

StÃ©phan Fuchs

List of Publications by Year in descending order

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30
papers

1,087
citations

430874

18
h-index

642732

23
g-index

34
all docs

34
docs citations

34
times ranked

1638
citing authors

#	ARTICLE	IF	CITATIONS
1	Exploring functional contexts of symbiotic sustain within lichen-associated bacteria by comparative omics. ISME Journal, 2015, 9, 412-424.	9.8	238
2	Challenges and promise at the interface of metaproteomics and genomics: an overview of recent progress in metaproteogenomic data analysis. Expert Review of Proteomics, 2019, 16, 375-390.	3.0	86
3	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
4	A Metaproteomics Approach to Elucidate Host and Pathogen Protein Expression during Catheter-Associated Urinary Tract Infections (CAUTIs). Molecular and Cellular Proteomics, 2015, 14, 989-1008.	3.8	63
5	A proteomic view of cell physiology and virulence of Staphylococcus aureus. International Journal of Medical Microbiology, 2010, 300, 76-87.	3.6	62
6	Physiological proteomics and stress/starvation responses in Bacillus subtilis and Staphylococcus aureus. Research in Microbiology, 2009, 160, 245-258.	2.1	57
7	Soil and leaf litter metaproteomics—a brief guideline from sampling to understanding. FEMS Microbiology Ecology, 2016, 92, fiw180.	2.7	54
8	Microbial functionality as affected by experimental warming of a temperate mountain forest soil—a metaproteomics survey. Applied Soil Ecology, 2017, 117-118, 196-202.	4.3	48
9	Symbiotic Interplay of Fungi, Algae, and Bacteria within the Lung Lichen <i>Lobaria pulmonaria</i> L. Hoffm. as Assessed by State-of-the-Art Metaproteomics. Journal of Proteome Research, 2017, 16, 2160-2173.	3.7	43
10	A complete and flexible workflow for metaproteomics data analysis based on MetaProteomeAnalyzer and Prophan. Nature Protocols, 2020, 15, 3212-3239.	12.0	42
11	Costs of life - Dynamics of the protein inventory of Staphylococcus aureus during anaerobiosis. Scientific Reports, 2016, 6, 28172.	3.3	38
12	Response of Microbial Communities and Their Metabolic Functions to Drying—Rewetting Stress in a Temperate Forest Soil. Microorganisms, 2019, 7, 129.	3.6	35
13	Critical Assessment of MetaProteome Investigation (CAMPI): a multi-laboratory comparison of established workflows. Nature Communications, 2021, 12, 7305.	12.8	34
14	Aureolib — A Proteome Signature Library: Towards an Understanding of Staphylococcus aureus Pathophysiology. PLoS ONE, 2013, 8, e70669.	2.5	28
15	Survey of metaproteomics software tools for functional microbiome analysis. PLoS ONE, 2020, 15, e0241503.	2.5	28
16	<i>Staphylococcus aureus</i> physiological growth limitations: Insights from flux calculations built on proteomics and external metabolite data. Proteomics, 2011, 11, 1915-1935.	2.2	27
17	Metaproteomics analysis of microbial diversity of human saliva and tongue dorsum in young healthy individuals. Journal of Oral Microbiology, 2019, 11, 1654786.	2.7	27
18	Data visualization in environmental proteomics. Proteomics, 2013, 13, 2805-2821.	2.2	21

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19	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
20	Aurantimycin resistance genes contribute to survival of <i>Listeria monocytogenes</i> during life in the environment. <i>Molecular Microbiology</i> , 2019, 111, 1009-1024.	2.5	16
21	A <i>Staphylococcus aureus</i> Proteome Overview: Shared and Specific Proteins and Protein Complexes from Representative Strains of All Three Clades. <i>Proteomes</i> , 2016, 4, 8.	3.5	10
22	Comparative analysis of Salivette® and paraffin gum preparations for establishment of a metaproteomics analysis pipeline for stimulated human saliva. <i>Journal of Oral Microbiology</i> , 2018, 10, 1428006.	2.7	10
23	PadR-type repressors controlling production of a non-canonical FtsW/RodA homologue and other trans-membrane proteins. <i>Scientific Reports</i> , 2019, 9, 10023.	3.3	9
24	Protein expression profiling of <i>Staphylococcus aureus</i> in response to the bacteriocin bovicin HC5. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 7857-7869.	3.6	0
25	Survey of metaproteomics software tools for functional microbiome analysis. , 2020, 15, e0241503.		0
26	Survey of metaproteomics software tools for functional microbiome analysis. , 2020, 15, e0241503.		0
27	Survey of metaproteomics software tools for functional microbiome analysis. , 2020, 15, e0241503.		0
28	Survey of metaproteomics software tools for functional microbiome analysis. , 2020, 15, e0241503.		0
29	Survey of metaproteomics software tools for functional microbiome analysis. , 2020, 15, e0241503.		0
30	Survey of metaproteomics software tools for functional microbiome analysis. , 2020, 15, e0241503.		0