Ruben Props

List of Publications by Year
in descending order

36 papers	1,437 citations	394421 19 h-index	361022 35 g-index
52 all docs	52 docs citations	52 times ranked	2453 citing authors

#	Article	IF	Citations
1	Lignocellulose Fermentation Products Generated by Giant Panda Gut Microbiomes Depend Ultimately on pH Rather than Portion of Bamboo: A Preliminary Study. Microorganisms, 2022, 10, 978.	3.6	0
2	Rearing water microbiomes in white leg shrimp (<scp>Litopenaeus vannamei</scp>) larviculture assemble stochastically and are influenced by the microbiomes of live feed products. Environmental Microbiology, 2021, 23, 281-298.	3.8	17
3	Cytometric fingerprints of gut microbiota predict Crohnâ€™s disease state. ISME Journal, 2021, 15, 354-358.	9.8	19
4	PhenoGMM: Gaussian Mixture Modeling of Cytometry Data Quantifies Changes in Microbial Community Structure. MSphere, 2021, 6, .	2.9	21
5	Computational Analysis of Microbial Flow Cytometry Data. MSystems, 2021, 6, .	3.8	20
6	Predicting the Presence and Abundance of Bacterial Taxa in Environmental Communities through Flow Cytometric Fingerprinting. MSystems, 2021, 6, e0055121.	3.8	9
7	Triangulation of microbial fingerprinting in anaerobic digestion reveals consistent fingerprinting profiles. Water Research, 2021, 202, 117422.	11.3	12
8	Flow cytometry for rapid characterisation of microbial community dynamics in waste stabilisation ponds. Water Research, 2020, 169, 115243.	11.3	26
9	Adaptation and characterization of thermophilic anammox in bioreactors. Water Research, 2020, 172, 115462.	11.3	21
10	Discriminating Bacterial Phenotypes at the Population and Singleâ€€Cell Level: A Comparison of Flow Cytometry and Raman Spectroscopy Fingerprinting. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2020, 97, 713-726.	1.5	16
11	Raman Spectroscopy-Based Measurements of Single-Cell Phenotypic Diversity in Microbial Populations. MSphere, 2020, 5, .	2.9	17
12	Microhabitats are associated with diversityâ€“productivity relationships in freshwater bacterial communities. FEMS Microbiology Ecology, 2020, 96, .	2.7	13
13	Short-term supplementation of celecoxib-shifted butyrate production on a simulated model of the gut microbial ecosystem and ameliorated in vitro inflammation. Npj Biofilms and Microbiomes, 2020, 6, 9.	6.4	24
14	Substrate-Dependent Fermentation of Bamboo in Giant Panda Gut Microbiomes: Leaf Primarily to Ethanol and Pith to Lactate. Frontiers in Microbiology, 2020, 11, 530.	3.5	7
15	Temperature and Nutrient Levels Correspond with Lineage-Specific Microdiversification in the Ubiquitous and Abundant Freshwater Genus Limnohabitans. Applied and Environmental Microbiology, 2020, 86, .	3.1	16
16	Propionate-Producing Consortium Restores Antibiotic-Induced Dysbiosis in a Dynamic in vitro Model of the Human Intestinal Microbial Ecosystem. Frontiers in Microbiology, 2019, 10, 1206.	3.5	84
17	Gene Expansion and Positive Selection as Bacterial Adaptations to Oligotrophic Conditions. MSphere, 2019, 4, .	2.9	28
18	Coculturing Bacteria Leads to Reduced Phenotypic Heterogeneities. Applied and Environmental Microbiology, 2019, 85, .	3.1	37

#	Article	IF	Citations
19	Granular fermentation enables high rate caproic acid production from solid-free thin stillage. Green Chemistry, 2019, 21, 1330-1339.	9.0	60
20	Randomized Lasso Links Microbial Taxa with Aquatic Functional Groups Inferred from Flow Cytometry. MSystems, 2019, 4, .	3.8	14
21	Initial evenness determines diversity and cell density dynamics in synthetic microbial ecosystems. Scientific Reports, 2018, 8, 340.	3.3	12
22	Plant and soil microbe responses to light, warming and nitrogen addition in a temperate forest. Functional Ecology, 2018, 32, 1293-1303.	3.6	38
23	Flow cytometric monitoring of bacterioplankton phenotypic diversity predicts high populationâ€specific feeding rates by invasive dreissenid mussels. Environmental Microbiology, 2018, 20, 521-534.	3.8	31
24	Drinking water bacterial communities exhibit specific and selective necrotrophic growth. Npj Clean Water, 2018, 1, .	8.0	17
25	Detection of microbial disturbances in a drinking water microbial community through continuous acquisition and advanced analysis of flow cytometry data. Water Research, 2018, 145, 73-82.	11.3	29
26	Stripping flow cytometry: How many detectors do we need for bacterial identification?. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2017, 91, 1184-1191.	1.5	17
27	Absolute quantification of microbial taxon abundances. ISME Journal, 2017, 11, 584-587.	9.8	273
28	Reconciliation between operational taxonomic units and species boundaries. FEMS Microbiology Ecology, 2017, 93, .	2.7	71
29	A Clostridium Group IV Species Dominates and Suppresses a Mixed Culture Fermentation by Tolerance to Medium Chain Fatty Acids Products. Frontiers in Bioengineering and Biotechnology, 2017, 5, 8.	4.1	71
30	Laboratory-Scale Simulation and Real-Time Tracking of a Microbial Contamination Event and Subsequent Shock-Chlorination in Drinking Water. Frontiers in Microbiology, 2017, 8, 1900.	3.5	37
31	Biological Recovery of Platinum Complexes from Diluted Aqueous Streams by Axenic Cultures. PLoS ONE, 2017, 12, e0169093.	2.5	29
32	Flow Cytometric Single-Cell Identification of Populations in Synthetic Bacterial Communities. PLoS ONE, 2017, 12, e0169754.	2.5	31
33	Presence does not imply activity: DNA and RNA patterns differ in response to salt perturbation in anaerobic digestion. Biotechnology for Biofuels, 2016, 9, 244.	6.2	81
34	Measuring the biodiversity of microbial communities by flow cytometry. Methods in Ecology and Evolution, 2016, 7, 1376-1385.	5.2	161
35	Platinum Recovery from Synthetic Extreme Environments by Halophilic Bacteria. Environmental Science & Technology, 2016, 50, 2619-2626.	10.0	28
36	5-Fluorouracil sensitivity varies among oral micro-organisms. Journal of Medical Microbiology, 2016, 65, 775-783.	1.8	21