Elizabeth Ann Dinsdale

List of Publications by Year in descending order

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80 papers

8,095 citations

34 h-index 79698 73 g-index

91 all docs 91 docs citations

91 times ranked 9703 citing authors

#	Article	IF	CITATIONS
1	The Epidermal Microbiome Within an Aggregation of Leopard Sharks (Triakis semifasciata) Has Taxonomic Flexibility with Gene Functional Stability Across Three Time-points. Microbial Ecology, 2023, 85, 747-764.	2.8	6
2	Exploring the taxonomical and functional profile of As Burgas hot spring focusing on thermostable \hat{l}^2 -galactosidases. Scientific Reports, 2021, 11, 101.	3.3	11
3	Reducing Data Deficiencies: Preliminary Elasmobranch Fisheries Surveys in India, Identify Range Extensions and Large Proportions of Female and Juvenile Landings. Frontiers in Marine Science, 2021, 8,	2.5	3
4	Elasmobranch microbiomes: emerging patterns and implications for host health and ecology. Animal Microbiome, 2021, 3, 61.	3.8	11
5	There Is More than Multiple Choice: Crowd-Sourced Assessment Tips for Online, Hybrid, and Face-to-Face Environments. Journal of Microbiology and Biology Education, 2021, 22, .	1.0	2
6	Microbial abundance, composition, and function in nectar are shaped by flower visitor identity. FEMS Microbiology Ecology, 2020, 96, .	2.7	46
7	The skin microbiome of elasmobranchs follows phylosymbiosis, but in teleost fishes, the microbiomes converge. Microbiome, 2020, 8, 93.	11.1	37
8	Mitochondrial genome of the Smoothnose wedgefish Rhynchobatus laevis from the Western Indian Ocean. Mitochondrial DNA Part B: Resources, 2020, 5, 2083-2084.	0.4	5
9	Complete mitochondrial genome of the whitetip reef shark Triaenodon obesus from the British Indian Ocean Territory Marine Protected Area. Mitochondrial DNA Part B: Resources, 2020, 5, 2347-2349.	0.4	O
10	Incubators: Building community networks and developing open educational resources to integrate bioinformatics into life science education. Biochemistry and Molecular Biology Education, 2020, 48, 381-390.	1.2	18
11	Latitude and chlorophyll a density drive the distribution of carbohydrateâ€active enzymes in the planktonic microbial fraction of the epipelagic zone. Environmental Microbiology Reports, 2020, 12, 473-485.	2.4	2
12	Mitochondrial genome of the silky shark Carcharhinus falciformis from the British Indian Ocean Territory Marine Protected Area. Mitochondrial DNA Part B: Resources, 2020, 5, 2416-2417.	0.4	2
13	Genomic and ecological attributes of marine bacteriophages encoding bacterial virulence genes. BMC Genomics, 2020, 21, 126.	2.8	26
14	Mitochondrial genome to aid species delimitation and effective conservation of the Sharpnose Guitarfish (Glaucostegus granulatus). Meta Gene, 2020, 24, 100648.	0.6	13
15	Modeling of the Coral Microbiome: the Influence of Temperature and Microbial Network. MBio, 2020, 11, .	4.1	30
16	Complete mitochondrial genome of the gray reef shark, <i>Carcharhinus amblyrhynchos</i> (Carcharhiniformes: Carcharhinidae). Mitochondrial DNA Part B: Resources, 2020, 5, 2080-2082.	0.4	7
17	Mitochondrial genome of the Silvertip shark, <i>Carcharhinus albimarginatus, </i> from the British Indian Ocean Territory. Mitochondrial DNA Part B: Resources, 2020, 5, 2085-2086.	0.4	6
18	Global phylogeography and ancient evolution of the widespread human gut virus crAssphage. Nature Microbiology, 2019, 4, 1727-1736.	13.3	184

