

Suhelen Egan

List of Publications by Year in descending order

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Version: 2024-02-01

76
papers

5,278
citations

126907

33
h-index

88630

70
g-index

78
all docs

78
docs citations

78
times ranked

5893
citing authors

#	ARTICLE	IF	CITATIONS
1	Differential priority effects impact taxonomy and functionality of host-associated microbiomes. <i>Molecular Ecology</i> , 2023, 32, 6278-6293.	3.9	6
2	Bacterial controlled mitigation of dysbiosis in a seaweed disease. <i>ISME Journal</i> , 2022, 16, 378-387.	9.8	21
3	Cross-Host Protection of Marine Bacteria Against Macroalgal Disease. <i>Microbial Ecology</i> , 2022, 84, 1288-1293.	2.8	9
4	Pathogen exposure leads to a transcriptional downregulation of core cellular functions that may dampen the immune response in a macroalga. <i>Molecular Ecology</i> , 2022, 31, 3468-3480.	3.9	3
5	Epimicrobiome Shifts With Bleaching Disease Progression in the Brown Seaweed <i>Saccharina japonica</i> . <i>Frontiers in Marine Science</i> , 2022, 9, .	2.5	8
6	Opportunistic diseases in marine eukaryotes: Could Bacteroidota be the next threat to ocean life?. <i>Environmental Microbiology</i> , 2022, 24, 4505-4518.	3.8	18
7	Opportunities for microbiome research to enhance farmed freshwater fish quality and production. <i>Reviews in Aquaculture</i> , 2021, 13, 2027-2037.	9.0	11
8	Genomic Evolution of the Marine Bacterium <i>Phaeobacter inhibens</i> during Biofilm Growth. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0076921.	3.1	3
9	Novel Nematode-Killing Protein-1 (Nkp-1) from a Marine Epiphytic Bacterium <i>Pseudoalteromonas tunicata</i> . <i>Biomedicines</i> , 2021, 9, 1586.	3.2	2
10	Age, gut location and diet impact the gut microbiome of a tropical herbivorous surgeonfish. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	2.7	18
11	Novel multifunctional iron chelators of the aroyl nicotinoyl hydrazone class that markedly enhance cellular NAD ⁺ /NADH ratios. <i>British Journal of Pharmacology</i> , 2020, 177, 1967-1987.	5.4	7
12	Slr4, a newly identified S-layer protein from marine Gammaproteobacteria, is a major biofilm matrix component. <i>Molecular Microbiology</i> , 2020, 114, 979-990.	2.5	4
13	Diet type influences the gut microbiome and nutrient assimilation of Genetically Improved Farmed Tilapia (<i>Oreochromis niloticus</i>). <i>PLoS ONE</i> , 2020, 15, e0237775.	2.5	32
14	Combating Parasitic Nematode Infections, Newly Discovered Antinematode Compounds from Marine Epiphytic Bacteria. <i>Microorganisms</i> , 2020, 8, 1963.	3.6	10
15	Opportunities and Challenges to Microbial Symbiosis Research in the Microbiome Era. <i>Frontiers in Microbiology</i> , 2020, 11, 1150.	3.5	5
16	Diversity of the epiphytic bacterial communities associated with commercially cultivated healthy and diseased <i>Saccharina japonica</i> during the harvest season. <i>Journal of Applied Phycology</i> , 2020, 32, 2071-2080.	2.8	29
17	Revisiting Australian <i>Ectocarpus subulatus</i> (Phaeophyceae) From the Hopkins River: Distribution, Abiotic Environment, and Associated Microbiota. <i>Journal of Phycology</i> , 2020, 56, 719-729.	2.3	9
18	The effect of elevated pCO ₂ on cadmium resistance of a globally important diatom. <i>Journal of Hazardous Materials</i> , 2020, 396, 122749.	12.4	10

