Jakob Herschend

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/10965245/publications.pdf

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25 1,088 11 18
papers citations h-index g-index

25 25 25 1469 all docs docs citations times ranked citing authors

#	Article	IF	CITATIONS
1	Metabolic Profiling of Interspecies Interactions During Sessile Bacterial Cultivation Reveals Growth and Sporulation Induction in Paenibacillus amylolyticus in Response to Xanthomonas retroflexus. Frontiers in Cellular and Infection Microbiology, 2022, 12, 805473.	3.9	1
2	Metagenomic analysis of a keratin-degrading bacterial consortium provides insight into the keratinolytic mechanisms. Science of the Total Environment, 2021, 761, 143281.	8.0	25
3	Impact of Tellurite on the Metabolism of Paenibacillus pabuli AL109b With Flagellin Production Explaining High Reduction Capacity. Frontiers in Microbiology, 2021, 12, 718963.	3.5	2
4	Biofilms can act as plasmid reserves in the absence of plasmid specific selection. Npj Biofilms and Microbiomes, 2021, 7, 78.	6.4	14
5	The T-shirt microbiome is distinct between individuals and shaped by washing and fabric type. Environmental Research, 2020, 185, 109449.	7.5	15
6	Community-intrinsic properties enhance keratin degradation from bacterial consortia. PLoS ONE, 2020, 15, e0228108.	2.5	16
7	Community-intrinsic properties enhance keratin degradation from bacterial consortia., 2020, 15, e0228108.		O
8	Community-intrinsic properties enhance keratin degradation from bacterial consortia., 2020, 15, e0228108.		0
9	Community-intrinsic properties enhance keratin degradation from bacterial consortia., 2020, 15, e0228108.		O
10	Community-intrinsic properties enhance keratin degradation from bacterial consortia., 2020, 15, e0228108.		0
11	Heavy metal exposure causes changes in the metabolic health-associated gut microbiome and metabolites. Environment International, 2019, 126, 454-467.	10.0	125
12	Construction of Simplified Microbial Consortia to Degrade Recalcitrant Materials Based on Enrichment and Dilution-to-Extinction Cultures. Frontiers in Microbiology, 2019, 10, 3010.	3.5	39
13	Disease-induced assemblage of a plant-beneficial bacterial consortium. ISME Journal, 2018, 12, 1496-1507.	9.8	603
14	Biological control of rice sheath blight using hyphae-associated bacteria: development of an in planta screening assay to predict biological control agent performance under field conditions. BioControl, 2018, 63, 843-853.	2.0	10
15	Enrichment and characterization of an environmental microbial consortium displaying efficient keratinolytic activity. Bioresource Technology, 2018, 270, 303-310.	9.6	42
16	Enhanced bacterial mutualism through an evolved biofilm phenotype. ISME Journal, 2018, 12, 2608-2618.	9.8	34
17	<i>In Vitro</i> Community Synergy between Bacterial Soil Isolates Can Be Facilitated by pH Stabilization of the Environment. Applied and Environmental Microbiology, 2018, 84, .	3.1	18
18	A meta-proteomics approach to study the interspecies interactions affecting microbial biofilm development in a model community. Scientific Reports, 2017, 7, 16483.	3.3	51

#	Article	IF	CITATIONS
19	Genome Sequence of <i>Kocuria palustris</i> Strain W4. Genome Announcements, 2016, 4, .	0.8	0
20	Genome Sequence of Kocuria varians G6 Isolated from a Slaughterhouse in Denmark. Genome Announcements, $2016, 4, .$	0.8	2
21	Draft Genome Assembly of Two Pseudoclavibacter helvolus Strains, G8 and W3, Isolated from Slaughterhouse Environments. Genome Announcements, 2016, 4, .	0.8	0
22	Genome Sequence of Psychrobacter cibarius Strain W1. Genome Announcements, 2016, 4, .	0.8	1
23	Genome Sequence of Arthrobacter antarcticus Strain W2, Isolated from a Slaughterhouse. Genome Announcements, 2016, 4, .	0.8	1
24	Draft Genome Sequences of Two <i>Kocuria</i> Isolates, <i>K. salsicia</i> G1 and <i>K. rhizophila</i> G2, Isolated from a Slaughterhouse in Denmark. Genome Announcements, 2016, 4, .	0.8	1
25	Interspecies interactions result in enhanced biofilm formation by co-cultures of bacteria isolated from a food processing environment. Food Microbiology, 2015, 51, 18-24.	4.2	88