Thomas Mock

List of Publications by Year
in descending order

#	Article	IF	Citations
1	Diversity, prevalence, and expression of cyanase genes (<i>cynS</i>) in planktonic marine microorganisms. ISME Journal, 2022, 16, 602-605.	9.8	15
2	Diatoms and Their Microbiomes in Complex and Changing Polar Oceans. Frontiers in Microbiology, 2022, 13, 786764.	3.5	7
3	Metagenome-assembled genomes of phytoplankton microbiomes from the Arctic and Atlantic Oceans. Microbiome, 2022, 10, 67.	11.1	17
4	Genome evolution of a nonparasitic secondary heterotroph, the diatom <i>Nitzschia putrida</i>. Science Advances, 2022, 8, eabi5075.	10.3	9
5	The role of zinc in the adaptive evolution of polar phytoplankton. Nature Ecology and Evolution, 2022, 6, 965-978.	7.8	14
6	A genomic catalog of Earthâ€™s microbiomes. Nature Biotechnology, 2021, 39, 499-509.	17.5	457
7	Integrative analysis of chloroplast DNA methylation in a marine algaâ€”Saccharina japonica. Plant Molecular Biology, 2021, 105, 611-623.	3.9	5
8	Healthy herds in the phytoplankton: the benefit of selective parasitism. ISME Journal, 2021, 15, 2163-2166.	9.8	14
9	Silicon drives the evolution of complex crystal morphology in calcifying algae. New Phytologist, 2021, 231, 1663-1666.	7.3	3
10	Mitotic recombination between homologous chromosomes drives genomic diversity in diatoms. Current Biology, 2021, 31, 3221-3232.e9.	3.9	29
11	Biochemical Characterization of a Novel Redox-Regulated Metacaspase in a Marine Diatom. Frontiers in Microbiology, 2021, 12, 688199.	3.5	13
12	The biogeographic differentiation of algal microbiomes in the upper ocean from pole to pole. Nature Communications, 2021, 12, 5483.	12.8	29
13	Singleâ€base methylome profiling of the giant kelp <i>Saccharina japonica</i> reveals significant differences in DNA methylation to microalgae and plants. New Phytologist, 2020, 225, 234-249.	7.3	38
14	Adaptive divergence across Southern Ocean gradients in the pelagic diatom <i>Fragilariopsis kerguelensis</i>. Molecular Ecology, 2020, 29, 4913-4924.	3.9	15
15	The Seminavis robusta genome provides insights into the evolutionary adaptations of benthic diatoms. Nature Communications, 2020, 11, 3320.	12.8	55
16	Evolutionary genomics can improve prediction of speciesâ€™ responses to climate change. Evolution Letters, 2020, 4, 4-18.	3.3	190
17	Genetic tool development in marine protists: emerging model organisms for experimental cell biology. Nature Methods, 2020, 17, 481-494.	19.0	97
18	Diatom Molecular Research Comes of Age: Model Species for Studying Phytoplankton Biology and Diversity. Plant Cell, 2020, 32, 547-572.	6.6	94