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19	Genome sequence of <i>Epibacterium ulvae</i> strain DSM 24752T, an indigoidine-producing, macroalga-associated member of the marine Roseobacter group. <i>Environmental Microbiomes</i> , 2019, 14, 4.	5.0	6
20	A horizon scan of priorities for coastal marine microbiome research. <i>Nature Ecology and Evolution</i> , 2019, 3, 1509-1520.	7.8	77
21	Tropodithietic acid induces oxidative stress response, cell envelope biogenesis and iron uptake in <i>Vibrio vulnificus</i> . <i>Environmental Microbiology Reports</i> , 2019, 11, 581-588.	2.4	12
22	Diversity and Distribution of Bacteria Producing Known Secondary Metabolites. <i>Microbial Ecology</i> , 2019, 78, 885-894.	2.8	4
23	<i>Phaeobacter inhibens</i> controls bacterial community assembly on a marine diatom. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	2.7	24
24	Comparative genome analysis provides novel insight into the interaction of <i>Aquimarina</i> sp. AD1, BL5 and AD10 with their macroalgal host. <i>Marine Genomics</i> , 2019, 46, 8-15.	1.1	33
25	Diet and diet-associated bacteria shape early microbiome development in Yellowtail Kingfish (<i>Seriola lalandi</i>). <i>Microbial Biotechnology</i> , 2019, 12, 275-288.	4.2	68
26	Impact of <i>Phaeobacter inhibens</i> on marine eukaryote-associated microbial communities. <i>Environmental Microbiology Reports</i> , 2019, 11, 401-413.	2.4	28
27	Transcriptional response of <i>Nautella italica</i> R11 towards its macroalgal host uncovers new mechanisms of host-pathogen interaction. <i>Molecular Ecology</i> , 2018, 27, 1820-1832.	3.9	9
28	Causes and Consequences of a Variant Strain of <i>Phaeobacter inhibens</i> With Reduced Competition. <i>Frontiers in Microbiology</i> , 2018, 9, 2601.	3.5	11
29	Rational Design of Single-Chain Polymeric Nanoparticles That Kill Planktonic and Biofilm Bacteria. <i>ACS Infectious Diseases</i> , 2017, 3, 237-248.	3.8	134
30	Microbial community function in the bleaching disease of the marine macroalgae <i>Delisea pulchra</i> . <i>Environmental Microbiology</i> , 2017, 19, 3012-3024.	3.8	42
31	Microbial Diversity and Symbiotic Interactions with Macroalgae. , 2017, , 493-546.		2
32	Exploring the Complexity of Macroalgal-Bacterial Interactions Through Interkingdom Signalling System. , 2017, , 301-315.		1
33	Exoproteome Analysis of the Seaweed Pathogen <i>Nautella italica</i> R11 Reveals Temperature-Dependent Regulation of RTX-Like Proteins. <i>Frontiers in Microbiology</i> , 2017, 8, 1203.	3.5	8
34	Microbiome patterns across the gastrointestinal tract of the rabbitfish <i>Siganus fuscescens</i> . <i>PeerJ</i> , 2017, 5, e3317.	2.0	60
35	Microbial Dysbiosis: Rethinking Disease in Marine Ecosystems. <i>Frontiers in Microbiology</i> , 2016, 7, 991.	3.5	212
36	Tiny Microbes with a Big Impact: The Role of Cyanobacteria and Their Metabolites in Shaping Our Future. <i>Marine Drugs</i> , 2016, 14, 97.	4.6	101

