

StÃ©phan Fuchs

List of Publications by Year in descending order

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Version: 2024-02-01

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	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
2	Critical Assessment of MetaProteome Investigation (CAMPI): a multi-laboratory comparison of established workflows. <i>Nature Communications</i> , 2021, 12, 7305.	12.8	34
3	A complete and flexible workflow for metaproteomics data analysis based on MetaProteomeAnalyzer and Prophane. <i>Nature Protocols</i> , 2020, 15, 3212-3239.	12.0	42
4	Survey of metaproteomics software tools for functional microbiome analysis. <i>PLoS ONE</i> , 2020, 15, e0241503.	2.5	28
5	Survey of metaproteomics software tools for functional microbiome analysis. , 2020, 15, e0241503.		0
6	Survey of metaproteomics software tools for functional microbiome analysis. , 2020, 15, e0241503.		0
7	Survey of metaproteomics software tools for functional microbiome analysis. , 2020, 15, e0241503.		0
8	Survey of metaproteomics software tools for functional microbiome analysis. , 2020, 15, e0241503.		0
9	Survey of metaproteomics software tools for functional microbiome analysis. , 2020, 15, e0241503.		0
10	Survey of metaproteomics software tools for functional microbiome analysis. , 2020, 15, e0241503.		0
11	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
12	Metaproteomics analysis of microbial diversity of human saliva and tongue dorsum in young healthy individuals. <i>Journal of Oral Microbiology</i> , 2019, 11, 1654786.	2.7	27
13	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
14	Response of Microbial Communities and Their Metabolic Functions to Drying–Rewetting Stress in a Temperate Forest Soil. <i>Microorganisms</i> , 2019, 7, 129.	3.6	35
15	Challenges and promise at the interface of metaproteomics and genomics: an overview of recent progress in metaproteogenomic data analysis. <i>Expert Review of Proteomics</i> , 2019, 16, 375-390.	3.0	86
16	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
17	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
18	Microbial functionality as affected by experimental warming of a temperate mountain forest soil—A metaproteomics survey. <i>Applied Soil Ecology</i> , 2017, 117-118, 196-202.	4.3	48

#	ARTICLE	IF	CITATIONS
19	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. <i>Journal of Proteome Research</i> , 2017, 16, 2160-2173.	3.7	43
20	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
21	Soil and leaf litter metaproteomics—a brief guideline from sampling to understanding. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw180.	2.7	54
22	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
23	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
24	Exploring functional contexts of symbiotic sustain within lichen-associated bacteria by comparative omics. <i>ISME Journal</i> , 2015, 9, 412-424.	9.8	238
25	Data visualization in environmental proteomics. <i>Proteomics</i> , 2013, 13, 2805-2821.	2.2	21
26	Aureolib – A Proteome Signature Library: Towards an Understanding of <i>Staphylococcus aureus</i> Pathophysiology. <i>PLoS ONE</i> , 2013, 8, e70669.	2.5	28
27	<i>Staphylococcus aureus</i> physiological growth limitations: Insights from flux calculations built on proteomics and external metabolite data. <i>Proteomics</i> , 2011, 11, 1915-1935.	2.2	27
28	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
29	Physiological proteomics and stress/starvation responses in <i>Bacillus subtilis</i> and <i>Staphylococcus aureus</i> . <i>Research in Microbiology</i> , 2009, 160, 245-258.	2.1	57
30	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