#	Article	IF	Citations
19	A novel tri-unsaturated highly branched isoprenoid (HBI) alkene from the marine diatom Navicula salinicola. Organic Geochemistry, 2020, 146, 104050.	1.8	1
20	Ocean acidification increases iodine accumulation in kelpâ€based coastal food webs. Global Change Biology, 2019, 25, 629-639.	9.5	26
21	Identifying metabolic pathways for production of extracellular polymeric substances by the diatom <i>Fragilariopsis cylindrus</i> inhabiting sea ice. ISME Journal, 2018, 12, 1237-1251.	9.8	43
22	Phycoremediation of municipal wastewater by microalgae to produce biofuel. International Journal of Phytoremediation, 2017, 19, 805-812.	3.1	39
23	Evolutionary genomics of the cold-adapted diatom Fragilariopsis cylindrus. Nature, 2017, 541, 536-540.	27.8	332
24	Finding a partner in the ocean: molecular and evolutionary bases of the response to sexual cues in a planktonic diatom. New Phytologist, 2017, 215, 140-156.	7.3	115
25	The Algal Revolution. Trends in Plant Science, 2017, 22, 726-738.	8.8	73
26	The effect of extrinsic mortality on genome size evolution in prokaryotes. ISME Journal, 2017, 11, 1011-1018.	9.8	16
27	Building a locally diploid genome and transcriptome of the diatom Fragilariopsis cylindrus. Scientific Data, 2017, 4, 170149.	5.3	14
28	Biotic interactions as drivers of algal origin and evolution. New Phytologist, 2017, 216, 670-681.	7.3	25
29	A role for the cell-wall protein silacidin in cell size of the diatom <i>Thalassiosira pseudonana</i>. ISME Journal, 2017, 11, 2452-2464.	9.8	15
30	Identification of Genes under Positive Selection Reveals Differences in Evolutionary Adaptation between Brown-Algal Species. Frontiers in Plant Science, 2017, 8, 1429.	3.6	17
31	Polar Microalgae: Functional Genomics, Physiology, and the Environment. , 2017, , 305-344.		4
32	Genome Editing in Diatoms Using CRISPR-Cas to Induce Precise Bi-allelic Deletions. Bio-protocol, 2017, 7, e2625.	0.4	11
33	Editing of the urease gene by CRISPR-Cas in the diatom Thalassiosira pseudonana. Plant Methods, 2016, 12, 49.	4.3	137
34	Bridging the gap between omics and earth system science to better understand how environmental change impacts marine microbes. Global Change Biology, 2016, 22, 61-75.	9.5	58
35	Characterization of the Small RNA Transcriptome of the Marine Coccolithophorid, Emiliania huxleyi. PLoS ONE, 2016, 11, e0154279.	2.5	12
36	Plastid proteome prediction for diatoms and other algae with secondary plastids of the red lineage. Plant Journal, 2015, 81, 519-528.	5.7	174

#	Article	IF	Citations
37	<i>In situ</i> expression of eukaryotic ice-binding proteins in microbial communities of Arctic and Antarctic sea ice. ISME Journal, 2015, 9, 2537-2540.	9.8	18
38	A Model of Genome Size Evolution for Prokaryotes in Stable and Fluctuating Environments. Genome Biology and Evolution, 2015, 7, 2344-2351.	2.5	55
39	Polar Microalgae: New Approaches towards Understanding Adaptations to an Extreme and Changing Environment. Biology, 2014, 3, 56-80.	2.8	94
40	Metatranscriptomes from diverse microbial communities: assessment of data reduction techniques for rigorous annotation. BMC Genomics, 2014, 15, 901.	2.8	11
41	Alternatives to vitamin B1 uptake revealed with discovery of riboswitches in multiple marine eukaryotic lineages. ISME Journal, 2014, 8, 2517-2529.	9.8	69
42	The Marine Microbial Eukaryote Transcriptome Sequencing Project (MMETSP): Illuminating the Functional Diversity of Eukaryotic Life in the Oceans through Transcriptome Sequencing. PLoS Biology, 2014, 12, e1001889.	5.6	885
43	The first evidence for genotypic stability in a cryopreserved transgenic diatom. Journal of Applied Phycology, 2014, 26, 65-71.	2.8	12
44	Global discovery and characterization of small non-coding RNAs in marine microalgae. BMC Genomics, 2014, 15, 697.	2.8	21
45	A novel cost effective and high-throughput isolation and identification method for marine microalgae. Plant Methods, 2014, 10, 26.	4.3	11
46	The impact of temperature on marine phytoplankton resource allocation and metabolism. Nature Climate Change, 2013, 3, 979-984.	18.8	358
47	Algal genomes reveal evolutionary mosaicism and the fate of nucleomorphs. Nature, 2012, 492, 59-65.	27.8	377
48	The Response of Diatom Central Carbon Metabolism to Nitrogen Starvation Is Different from That of Green Algae and Higher Plants Â. Plant Physiology, 2012, 158, 299-312.	4.8	318
49	Genomics and Genetics ofÂDiatoms. Advances in Botanical Research, 2012, 64, 245-284.	1.1	15
50	Frustule-related gene transcription and the influence of diatom community composition on silica precipitation in an iron-limited environment. Limnology and Oceanography, 2012, 57, 1619-1633.	3.1	37
51	What can we learn from genomics approaches in marine ecology? From sequences to ecoâ€systems biology!. Marine Ecology, 2012, 33, 131-148.	1.1	11
52	Antifreeze proteins in polar sea ice diatoms: diversity and gene expression in the genus <i>Fragilariopsis</i>. Environmental Microbiology, 2010, 12, 1041-1052.	3.8	81
53	Digital expression profiling of novel diatom transcripts provides insight into their biological functions. Genome Biology, 2010, 11, R85.	9.6	97
54	Chitin in Diatoms and Its Association with the Cell Wall. Eukaryotic Cell, 2009, 8, 1038-1050.	3.4	155