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37	Multiple opportunistic pathogens can cause a bleaching disease in the red seaweed <i>Delisea pulchra</i> . <i>Environmental Microbiology</i> , 2016, 18, 3962-3975.	3.8	113
38	Effect of interspecific competition on trait variation in <i>Pseudomonas fluorescens Pf0-1</i> biofilms. <i>Environmental Microbiology</i> , 2016, 18, 1635-1645.	3.8	11
39	<i>Caenorhabditis elegans</i> employs innate and learned aversion in response to bacterial toxic metabolites tambjamine and violacein. <i>Scientific Reports</i> , 2016, 6, 29284.	3.3	19
40	Editorial for: Microbial symbiosis of marine sessile hosts- diversity and function. <i>Frontiers in Microbiology</i> , 2015, 6, 585.	3.5	7
41	VarR controls colonization and virulence in the marine macroalgal pathogen <i>Nautella italica</i> R11. <i>Frontiers in Microbiology</i> , 2015, 6, 1130.	3.5	19
42	A glutathione peroxidase (GpoA) plays a role in the pathogenicity of <i>Nautella italica</i> strain R11 towards the red alga <i>Delisea pulchra</i> . <i>FEMS Microbiology Ecology</i> , 2015, 91, .	2.7	24
43	A comprehensive analysis of the microbial communities of healthy and diseased marine macroalgae and the detection of known and potential bacterial pathogens. <i>Frontiers in Microbiology</i> , 2015, 6, 146.	3.5	102
44	Bacterial pathogens, virulence mechanism and host defence in marine macroalgae. <i>Environmental Microbiology</i> , 2014, 16, 925-938.	3.8	114
45	Antinematode Activity of Violacein and the Role of the Insulin/IGF-1 Pathway in Controlling Violacein Sensitivity in <i>Caenorhabditis elegans</i> . <i>PLoS ONE</i> , 2014, 9, e109201.	2.5	37
46	An ortholog of the <i>Leptospira interrogans</i> lipoprotein LipL32 aids in the colonization of <i>Pseudoalteromonas tunicata</i> to host surfaces. <i>Frontiers in Microbiology</i> , 2014, 5, 323.	3.5	9
47	The seaweed holobiont: understanding seaweed-bacteria interactions. <i>FEMS Microbiology Reviews</i> , 2013, 37, 462-476.	8.6	560
48	<i>Epibacterium ulvae</i> gen. nov., sp. nov., epibiotic bacteria isolated from the surface of a marine alga. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2013, 63, 1589-1596.	1.7	25
49	Assessing the Effectiveness of Functional Genetic Screens for the Identification of Bioactive Metabolites. <i>Marine Drugs</i> , 2013, 11, 40-49.	4.6	16
50	Chemical Mediation of Ternary Interactions Between Marine Holobionts and Their Environment as Exemplified by the Red Alga <i>Delisea pulchra</i> . <i>Journal of Chemical Ecology</i> , 2012, 38, 442-450.	1.8	68
51	Identification of the Antibacterial Compound Produced by the Marine Epiphytic Bacterium <i>Pseudovibrio</i> sp. D323 and Related Sponge-Associated Bacteria. <i>Marine Drugs</i> , 2011, 9, 1391-1402.	4.6	82
52	Membrane proteins of <i>Pseudoalteromonas tunicata</i> during the transition from planktonic to extracellular matrix-adherent state. <i>Environmental Microbiology Reports</i> , 2011, 3, 405-413.	2.4	6
53	Functional genomic signatures of sponge bacteria reveal unique and shared features of symbiosis. <i>ISME Journal</i> , 2010, 4, 1557-1567.	9.8	278
54	Identification of Compounds with Bioactivity against the Nematode <i>Caenorhabditis elegans</i> by a Screen Based on the Functional Genomics of the Marine Bacterium <i>Pseudoalteromonas tunicata</i> D2. <i>Applied and Environmental Microbiology</i> , 2010, 76, 5710-5717.	3.1	46

