

Damien Eveillard

List of Publications by Year in descending order

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Version: 2024-02-01

58
papers

2,799
citations

346980

22
h-index

232693

48
g-index

75
all docs

75
docs citations

75
times ranked

5224
citing authors

#	ARTICLE	IF	CITATIONS
1	Contribution of genome-scale metabolic modelling to niche theory. <i>Ecology Letters</i> , 2022, 25, 1352-1364.	3.0	11
2	Diversity and ecological footprint of Global Ocean RNA viruses. <i>Science</i> , 2022, 376, 1202-1208.	6.0	41
3	Priorities for ocean microbiome research. <i>Nature Microbiology</i> , 2022, 7, 937-947.	5.9	27
4	A community perspective on the concept of marine holobionts: current status, challenges, and future directions. <i>PeerJ</i> , 2021, 9, e10911.	0.9	44
5	Investigating the microbial ecology of coastal hotspots of marine nitrogen fixation in the western North Atlantic. <i>Scientific Reports</i> , 2021, 11, 5508.	1.6	4
6	Environmental vulnerability of the global ocean epipelagic plankton community interactome. <i>Science Advances</i> , 2021, 7, .	4.7	54
7	Decline in plankton diversity and carbon flux with reduced sea ice extent along the Western Antarctic Peninsula. <i>Nature Communications</i> , 2021, 12, 4948.	5.8	24
8	Compendium of 530 metagenome-assembled bacterial and archaeal genomes from the polar Arctic Ocean. <i>Nature Microbiology</i> , 2021, 6, 1561-1574.	5.9	57
9	Probabilistic modeling to estimate jellyfish ecophysiological properties and size distributions. <i>Scientific Reports</i> , 2020, 10, 6074.	1.6	9
10	Synergic Effects of Temperature and Irradiance on the Physiology of the Marine Synechococcus Strain WH7803. <i>Frontiers in Microbiology</i> , 2020, 11, 1707.	1.5	18
11	Evolutionary Mechanisms of Long-Term Genome Diversification Associated With Niche Partitioning in Marine Picocyanobacteria. <i>Frontiers in Microbiology</i> , 2020, 11, 567431.	1.5	37
12	Linking Spatial and Temporal Dynamic of Bacterioplankton Communities With Ecological Strategies Across a Coastal Frontal Area. <i>Frontiers in Marine Science</i> , 2020, 7, .	1.2	7
13	Tara Oceans: towards global ocean ecosystems biology. <i>Nature Reviews Microbiology</i> , 2020, 18, 428-445.	13.6	227
14	Uncovering the Core Microbiome and Distribution of Palmerolide in <i>Synocicum adareanum</i> Across the Anvers Island Archipelago, Antarctica. <i>Marine Drugs</i> , 2020, 18, 298.	2.2	12
15	Roadmap for naming uncultivated Archaea and Bacteria. <i>Nature Microbiology</i> , 2020, 5, 987-994.	5.9	115
16	Community-level Responses to Iron Availability in Open Ocean Plankton Ecosystems. <i>Global Biogeochemical Cycles</i> , 2019, 33, 391-419.	1.9	76
17	Probabilistic Modeling of Microbial Metabolic Networks for Integrating Partial Quantitative Knowledge Within the Nitrogen Cycle. <i>Frontiers in Microbiology</i> , 2019, 9, 3298.	1.5	0
18	Observational Needs Supporting Marine Ecosystems Modeling and Forecasting: From the Global Ocean to Regional and Coastal Systems. <i>Frontiers in Marine Science</i> , 2019, 6, .	1.2	32

#	ARTICLE	IF	CITATIONS
19	Modelling the complexity of plankton communities exploiting omics potential: From present challenges to an integrative pipeline. <i>Current Opinion in Systems Biology</i> , 2019, 13, 68-74.	1.3	27
20	Structure and co-occurrence patterns in microbial communities under acute environmental stress reveal ecological factors fostering resilience. <i>Scientific Reports</i> , 2018, 8, 5875.	1.6	123
21	Identification of transcription factors involved in the phenotype of a domesticated oleaginous microalgae strain of <i>Tisochrysis lutea</i> . <i>Algal Research</i> , 2018, 30, 59-72.	2.4	19
22	Gene Expression Analysis of <i>Zobellia galactanivorans</i> during the Degradation of Algal Polysaccharides Reveals both Substrate-Specific and Shared Transcriptome-Wide Responses. <i>Frontiers in Microbiology</i> , 2017, 8, 1808.	1.5	58
23	On the Power of Uncertainties in Microbial System Modeling: No Need To Hide Them Anymore. <i>MSystems</i> , 2017, 2, .	1.7	6
24	Meneco, a Topology-Based Gap-Filling Tool Applicable to Degraded Genome-Wide Metabolic Networks. <i>PLoS Computational Biology</i> , 2017, 13, e1005276.	1.5	77
25	A multi-objective constraint-based approach for modeling genome-scale microbial ecosystems. <i>PLoS ONE</i> , 2017, 12, e0171744.	1.1	47
26	Combining graph and flux-based structures to decipher phenotypic essential metabolites within metabolic networks. <i>PeerJ</i> , 2017, 5, e3860.	0.9	10
27	Putative bacterial interactions from metagenomic knowledge with an integrative systems ecology approach. <i>MicrobiologyOpen</i> , 2016, 5, 106-117.	1.2	16
28	Deciphering transcriptional regulations coordinating the response to environmental changes. <i>BMC Bioinformatics</i> , 2016, 17, 35.	1.2	2
29	Plankton networks driving carbon export in the oligotrophic ocean. <i>Nature</i> , 2016, 532, 465-470.	13.7	670
30	Beyond the Black Queen Hypothesis. <i>ISME Journal</i> , 2016, 10, 2085-2091.	4.4	105
31	REVIEW: Predictive ecology in a changing world. <i>Journal of Applied Ecology</i> , 2015, 52, 1293-1310.	1.9	237
32	Marine systems biology. <i>Frontiers in Genetics</i> , 2015, 6, 181.	1.1	1
33	Using hybrid automata modelling to study phenotypic plasticity and allocation strategies in the plant mycorrhizal mutualism. <i>Ecological Modelling</i> , 2015, 311, 11-19.	1.2	4
34	OPINION PAPER Evolutionary Constraint-Based Formulation Requires New Bi-level Solving Techniques. <i>Lecture Notes in Computer Science</i> , 2015, , 279-281.	1.0	0
35	A shift in the archaeal nitrifier community in response to natural and anthropogenic disturbances in the northern Gulf of Mexico. <i>Environmental Microbiology Reports</i> , 2014, 6, 106-112.	1.0	25
36	A metabolic approach to study algal-bacterial interactions in changing environments. <i>Molecular Ecology</i> , 2014, 23, 1656-1660.	2.0	52

