

Jacob A Cram

List of Publications by Year in descending order

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Version: 2024-02-01

26
papers

2,797
citations

567281

15
h-index

610901

24
g-index

35
all docs

35
docs citations

35
times ranked

4058
citing authors

#	ARTICLE	IF	CITATIONS
1	Hatchery crashes among shellfish research hatcheries along the Atlantic coast of the United States: A case study of production analysis at Horn Point Laboratory. <i>Aquaculture</i> , 2022, 546, 737259.	3.5	14
2	Microbiota of <i>Crassostrea virginica</i> larvae during a hatchery crash and under normal production: Amplicon sequence data. <i>Data in Brief</i> , 2022, 40, 107755.	1.0	1
3	Slow Particle Remineralization, Rather Than Suppressed Disaggregation, Drives Efficient Flux Transfer Through the Eastern Tropical North Pacific Oxygen Deficient Zone. <i>Global Biogeochemical Cycles</i> , 2022, 36, .	4.9	11
4	NetGAM: Using generalized additive models to improve the predictive power of ecological network analyses constructed using time-series data. <i>ISME Communications</i> , 2022, 2, .	4.2	1
5	Variable particle size distributions reduce the sensitivity of global export flux to climate change. <i>Biogeosciences</i> , 2021, 18, 229-250.	3.3	10
6	Explore mediated co-varying dynamics in microbial community using integrated local similarity and liquid association analysis. <i>BMC Genomics</i> , 2019, 20, 185.	2.8	20
7	Human gut microbiota is associated with HIV-reactive immunoglobulin at baseline and following HIV vaccination. <i>PLoS ONE</i> , 2019, 14, e0225622.	2.5	20
8	Vertical and Seasonal Patterns Control Bacterioplankton Communities at Two Horizontally Coherent Coastal Upwelling Sites off Galicia (NW Spain). <i>Microbial Ecology</i> , 2018, 76, 866-884.	2.8	25
9	Utilizing gnotobiotic models to inform the role of the microbiome in vaccine response heterogeneity. <i>Current Opinion in HIV and AIDS</i> , 2018, 13, 1-8.	3.8	8
10	The Role of Particle Size, Ballast, Temperature, and Oxygen in the Sinking Flux to the Deep Sea. <i>Global Biogeochemical Cycles</i> , 2018, 32, 858-876.	4.9	65
11	Dynamics and interactions of highly resolved marine plankton via automated high-frequency sampling. <i>ISME Journal</i> , 2018, 12, 2417-2432.	9.8	66
12	Deep ocean nutrients imply large latitudinal variation in particle transfer efficiency. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 8606-8611.	7.1	118
13	Dilution reveals how viral lysis and grazing shape microbial communities. <i>Limnology and Oceanography</i> , 2016, 61, 889-905.	3.1	39
14	Correlation detection strategies in microbial data sets vary widely in sensitivity and precision. <i>ISME Journal</i> , 2016, 10, 1669-1681.	9.8	593
15	New insights into relationships between active and dormant organisms, phylogenetic diversity and ecosystem productivity. <i>Molecular Ecology</i> , 2015, 24, 5767-5769.	3.9	8
16	Statistical significance approximation in local trend analysis of high-throughput time-series data using the theory of Markov chains. <i>BMC Bioinformatics</i> , 2015, 16, 301.	2.6	13
17	Cross-depth analysis of marine bacterial networks suggests downward propagation of temporal changes. <i>ISME Journal</i> , 2015, 9, 2573-2586.	9.8	105
18	Marine microbial community dynamics and their ecological interpretation. <i>Nature Reviews Microbiology</i> , 2015, 13, 133-146.	28.6	681

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19	Seasonal and interannual variability of the marine bacterioplankton community throughout the water column over ten years. ISME Journal, 2015, 9, 563-580.	9.8	219
20	Marine Bacterial, Archaeal, and Protistan Association Networks. , 2015, , 305-313.		0
21	Temporal variability and coherence of euphotic zone bacterial communities over a decade in the Southern California Bight. ISME Journal, 2013, 7, 2259-2273.	9.8	162
22	Short-term observations of marine bacterial and viral communities: patterns, connections and resilience. ISME Journal, 2013, 7, 1274-1285.	9.8	144
23	Efficient statistical significance approximation for local similarity analysis of high-throughput time series data. Bioinformatics, 2013, 29, 230-237.	4.1	137
24	Marine Bacterial, Archaeal, and Protistan Association Networks. , 2013, , 1-10.		2
25	Accurate Genome Relative Abundance Estimation Based on Shotgun Metagenomic Reads. PLoS ONE, 2011, 6, e27992.	2.5	105
26	Extended local similarity analysis (eLSA) of microbial community and other time series data with replicates. BMC Systems Biology, 2011, 5, S15.	3.0	223