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55	Development of Novel Drugs from Marine Surface Associated Microorganisms. <i>Marine Drugs</i> , 2010, 8, 438-459.	4.6	193
56	The genomic basis of trophic strategy in marine bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 15527-15533.	7.1	685
57	Phylogenetic screening of a bacterial, metagenomic library using homing endonuclease restriction and marker insertion. <i>Nucleic Acids Research</i> , 2009, 37, e144-e144.	14.5	16
58	Antimicrobial activity observed among cultured marine epiphytic bacteria reflects their potential as a source of new drugs. <i>FEMS Microbiology Ecology</i> , 2009, 69, 113-124.	2.7	113
59	Ecology of type II secretion in marine <i>γ</i> -proteobacteria. <i>Environmental Microbiology</i> , 2008, 10, 1101-1107.	3.8	36
60	Unlocking the diversity and biotechnological potential of marine surface associated microbial communities. <i>Current Opinion in Microbiology</i> , 2008, 11, 219-225.	5.1	183
61	Hydrogen Peroxide Linked to Lysine Oxidase Activity Facilitates Biofilm Differentiation and Dispersal in Several Gram-Negative Bacteria. <i>Journal of Bacteriology</i> , 2008, 190, 5493-5501.	2.2	119
62	LipL32 Is an Extracellular Matrix-Interacting Protein of <i>Leptospira</i> spp. and <i>Pseudoalteromonas tunicata</i> . <i>Infection and Immunity</i> , 2008, 76, 2063-2069.	2.2	121
63	Marine Biofilm Bacteria Evade Eukaryotic Predation by Targeted Chemical Defense. <i>PLoS ONE</i> , 2008, 3, e2744.	2.5	176
64	Analysis of the <i>Pseudoalteromonas tunicata</i> Genome Reveals Properties of a Surface-Associated Life Style in the Marine Environment. <i>PLoS ONE</i> , 2008, 3, e3252.	2.5	126
65	Profiling the Secretome of the Marine Bacterium <i>Pseudoalteromonas tunicata</i> Using Amine-Specific Isobaric Tagging (iTRAQ). <i>Journal of Proteome Research</i> , 2007, 6, 967-975.	3.7	44
66	The use of functional genomics for the identification of a gene cluster encoding for the biosynthesis of an antifungal tambjamine in the marine bacterium <i>Pseudoalteromonas tunicata</i> . <i>Environmental Microbiology</i> , 2007, 9, 814-818.	3.8	63
67	A mannose-sensitive haemagglutinin (MSHA)-like pilus promotes attachment of <i>Pseudoalteromonas tunicata</i> cells to the surface of the green alga <i>Ulva australis</i> . <i>Microbiology (United Kingdom)</i> , 2006, 152, 2875-2883.	1.8	31
68	Unravelling the role of the ToxR-like transcriptional regulator WmpR in the marine antifouling bacterium <i>Pseudoalteromonas tunicata</i> . <i>Microbiology (United Kingdom)</i> , 2006, 152, 1385-1394.	1.8	27
69	Isolation and Structure Elucidation of a Novel Yellow Pigment from the Marine Bacterium <i>Pseudoalteromonas tunicata</i> . <i>Molecules</i> , 2005, 10, 1286-1291.	3.8	95
70	Biofilm Development and Cell Death in the Marine Bacterium <i>Pseudoalteromonas tunicata</i> . <i>Applied and Environmental Microbiology</i> , 2004, 70, 3232-3238.	3.1	120
71	Identification and Characterization of a Putative Transcriptional Regulator Controlling the Expression of Fouling Inhibitors in <i>Pseudoalteromonas tunicata</i> . <i>Applied and Environmental Microbiology</i> , 2002, 68, 372-378.	3.1	55
72	Correlation between pigmentation and antifouling compounds produced by <i>Pseudoalteromonas tunicata</i> . <i>Environmental Microbiology</i> , 2002, 4, 433-442.	3.8	116

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73	Antifouling activities expressed by marine surface associated <i>Pseudoalteromonas</i> species. FEMS Microbiology Ecology, 2002, 41, 47-58.	2.7	124
74	Inhibition of algal spore germination by the marine bacterium <i>Pseudoalteromonas tunicata</i> . FEMS Microbiology Ecology, 2001, 35, 67-73.	2.7	113
75	Inhibition of algal spore germination by the marine bacterium <i>Pseudoalteromonas tunicata</i> . FEMS Microbiology Ecology, 2001, 35, 67-73.	2.7	4
76	Phylogenetic relationship and antifouling activity of bacterial epiphytes from the marine alga <i>Ulva lactuca</i> . Brief report. Environmental Microbiology, 2000, 2, 343-347.	3.8	137