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37	The genome-scale metabolic network of <i>Ectocarpus siliculosus</i> (EctoGEM): a resource to study brown algal physiology and beyond. <i>Plant Journal</i> , 2014, 80, 367-381.	2.8	39
38	Antagonistic interactions between heterotrophic bacteria as a potential regulator of community structure of hypersaline microbial mats. <i>FEMS Microbiology Ecology</i> , 2013, 83, 74-81.	1.3	20
39	Extending the Metabolic Network of <i>Ectocarpus Siliculosus</i> Using Answer Set Programming. <i>Lecture Notes in Computer Science</i> , 2013, , 245-256.	1.0	11
40	An ASP Application in Integrative Biology: Identification of Functional Gene Units. <i>Lecture Notes in Computer Science</i> , 2013, , 206-218.	1.0	0
41	Environmental factors determining ammonia-oxidizing organism distribution and diversity in marine environments. <i>Environmental Microbiology</i> , 2012, 14, 714-729.	1.8	146
42	Mathematical modeling of one-carbon metabolism in trisomy 21. <i>FASEB Journal</i> , 2012, 26, lb420.	0.2	0
43	SIPPER: A flexible method to integrate heterogeneous data into a metabolic network. , 2011, , .		2
44	Toward Systems Biology in Brown Algae to Explore Acclimation and Adaptation to the Shore Environment. <i>OMICS A Journal of Integrative Biology</i> , 2011, 15, 883-892.	1.0	15
45	Using logic programming for modeling the one-carbon metabolism network to study the impact of folate deficiency on methylation processes. <i>Molecular BioSystems</i> , 2011, 7, 2508.	2.9	10
46	Seasonal and annual reoccurrence in betaproteobacterial ammonia-oxidizing bacterial population structure. <i>Environmental Microbiology</i> , 2011, 13, 872-886.	1.8	39
47	Integrated analysis of the gene neighbouring impact on bacterial metabolic networks. <i>IET Systems Biology</i> , 2011, 5, 261-268.	0.8	5
48	Integrating Quantitative Knowledge into a Qualitative Gene Regulatory Network. <i>PLoS Computational Biology</i> , 2011, 7, e1002157.	1.5	8
49	Hybrid modeling of biological networks: mixing temporal and qualitative biological properties. <i>BMC Systems Biology</i> , 2010, 4, 79.	3.0	16
50	Targeting human Rad51 by specific DNA aptamers induces inhibition of homologous recombination. <i>Biochimie</i> , 2010, 92, 1832-1838.	1.3	14
51	Including Ordinary Differential Equations Based Constraints in the Standard CP Framework. <i>Lecture Notes in Computer Science</i> , 2010, , 221-235.	1.0	15
52	Homogeneous decomposition of protein interaction networks: refining the description of intra-modular interactions. <i>Bioinformatics</i> , 2009, 25, 926-932.	1.8	2
53	Time course gene expression in the one-carbon metabolism network using HepG2 cell line grown in folate-deficient medium. <i>Journal of Nutritional Biochemistry</i> , 2009, 20, 312-320.	1.9	16
54	Temporal constraints of a gene regulatory network: Refining a qualitative simulation. <i>BioSystems</i> , 2009, 98, 149-159.	0.9	16

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55	Comparing Bacterial Genomes by Searching Their Common Intervals. Lecture Notes in Computer Science, 2009, , 102-113.	1.0	1
56	Ammonia-oxidizing bacterial community composition in estuarine and oceanic environments assessed using a functional gene microarray. Environmental Microbiology, 2007, 9, 2522-2538.	1.8	72
57	Building and Analysing an Integrative Model of HIV-1 RNA Alternative Splicing. Lecture Notes in Computer Science, 2005, , 43-57.	1.0	1
58	A multi-scale constraint programming model of alternative splicing regulation. Theoretical Computer Science, 2004, 325, 3-24.	0.5	7