## **Christopher Dupont**

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Petrobactin, a siderophore produced by <i>Alteromonas</i> , mediates community iron acquisition in the global ocean. ISME Journal, 2022, 16, 358-369.	9.8	30
2	Biogeochemical profiling and taxonomic characterization of municipal landfill site by metagenomic sequencing. Bioresource Technology, 2022, 351, 126936.	9.6	13
3	A Silent Operon of Photorhabdus luminescens Encodes a Prodrug Mimic of GTP. MBio, 2022, 13, e0070022.	4.1	7
4	Genomic insights into waste valorized extracellular polymeric substances (EPS) produced by Bacillus sp. ISTL8. Environmental Research, 2021, 192, 110277.	7.5	20
5	Metabolic versatility of the nitrite-oxidizing bacterium <i>Nitrospira marina</i> and its proteomic response to oxygen-limited conditions. ISME Journal, 2021, 15, 1025-1039.	9.8	62
6	Development of an Ocean Protein Portal for Interactive Discovery and Education. Journal of Proteome Research, 2021, 20, 326-336.	3.7	9
7	Reference-guided metagenomics reveals genome-level evidence of potential microbial transmission from the ISS environment to an astronaut's microbiome. IScience, 2021, 24, 102114.	4.1	6
8	Predicting antimicrobial mechanism-of-action from transcriptomes: A generalizable explainable artificial intelligence approach. PLoS Computational Biology, 2021, 17, e1008857.	3.2	16
9	Coral microbiome manipulation elicits metabolic and genetic restructuring to mitigate heat stress and evade mortality. Science Advances, 2021, 7, .	10.3	114
10	Dinoflagellates alter their carbon and nutrient metabolic strategies across environmental gradients in the central Pacific Ocean. Nature Microbiology, 2021, 6, 173-186.	13.3	45
11	Interactions between fecal gut microbiome, enteric pathogens, and energy regulating hormones among acutely malnourished rural Gambian children. EBioMedicine, 2021, 73, 103644.	6.1	12
12	Global ecotypes in the ubiquitous marine clade SAR86. ISME Journal, 2020, 14, 178-188.	9.8	49
13	METATRYP v 2.0: Metaproteomic Least Common Ancestor Analysis for Taxonomic Inference Using Specialized Sequence Assemblies—Standalone Software and Web Servers for Marine Microorganisms and Coronaviruses. Journal of Proteome Research, 2020, 19, 4718-4729.	3.7	13
14	Revealing ocean-scale biochemical structure with a deep-diving vertical profiling autonomous vehicle. Science Robotics, 2020, 5, .	17.6	12
15	Bidirectional C and N transfer and a potential role for sulfur in an epiphytic diazotrophic mutualism. ISME Journal, 2020, 14, 3068-3078.	9.8	33
16	Abundant nitrite-oxidizing metalloenzymes in the mesopelagic zone of the tropical Pacific Ocean. Nature Geoscience, 2020, 13, 355-362.	12.9	41
17	A comparative metagenomic study reveals microbial diversity and their role in the biogeochemical cycling of Pangong lake. Science of the Total Environment, 2020, 731, 139074.	8.0	58
18	Applications of weighted association networks applied to compositional data in biology. Environmental Microbiology, 2020, 22, 3020-3038.	3.8	11

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19	Transcriptomic Study of Substrate-Specific Transport Mechanisms for Iron and Carbon in the Marine Copiotroph Alteromonas macleodii. MSystems, 2020, 5, .	3.8	19
20	Genomic and phenotypic characterization of Burkholderia isolates from the potable water system of the International Space Station. PLoS ONE, 2020, 15, e0227152.	2.5	11
21	Genetic tool development in marine protists: emerging model organisms for experimental cell biology. Nature Methods, 2020, 17, 481-494.	19.0	97
22	Mechanism-of-Action Classification of Antibiotics by Global Transcriptome Profiling. Antimicrobial Agents and Chemotherapy, 2020, 64, .	3.2	56
23	Microbiome disturbance and resilience dynamics of the upper respiratory tract during influenza A virus infection. Nature Communications, 2020, 11, 2537.	12.8	72
24	Genetic diversity of clinical and environmental Mucorales isolates obtained from an investigation of mucormycosis cases among solid organ transplant recipients. Microbial Genomics, 2020, 6, .	2.0	10
25	The Airplane Cabin Microbiome. Microbial Ecology, 2019, 77, 87-95.	2.8	19
26	Planktonic Marine Archaea. Annual Review of Marine Science, 2019, 11, 131-158.	11.6	129
27	Genomic Changes Associated with the Evolutionary Transitions of Nostoc to a Plant Symbiont. Molecular Biology and Evolution, 2018, 35, 1160-1175.	8.9	54
28	Supragingival Plaque Microbiome Ecology and Functional Potential in the Context of Health and Disease. MBio, 2018, 9, .	4.1	58
29	Taxon-specific aerosolization of bacteria and viruses in an experimental ocean-atmosphere mesocosm. Nature Communications, 2018, 9, 2017.	12.8	103
30	Tracking the rise of eukaryotes to ecological dominance with zinc isotopes. Geobiology, 2018, 16, 341-352.	2.4	65
31	Speciation and ecological success in dimly lit waters: horizontal gene transfer in a green sulfur bacteria bloom unveiled by metagenomic assembly. ISME Journal, 2017, 11, 201-211.	9.8	40
32	Evolutionary genomics of the cold-adapted diatom Fragilariopsis cylindrus. Nature, 2017, 541, 536-540.	27.8	332
33	Integrated Regulatory and Metabolic Networks of the Marine Diatom <i>Phaeodactylum tricornutum</i> Predict the Response to Rising CO <sub>2</sub> Levels. MSystems, 2017, 2, .	3.8	40
34	Thaumarchaeal ecotype distributions across the equatorial Pacific Ocean and their potential roles in nitrification and sinking flux attenuation. Limnology and Oceanography, 2017, 62, 1984-2003.	3.1	83
35	Host Genetic Control of the Oral Microbiome in Health and Disease. Cell Host and Microbe, 2017, 22, 269-278.e3.	11.0	165
36	Nitrate Reductase Knockout Uncouples Nitrate Transport from Nitrate Assimilation and Drives Repartitioning of Carbon Flux in a Model Pennate Diatom. Plant Cell, 2017, 29, 2047-2070.	6.6	102