#	Article	IF	Citations
55	Update of the Diatom EST Database: a new tool for digital transcriptomics. Nucleic Acids Research, 2009, 37, D1001-D1005.	14.5	69
56	Green Evolution and Dynamic Adaptations Revealed by Genomes of the Marine Picoeukaryotes <i>Micromonas</i>. Science, 2009, 324, 268-272.	12.6	591
57	The Phaeodactylum genome reveals the evolutionary history of diatom genomes. Nature, 2008, 456, 239-244.	27.8	1,458
58	A Model for Carbohydrate Metabolism in the Diatom Phaeodactylum tricornutum Deduced from Comparative Whole Genome Analysis. PLoS ONE, 2008, 3, e1426.	2.5	394
59	Genomic Insights into Marine Microalgae. Annual Review of Genetics, 2008, 42, 619-645.	7.6	145
60	Microalgae in Polar Regions: Linking Functional Genomics and Physiology with Environmental Conditions. , 2008, , 285-312.		10
61	A new class of ice-binding proteins discovered in a salt-stress-induced cDNA library of the psychrophilic diatom<i>Fragilariopsis cylindrus</i>(Bacillariophyceae). European Journal of Phycology, 2008, 43, 423-433.	2.0	56
62	Whole-genome expression profiling of the marine diatom <i>Thalassiosira pseudonana</i> identifies genes involved in silicon bioprocesses. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 1579-1584.	7.1	247
63	Psychrophilic Diatoms. Cellular Origin and Life in Extreme Habitats, 2007, , 343-364.	0.3	10
64	ANALYSIS OF EXPRESSED SEQUENCE TAGS (ESTS) FROM THE POLAR DIATOM FRAGILARIOPSIS CYLINDRUS1. Journal of Phycology, 2006, 42, 78-85.	2.3	46
65	ICE-BINDING PROTEINS FROM SEA ICE DIATOMS (BACILLARIOPHYCEAE)1. Journal of Phycology, 2006, 42, 410-416.	2.3	179
66	Recent advances in sea-ice microbiology. Environmental Microbiology, 2005, 7, 605-619.	3.8	132
67	Long-Term Temperature Acclimation of Photosynthesis in Steady-State Cultures of the Polar Diatom Fragilariopsis cylindrus. Photosynthesis Research, 2005, 85, 307-317.	2.9	98
68	PHOTOSYNTHESIS AND COLD ACCLIMATION: MOLECULAR EVIDENCE FROM A POLAR DIATOM1. Journal of Phycology, 2004, 40, 732-741.	2.3	102
69	A new microcosm to investigate oxygen dynamics at the sea ice water interface. Aquatic Microbial Ecology, 2003, 30, 197-205.	1.8	22
70	Micro-optodes in sea ice: a new approach to investigate oxygen dynamics during sea ice formation. Aquatic Microbial Ecology, 2002, 29, 297-306.	1.8	43
71	Photosynthetic energy conversion under extreme conditionsâ€”II: the significance of lipids under light limited growth in Antarctic sea ice diatoms. Phytochemistry, 2002, 61, 53-60.	2.9	102
72	Photosynthetic energy conversion under extreme conditionsâ€”I: important role of lipids as structural modulators and energy sink under N-limited growth in Antarctic sea ice diatoms. Phytochemistry, 2002, 61, 41-51.	2.9	121

#	Article	IF	Citations
73	In situ primary production in young Antarctic sea ice. Hydrobiologia, 2002, 470, 127-132.	2.0	30
74	A mesocosm study of physical-biological interactions in artificial sea ice: effects of brine channel surface evolution and brine movement on algal biomass. Polar Biology, 2001, 24, 356-364.	1.2	45
75	Changes in photosynthetic carbon allocation in algal assemblages of Arctic sea ice with decreasing nutrient concentrations and irradiance. Marine Ecology - Progress Series, 2000, 202, 1-11.	1.9	42
76	Determination of Arctic ice algal production with a new in situ incubation technique. Marine Ecology - Progress Series, 1999, 177, 15-26.	1.9	100
77	Bacteria in sea ice and underlying brackish water at 54Â°26'5"N (Baltic Sea, Kiel Bight). Marine Ecology - Progress Series, 1997, 158, 23-40.	1.9	32