | 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. | 1.9 | 2 |
| 104 | Nitrogen fixation in a chemoautotrophic lucinid symbiosis. <i>Nature Microbiology</i> , 2017, 2, 16193. | 5.9 | 56 |
| 105 | Metabolic and physiological interdependencies in the <i>Bathymodiolus azoricus</i> symbiosis. <i>ISME Journal</i> , 2017, 11, 463-477. | 4.4 | 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. | 0.4 | 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. | 1.8 | 18 |
| 108 | Insight into the evolution of microbial metabolism from the deep-branching bacterium, <i>Thermovibrio ammonificans</i> . <i>ELife</i> , 2017, 6, . | 2.8 | 40 |

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|-----|--|-----|-----------|
| 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. | 1.2 | 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. | 1.8 | 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. | 1.1 | 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. | 1.6 | 328 |
| 113 | A SDD1-like subtilase is exuded by tobacco roots. <i>Functional Plant Biology</i> , 2016, 43, 141. | 1.1 | 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. | 1.2 | 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. | 3.3 | 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. | 1.0 | 10 |
| 117 | Extracellular Proteome and Citrullinome of the Oral Pathogen <i>Porphyromonas gingivalis</i> . <i>Journal of Proteome Research</i> , 2016, 15, 4532-4543. | 1.8 | 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. | 0.8 | 36 |
| 119 | Proteomics of septicemic <i>Escherichia coli</i> . <i>Proteomics - Clinical Applications</i> , 2016, 10, 1020-1024. | 0.8 | 1 |
| 120 | Costs of life - Dynamics of the protein inventory of <i>Staphylococcus aureus</i> during anaerobiosis. <i>Scientific Reports</i> , 2016, 6, 28172. | 1.6 | 38 |
| 121 | Updating the proteome of the uncultivable hemotrophic <i>Mycoplasma</i> in experimentally infected pigs. <i>Proteomics</i> , 2016, 16, 609-613. | 1.3 | 3 |
| 122 | Decoding the complete arsenal for cellulose and hemicellulose deconstruction in the highly efficient cellulose decomposer <i>Paenibacillus</i> O199. <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. | 4.4 | 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. | 1.2 | 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. | 1.5 | 9 |
| 126 | Methods and applications of absolute protein quantification in microbial systems. <i>Journal of Proteomics</i> , 2016, 136, 222-233. | 1.2 | 16 |

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|-----|--|-----|-----------|
| 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. | 2.5 | 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. | 1.2 | 87 |
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