

Stephanie Markert

List of Publications by Year in descending order

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43
papers

2,282
citations

257450

24
h-index

254184

43
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53
all docs

53
docs citations

53
times ranked

2805
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	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
3	<i>Methanosaeta</i> and <i>Candidatus Velamenicoccus archaeovorus</i> . <i>Applied and Environmental Microbiology</i> , 2022, 88, e0240721.	3.1	7
4	Differential regulation of degradation and immune pathways underlies adaptation of the ectosymbiotic nematode <i>Laxus oneistus</i> to oxic-anoxic interfaces. <i>Scientific Reports</i> , 2022, 12, .	3.3	2
5	Bacterial symbiont subpopulations have different roles in a deep-sea symbiosis. <i>ELife</i> , 2021, 10, .	6.0	17
6	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
7	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
8	Anaerobic Sulfur Oxidation Underlies Adaptation of a Chemosynthetic Symbiont to Oxic-Anoxic Interfaces. <i>MSystems</i> , 2021, 6, e0118620.	3.8	10
9	Intrinsic Mechanisms Underlying Hypoxia-Tolerant Mitochondrial Phenotype During Hypoxia-Reoxygenation Stress in a Marine Facultative Anaerobe, the Blue Mussel <i>Mytilus edulis</i> . <i>Frontiers in Marine Science</i> , 2021, 8, .	2.5	8
10	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
11	An optimized metaproteomics protocol for a holistic taxonomic and functional characterization of microbial communities from marine particles. <i>Environmental Microbiology Reports</i> , 2020, 12, 367-376.	2.4	18
12	Verrucomicrobia use hundreds of enzymes to digest the algal polysaccharide fucoidan. <i>Nature Microbiology</i> , 2020, 5, 1026-1039.	13.3	182
13	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
14	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
15	A marine bacterial enzymatic cascade degrades the algal polysaccharide ulvan. <i>Nature Chemical Biology</i> , 2019, 15, 803-812.	8.0	97
16	Bioperculation of Interconnected Outer Membrane Vesicle Chains by a Marine <i>Flavobacterium</i> . <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	20
17	Host-Microbe Interactions in the Chemosynthetic <i>Riftia pachyptila</i> Symbiosis. <i>MBio</i> , 2019, 10, .	4.1	38
18	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

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19	Microbial metal-sulfide oxidation in inactive hydrothermal vent chimneys suggested by metagenomic and metaproteomic analyses. <i>Environmental Microbiology</i> , 2019, 21, 682-701.	3.8	50
20	Transcriptomic and proteomic insight into the mechanism of cyclooctasulfur versus thiosulfate oxidation by the chemolithoautotroph <i>Sulfurimonas denitrificans</i> . <i>Environmental Microbiology</i> , 2019, 21, 244-258.	3.8	16
21	Limonene dehydrogenase hydroxylates the allylic methyl group of cyclic monoterpenes in the anaerobic terpene degradation by <i>Castellaniella defragrans</i> . <i>Journal of Biological Chemistry</i> , 2018, 293, 9520-9529.	3.4	10
22	Centrifugation-Based Enrichment of Bacterial Cell Populations for Metaproteomic Studies on Bacteria-Invertebrate Symbioses. <i>Methods in Molecular Biology</i> , 2018, 1841, 319-334.	0.9	7
23	Alpha- and beta-mannan utilization by marine <i>Bacteroidetes</i> . <i>Environmental Microbiology</i> , 2018, 20, 4127-4140.	3.8	31
24	Adaptive mechanisms that provide competitive advantages to marine bacteroidetes during microalgal blooms. <i>ISME Journal</i> , 2018, 12, 2894-2906.	9.8	84
25	Metaproteogenomic Profiling of Microbial Communities Colonizing Actively Venting Hydrothermal Chimneys. <i>Frontiers in Microbiology</i> , 2018, 9, 680.	3.5	36
26	Anaerobic Degradation of Bicyclic Monoterpenes in <i>Castellaniella defragrans</i> . <i>Metabolites</i> , 2018, 8, 12.	2.9	1
27	Exploiting fine-scale genetic and physiological variation of closely related microbes to reveal unknown enzyme functions. <i>Journal of Biological Chemistry</i> , 2017, 292, 13056-13067.	3.4	18
28	Nitrogen fixation in a chemoautotrophic lucinid symbiosis. <i>Nature Microbiology</i> , 2017, 2, 16193.	13.3	56
29	Metabolic and physiological interdependencies in the <i>Bathymodiolus azoricus</i> symbiosis. <i>ISME Journal</i> , 2017, 11, 463-477.	9.8	116
30	Insight into the evolution of microbial metabolism from the deep-branching bacterium, <i>Thermovibrio ammonificans</i> . <i>ELife</i> , 2017, 6, .	6.0	40
31	Genome sequence of the sulfur-oxidizing <i>Bathymodiolus thermophilus</i> gill endosymbiont. <i>Standards in Genomic Sciences</i> , 2017, 12, 50.	1.5	32
32	The anaerobic linalool metabolism in <i>Thauera linaloolentis</i> 47 Lol. <i>BMC Microbiology</i> , 2016, 16, 76.	3.3	13
33	Linalool isomerase, a membrane-anchored enzyme in the anaerobic monoterpene degradation in <i>Thauera linaloolentis</i> 47Lol. <i>BMC Biochemistry</i> , 2016, 17, 6.	4.4	14
34	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
35	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
36	The oxygen-independent metabolism of cyclic monoterpenes in <i>Castellaniella defragrans</i> 65Phen. <i>BMC Microbiology</i> , 2014, 14, 164.	3.3	19

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37	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
38	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
39	Physiological homogeneity among the endosymbionts of <i>Riftia pachyptila</i> and <i>Tevnia jerichonana</i> revealed by proteogenomics. <i>ISME Journal</i> , 2012, 6, 766-776.	9.8	80
40	Status quo in physiological proteomics of the uncultured <i>Riftia pachyptila</i> endosymbiont. <i>Proteomics</i> , 2011, 11, 3106-3117.	2.2	34
41	Cytoplasmic and Periplasmic Proteomic Signatures of Exponentially Growing Cells of the Psychrophilic Bacterium <i>Pseudoalteromonas haloplanktis</i> TAC125. <i>Applied and Environmental Microbiology</i> , 2011, 77, 1276-1283.	3.1	30
42	Proteomics of marine bacteria. <i>Electrophoresis</i> , 2008, 29, 2603-2616.	2.4	28
43	Physiological Proteomics of the Uncultured Endosymbiont of <i>Riftia pachyptila</i> . <i>Science</i> , 2007, 315, 247-250.	12.6	207