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37	Feathermoss and epiphytic <i>Nostoc</i> cooperate differently: expanding the spectrum of plant–cyanobacteria symbiosis. ISME Journal, 2017, 11, 2821-2833.	9.8	69
38	Refinement of the Diatom Episome Maintenance Sequence and Improvement of Conjugation-Based DNA Delivery Methods. Frontiers in Bioengineering and Biotechnology, 2016, 4, 65.	4.1	74
39	Genome-Scale Model Reveals Metabolic Basis of Biomass Partitioning in a Model Diatom. PLoS ONE, 2016, 11, e0155038.	2.5	104
40	Trace Metal Acquisition by Marine Heterotrophic Bacterioplankton with Contrasting Trophic Strategies. Applied and Environmental Microbiology, 2016, 82, 1613-1624.	3.1	51
41	Pluses and minuses of ammonium and nitrate uptake and assimilation by phytoplankton and implications for productivity and community composition, with emphasis on nitrogen-enriched conditions. Limnology and Oceanography, 2016, 61, 165-197.	3.1	475
42	The physiology and genetics of CO2 concentrating mechanisms in model diatoms. Current Opinion in Plant Biology, 2016, 31, 51-57.	7.1	81
43	Trace elements at the intersection of marine biological and geochemical evolution. Earth-Science Reviews, 2016, 163, 323-348.	9.1	135
44	Global biogeography of <i>Prochlorococcus</i> genome diversity in the surface ocean. ISME Journal, 2016, 10, 1856-1865.	9.8	76
45	Using community metabolomics as a new approach to discriminate marine microbial particulate organic matter in the western English Channel. Progress in Oceanography, 2015, 137, 421-433.	3.2	27
46	Designer diatom episomes delivered by bacterial conjugation. Nature Communications, 2015, 6, 6925.	12.8	249
47	Genomic and proteomic characterization of " <i>Candidatus</i> Nitrosopelagicus brevis†An ammonia-oxidizing archaeon from the open ocean. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 1173-1178.	7.1	278
48	Genomes and gene expression across light and productivity gradients in eastern subtropical Pacific microbial communities. ISME Journal, 2015, 9, 1076-1092.	9.8	108
49	Inactivation of <i><scp>P</scp>haeodactylum tricornutum</i> urease gene using transcription activatorâ€like effector nucleaseâ€based targeted mutagenesis. Plant Biotechnology Journal, 2015, 13, 460-470.	8.3	128
50	Functional Tradeoffs Underpin Salinity-Driven Divergence in Microbial Community Composition. PLoS ONE, 2014, 9, e89549.	2.5	184
51	Bioavailability of zinc in marine systems through time. Nature Geoscience, 2013, 6, 125-128.	12.9	84
52	Candidate phylum TM6 genome recovered from a hospital sink biofilm provides genomic insights into this uncultivated phylum. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E2390-9.	7.1	192
53	Genomic insights to SAR86, an abundant and uncultivated marine bacterial lineage. ISME Journal, 2012, 6, 1186-1199.	9.8	511
54	Influence of cobalamin scarcity on diatom molecular physiology and identification of a cobalamin acquisition protein. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E1762-71.	7.1	104

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55	Copper toxicity and the origin of bacterial resistance—new insights and applications. Metallomics, 2011, 3, 1109.	2.4	297
56	Efficient de novo assembly of single-cell bacterial genomes from short-read data sets. Nature Biotechnology, 2011, 29, 915-921.	17.5	203
57	Evolution and metabolic significance of the urea cycle in photosynthetic diatoms. Nature, 2011, 473, 203-207.	27.8	453
58	Genomic and functional adaptation in surface ocean planktonic prokaryotes. Nature, 2010, 468, 60-66.	27.8	280
59	Targeted metagenomics and ecology of globally important uncultured eukaryotic phytoplankton. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 14679-14684.	7.1	257
60	Characterization of <i>Prochlorococcus</i> clades from iron-depleted oceanic regions. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 16184-16189.	7.1	183
61	Nickel utilization in phytoplankton assemblages from contrasting oceanic regimes. Deep-Sea Research Part I: Oceanographic Research Papers, 2010, 57, 553-566.	1.4	55
62	History of biological metal utilization inferred through phylogenomic analysis of protein structures. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 10567-10572.	7.1	264
63	Modern proteomes contain putative imprints of ancient shifts in trace metal geochemistry. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 17822-17827.	7.1	215
64	Dissection of Microbial Community Functions during a Cyanobacterial Bloom in the Baltic Sea via Metatranscriptomics. Frontiers in Marine Science, 0, 5, .	2.5	57