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19	Taking Advantage of the Genomics Revolution for Monitoring and Conservation of Chondrichthyan Populations. Diversity, 2019, 11, 49.	1.7	18
20	PHANOTATE: a novel approach to gene identification in phage genomes. Bioinformatics, 2019, 35, 4537-4542.	4.1	147
21	†Genome skimming' with the MinION hand-held sequencer identifies CITES-listed shark species in India' exports market. Scientific Reports, 2019, 9, 4476.	s 3.3	45
22	Barriers to integration of bioinformatics into undergraduate life sciences education: A national study of US life sciences faculty uncover significant barriers to integrating bioinformatics into undergraduate instruction. PLoS ONE, 2019, 14, e0224288.	2.5	40
23	Title is missing!. , 2019, 14, e0224288.		0
24	Title is missing!. , 2019, 14, e0224288.		0
25	Title is missing!. , 2019, 14, e0224288.		0
26	Title is missing!. , 2019, 14, e0224288.		0
27	Mitochondrial recovery from shotgun metagenome sequencing enabling phylogenetic analysis of the common thresher shark (Alopias vulpinus). Meta Gene, 2018, 15, 10-15.	0.6	11
28	Rhodoliths holobionts in a changing ocean: host-microbes interactions mediate coralline algae resilience under ocean acidification. BMC Genomics, 2018, 19, 701.	2.8	34
29	Novel ssDNA Viruses Detected in the Virome of Bleached, Habitat-Forming Kelp Ecklonia radiata. Frontiers in Marine Science, 2018, 4, .	2.5	14
30	Bioinformatics core competencies for undergraduate life sciences education. PLoS ONE, 2018, 13, e0196878.	2.5	93
31	Elevated temperature drives kelp microbiome dysbiosis, while elevated carbon dioxide induces water microbiome disruption. PLoS ONE, 2018, 13, e0192772.	2.5	95
32	Functional characterization of ligninolytic Klebsiella spp. strains associated with soil and freshwater. Archives of Microbiology, 2018, 200, 1267-1278.	2.2	18
33	Diversity of Microbial Carbohydrate-Active enZYmes (CAZYmes) Associated with Freshwater and Soil Samples from Caatinga Biome. Microbial Ecology, 2017, 74, 89-105.	2.8	19
34	The skin microbiome of the common thresher shark (<i>Alopias vulpinus</i>) has low taxonomic and gene function $\hat{1}^2\hat{a}\in d$ iversity. Environmental Microbiology Reports, 2017, 9, 357-373.	2.4	47
35	Microbial processes driving coral reef organic carbon flow. FEMS Microbiology Reviews, 2017, 41, 575-595.	8.6	67
36	Distinct biogeographical patterns of marine bacterial taxonomy and functional genes. Global Ecology and Biogeography, 2017, 26, 177-190.	5.8	65

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37	Bacterial Community Associated with the Reef Coral Mussismilia braziliensis's Momentum Boundary Layer over a Diel Cycle. Frontiers in Microbiology, 2017, 8, 784.	3.5	30
38	Optimizing and evaluating the reconstruction of Metagenome-assembled microbial genomes. BMC Genomics, 2017, 18, 915.	2.8	59
39	Aura-biomes are present in the water layer above coral reef benthic macro-organisms. PeerJ, 2017, 5, e3666.	2.0	23
40	Nearshore Pelagic Microbial Community Abundance Affects Recruitment Success of Giant Kelp, Macrocystis pyrifera. Frontiers in Microbiology, 2016, 7, 1800.	3.5	18
41	Global microbialization of coral reefs. Nature Microbiology, 2016, 1, 16042.	13.3	214
42	Can we measure beauty? Computational evaluation of coral reef aesthetics. PeerJ, 2015, 3, e1390.	2.0	31
43	Genomic Comparison of the Closely-Related Salmonella enterica Serovars Enteritidis, Dublin and Gallinarum. PLoS ONE, 2015, 10, e0126883.	2.5	39
44	Copper tolerance and distribution of epibiotic bacteria associated with giant kelp Macrocystis pyrifera in southern California. Ecotoxicology, 2015, 24, 1131-1140.	2.4	7
45	NIBLSE: A Network for Integrating Bioinformatics into Life Sciences Education. CBE Life Sciences Education, 2015, 14, le3.	2.3	30
46	Baseline Assessment of Mesophotic Reefs of the Vit \tilde{A}^3 ria-Trindade Seamount Chain Based on Water Quality, Microbial Diversity, Benthic Cover and Fish Biomass Data. PLoS ONE, 2015, 10, e0130084.	2.5	81
47	Experimental Metagenomics: Influence of Pulses of Carbon Dioxide on Kelp Forest Microbial Ecology. , 2015, , 176-182.		O
48	Local genomic adaptation of coral reef-associated microbiomes to gradients of natural variability and anthropogenic stressors. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 10227-10232.	7.1	220
49	A highly abundant bacteriophage discovered in the unknown sequences of human faecal metagenomes. Nature Communications, 2014, 5, 4498.	12.8	617
50	Sequencing at sea: challenges and experiences in Ion Torrent PGM sequencing during the 2013 Southern Line Islands Research Expedition. Peerl, 2014, 2, e520.	2.0	19
51	Microbes, metagenomes and marine mammals: enabling the next generation of scientist to enter the genomic era. BMC Genomics, 2013, 14, 600.	2.8	27
52	Combining de novo and reference-guided assembly with scaffold_builder. Source Code for Biology and Medicine, 2013, 8, 23.	1.7	59
53	Multivariate analysis of functional metagenomes. Frontiers in Genetics, 2013, 4, 41.	2.3	47
54	Metagenomic Insights into Anaerobic Metabolism along an Arctic Peat Soil Profile. PLoS ONE, 2013, 8, e64659.	2.5	121

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55	Black reefs: iron-induced phase shifts on coral reefs. ISME Journal, 2012, 6, 638-649.	9.8	65
56	Characterization of the ELPhiS Prophage from Salmonella enterica Serovar Enteritidis Strain LK5. Applied and Environmental Microbiology, 2012, 78, 1785-1793.	3.1	23
57	Oxygen minimum zones harbour novel viral communities with low diversity. Environmental Microbiology, 2012, 14, 3043-3065.	3.8	68
58	Abrolhos Bank Reef Health Evaluated by Means of Water Quality, Microbial Diversity, Benthic Cover, and Fish Biomass Data. PLoS ONE, 2012, 7, e36687.	2.5	125
59	Assembly Rules of Reef Corals Are Flexible along a Steep Climatic Gradient. Current Biology, 2012, 22, 736-741.	3.9	81
60	Fish or Germs? Microbial Dynamics Associated with Changing Trophic Structures on Coral Reefs., 2011,, 231-240.		33
61	Substrate Type Determines Metagenomic Profiles from Diverse Chemical Habitats. PLoS ONE, 2011, 6, e25173.	2.5	26
62	Microbes. Encyclopedia of Earth Sciences Series, 2011, , 697-698.	0.1	0
63	Viral and microbial community dynamics in four aquatic environments. ISME Journal, 2010, 4, 739-751.	9.8	387
64	The Lagoon at Caroline/Millennium Atoll, Republic of Kiribati: Natural History of a Nearly Pristine Ecosystem. PLoS ONE, 2010, 5, e10950.	2.5	22
65	Do the organic sulfur compounds DMSP and DMS drive coral microbial associations?. Trends in Microbiology, 2010, 18, 101-108.	7.7	203
66	Linking Ecological and Perceptual Assessments for Environmental Management: a Coral Reef Case Study. Ecology and Society, 2009, 14, .	2.3	6
67	Hyperspectral and Physiological Analyses of Coral-Algal Interactions. PLoS ONE, 2009, 4, e8043.	2.5	98
68	The GAAS Metagenomic Tool and Its Estimations of Viral and Microbial Average Genome Size in Four Major Biomes. PLoS Computational Biology, 2009, 5, e1000593.	3.2	177
69	Metagenomic and stable isotopic analyses of modern freshwater microbialites in Cuatro Ciénegas, Mexico. Environmental Microbiology, 2009, 11, 16-34.	3.8	204
70	Metagenomic analysis of stressed coral holobionts. Environmental Microbiology, 2009, 11, 2148-2163.	3.8	551
71	Gene-centric metagenomics of the fiber-adherent bovine rumen microbiome reveals forage specific glycoside hydrolases. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 1948-1953.	7.1	669
72	Functional metagenomic profiling of nine biomes. Nature, 2008, 452, 629-632.	27.8	842

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73	Dissecting microbial employment. Nature Biotechnology, 2008, 26, 997-998.	17.5	3
74	Baselines and Degradation of Coral Reefs in the Northern Line Islands. PLoS ONE, 2008, 3, e1548.	2.5	711
75	Microbial Ecology of Four Coral Atolls in the Northern Line Islands. PLoS ONE, 2008, 3, e1584.	2.5	383
76	Comparative Metagenomics Reveals Host Specific Metavirulomes and Horizontal Gene Transfer Elements in the Chicken Cecum Microbiome. PLoS ONE, 2008, 3, e2945.	2.5	247
77	Marine Environmental Genomics: Unlocking the Ocean's Secrets. Oceanography, 2007, 20, 56-61.	1.0	7
78	Assessing Coral Reef Condition: Eliciting Community Meanings. Society and Natural Resources, 2006, 19, 239-258.	1.9	14
79	Coral Disease on the Great Barrier Reef. , 2004, , 69-104.		269
80	Assessing Anchor Damage on Coral Reefs: A Case Study in Selection of Environmental Indicators. Environmental Management, 2004, 33, 126-139.	2.7	67